

130045

STIC-Biotech/ChemLib

From: Duffy, Patricia
Sent: Monday, August 16, 2004 5:49 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search 10/063546

Importance: High

CREF

In re:

10/063,546

Please search SEQ ID NO:38 and oligomers thereof.

Please include both a commercial and interference database search.

Please print out top ~~100~~ hits in each category.

70 scores

Thank you,

Patricia A. Duffy, Ph.D.

Art Unit 1645, Remsen 3B05

571-272-0855

STAFF USE ONLY

Searcher: SHAY
Searcher Phone: 2-
Date Searcher Picked up: 8/16/04
Date Completed: 8/16/04
Searcher Prep/Rev. Time:
Online Time:

Type of Search

NA Sequence: #
AA Sequence: #
Structure: #
Bibliographic:
Litigation:
Patent Family:
Other:

Vendors and cost where applicable

STN:
DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM: MS?
WWW/Internet:
Other(Specify):

Duffy, Patricia

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PRO 1344

Abs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:25:34 ; Search time 63 Seconds

(without alignments)
3229.114 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 720
Sequence: 1 MELGCWQTQLGTRFLQLLLIS.....LSTFTKVLKLPFKMIERNMK 720Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 700 summaries

Database : A Geneseq_29Jan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	720	100.0	720	3	AAV66695
2	720	100.0	720	4	AAU29108
3	720	100.0	720	4	AAU29108
4	720	100.0	720	4	AAU29108
5	720	100.0	720	4	AAU29108
6	720	100.0	720	4	AAU29108
7	720	100.0	720	4	AAU29108
8	720	100.0	720	4	AAU29108
9	720	100.0	720	4	AAU29108
10	720	100.0	720	4	AAU29108
11	720	100.0	720	4	AAU29108
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25	720	100.0	720	4	AAU29108

26	720	100.0	720	6	ABU85662	ABU85662	Human	PRO
27	720	100.0	720	6	ABU98822	ABU98822	Novel	hum
28	720	100.0	720	6	ABU98037	ABU98037	Novel	hum
29	720	100.0	720	6	ABU91743	ABU91743	Novel	hum
30	720	100.0	720	6	ABU89436	ABU89436	Human	PRO
31	720	100.0	720	6	ABU86277	ABU86277	Human	sec
32	720	100.0	720	6	ABU67490	ABU67490	Human	sec
33	720	100.0	720	6	ABU80518	ABU80518	Human	PRO
34	720	100.0	720	6	ABU72509	ABU72509	Novel	hum
35	720	100.0	720	6	ABU90894	ABU90894	Novel	hum
36	720	100.0	720	6	ABO33953	ABO33953	Human	sec
37	720	100.0	720	6	ABR99436	ABR99436	Human	sec
38	720	100.0	720	6	ABR98826	ABR98826	Human	sec
39	720	100.0	720	6	ABO16349	ABO16349	Human	sec
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42	720	100.0	720	6	ABR78311	ABR78311	Human	sec
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44	720	100.0	720	6	ABU85047	ABU85047	Novel	hum
45	720	100.0	720	6	ABO00186	ABO00186	Human	sec
46	720	100.0	720	6	ABO11518	ABO11518	Human	sec
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48	720	100.0	720	6	ABU88737	ABU88737	Novel	hum
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52	720	100.0	720	6	ABO09331	ABO09331	Human	sec
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54	720	100.0	720	6	ABO11213	ABO11213	Human	sec
55	720	100.0	720	6	ABR66831	ABR66831	Human	sec
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63	720	100.0	720	6	ABO15739	ABO15739	Human	sec
64	720	100.0	720	6	ABU56020	ABU56020	Human	sec
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67	720	100.0	720	6	ABU95293	ABU95293	Novel	hum
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69	720	100.0	720	6	ABO07806	ABO07806	Human	PRO
70	720	100.0	720	6	ABR70047	ABR70047	Human	sec
71	720	100.0	720	6	ABR69380	ABR69380	Human	sec
72	720	100.0	720	6	ABO01521	ABO01521	Human	PRO
73	720	100.0	720	6	ABR61323	ABR61323	Human	PRO
74	720	100.0	720	6	ABU90978	ABU90978	Human	PRO
75	720	100.0	720	6	ABR67855	ABR67855	Human	sec
76	720	100.0	720	6	ABR65243	ABR65243	Human	sec
77	720	100.0	720	6	ABR68465	ABR68465	Human	sec
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81	720	100.0	720	6	ABU83127	ABU83127	Human	sec
82	720	100.0	720	6	ABU98047	ABU98047	Human	sec
83	720	100.0	720	6	ABU94983	ABU94983	Novel	hum
84	720	100.0	720	6	ABU90531	ABU90531	Novel	hum
85	720	100.0	720	6	ABU84042	ABU84042	Human	sec
86	720	100.0	720	6	ABU93693	ABU93693	Novel	hum
87	720	100.0	720	6	ABO25955	ABO25955	Human	PRO
88	720	100.0	720	6	ABR64938	ABR64938	Human	sec
89	720	100.0	720	6	ABO27299	ABO27299	Human	sec
90	720	100.0	720	6	ABR68770	ABR68770	Human	sec
91	720	100.0	720	6	ABO06586	ABO06586	Human	sec
92	720	100.0	720	6	ABR99131	ABR99131	Human	sec
93	720	100.0	720	6	ABU57015	ABU57015	Human	PRO
94	720	100.0	720	6	ABU85967	ABU85967	Novel	hum
95	720	100.0	720	6	ABU82354	ABU82354	Novel	hum
96	720	100.0	720	6	ABU87265	ABU87265	Human	PRO
97	720	100.0	720	6	ABU83737	ABU83737	Human	sec
98	720	100.0	720	6	ABU83737	ABU83737	Human	sec

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101	720	100.0	720	6	ABU81822	AbU81822 Novel hum	174	720	100.0	720	6	ABR94394	AbR94394 Human sec
102	720	100.0	720	6	ABU65986	AbU65986 Novel hum	175	720	100.0	720	6	ABR95299	AbR95299 Human sec
103	720	100.0	720	6	ABU81164	AbU81164 Human sec	176	720	100.0	720	6	ADB17095	ADb17095 Human tra
104	720	100.0	720	6	ABR59815	AbR59815 Human sec	177	720	100.0	720	6	ABO21537	ABO21537 Human sec
105	720	100.0	720	6	ABU94003	AbU94003 Novel hum	178	720	100.0	720	6	ABR97801	AbR97801 Human sec
106	720	100.0	720	6	ABU99856	AbU99856 Novel hum	179	720	100.0	720	6	ABR87589	AbR87589 Human sec
107	720	100.0	720	6	ABR66526	AbR66526 Human sec	180	720	100.0	720	6	ABM77630	AbM77630 Human sec
108	720	100.0	720	6	ABR90944	AbR90944 Human sec	181	720	100.0	720	6	ABM27860	AbM27860 Human sec
109	720	100.0	720	6	ABO53279	ABO53279 Novel hum	182	720	100.0	720	6	ABM06141	ABM06141 Human sec
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111	720	100.0	720	6	ABU94371	AbU94371 Human PRO	184	720	100.0	720	6	ABM35098	ABM35098 Human sec
112	720	100.0	720	6	ABU79253	AbU79253 Human PRO	185	720	100.0	720	6	ABM26335	ABM26335 Human sec
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115	720	100.0	720	6	ABU94676	AbU94676 Human PRO	188	720	100.0	720	6	ABO24620	ABO24620 Human sec
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118	720	100.0	720	6	ABU92342	AbU92342 Novel hum	191	720	100.0	720	6	ABM02732	ABM02732 Human sec
119	720	100.0	720	6	ABU98517	AbU98517 Human PRO	192	720	100.0	720	6	ABM16028	ABM16028 Human sec
120	720	100.0	720	6	ABR65916	AbR65916 Human sec	193	720	100.0	720	6	ABO27589	ABO27589 Human sec
121	720	100.0	720	6	ABR64633	AbR64633 Human sec	194	720	100.0	720	6	ABM29080	ABM29080 Human sec
122	720	100.0	720	6	ABU59407	AbU59407 Novel hum	195	720	100.0	720	6	ABM07056	ABM07056 Human sec
123	720	100.0	720	6	ABU79558	AbU79558 Human PRO	196	720	100.0	720	6	ABM21150	ABM21150 Human sec
124	720	100.0	720	6	ABU92949	AbU92949 Human PRO	197	720	100.0	720	6	ABM09496	ABM09496 Human sec
125	720	100.0	720	6	ABU95908	AbU95908 Human PRO	198	720	100.0	720	6	ABO41366	ABO41366 Human sec
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127	720	100.0	720	6	ABU90221	AbU90221 Novel hum	200	720	100.0	720	6	ABO43710	ABO43710 Human PRO
128	720	100.0	720	6	ABO09636	ABO09636 Human sec	201	720	100.0	720	6	ABM76410	ABM76410 Human sec
129	720	100.0	720	6	ABO10908	ABO10908 Human sec	202	720	100.0	720	6	ABM25725	ABM25725 Human sec
130	720	100.0	720	6	ABR70962	AbR70962 Human sec	203	720	100.0	720	6	ABM25725	ABM25725 Human sec
131	720	100.0	720	6	ABU98281	AbU98281 Novel hum	204	720	100.0	720	6	ABM26030	ABM26030 Human sec
132	720	100.0	720	6	ABU87570	AbU87570 Human PRO	205	720	100.0	720	6	ADA21428	ADa21428 Human sec
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134	720	100.0	720	6	ABU89286	AbU89286 Novel hum	207	720	100.0	720	6	ABO02468	ABO02468 Human sec
135	720	100.0	720	6	ABU84652	AbU84652 Human sec	208	720	100.0	720	6	ABO44257	ABO44257 Human sec
136	720	100.0	720	6	ABR69742	AbR69742 Human sec	209	720	100.0	720	6	ABR90639	ABR90639 Human sec
137	720	100.0	720	6	ABU80119	AbU80119 Human PRO	210	720	100.0	720	6	ABR73707	ABR73707 Human sec
138	720	100.0	720	6	ABU82493	AbU82493 Novel hum	211	720	100.0	720	6	ABO16959	ABO16959 Human sec
139	720	100.0	720	6	ABU92173	AbU92173 Novel hum	212	720	100.0	720	6	ABR94384	ABR94384 Human sec
140	720	100.0	720	6	ABU93388	AbU93388 Human PRO	213	720	100.0	720	6	ABR75891	ABR75891 Human sec
141	720	100.0	720	6	ABO09941	ABO09941 Human sec	214	720	100.0	720	6	ABR71267	ABR71267 Human sec
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144	720	100.0	720	6	ABU10879	AbU10879 Human PRO	217	720	100.0	720	6	ADA10215	ADa10215 Human sec
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147	720	100.0	720	6	ABU72127	AbU72127 Human PRO	220	720	100.0	720	6	ABO30029	ABO30029 Human sec
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153	720	100.0	720	6	ABU88570	AbU88570 Human sec	226	720	100.0	720	6	ABO39536	ABO39536 Human sec
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158	720	100.0	720	6	ABR80901	AbR80901 Human sec	231	720	100.0	720	6	ADA19900	ADa19900 Novel hum
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160	720	100.0	720	6	ABM00902	ABM00902 Human sec	233	720	100.0	720	6	ADB17283	ADb17283 Human tra
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162	720	100.0	720	6	ABM77325	ABM77325 Human sec	235	720	100.0	720	6	ABR97191	ABR97191 Human sec
163	720	100.0	720	6	ABO28809	ABO28809 Human sec	236	720	100.0	720	6	ABR86979	ABR86979 Human sec
164	720	100.0	720	6	ABO31554	ABO31554 Human sec	237	720	100.0	720	6	ABM11021	ABM11021 Human sec
165	720	100.0	720	6	ABM07971	ABM07971 Human sec	238	720	100.0	720	6	ABR82816	ABR82816 Human sec
166	720	100.0	720	6	ABO40451	ABO40451 Human sec	239	720	100.0	720	6	ABO32164	ABO32164 Human sec
167	720	100.0	720	6	ABO35876	ABO35876 Human PRO	240	720	100.0	720	6	ABM15291	ABM15291 Human sec
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AbM17248	Human	sec
AbR94394	Human	sec
AbR95299	Human	sec
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ABR87589	Human	sec
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ABM35098	Human	sec
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ABO24620	Human	sec
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ABM11631	Human	sec
ABM02732	Human	sec
ABM16028	Human	sec
ABO27589	Human	sec
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ABR93164	Human	sec
ABR93469	Human	sec
ADA10215	Human	sec
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ABO27894	Human	sec
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ABO35571	Human	PRO
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ABM10411	Human	sec
ABM11936	Human	sec
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ABO52387	Human	PRO
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ABO23705	Human	sec
ADB17283	Human	tra
ADA17759	Human	PRO
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ABR86979	Human	sec
ABM11021	Human	sec
ABR82816	Human	sec
ABO32164	Human	sec
ABM15291	Human	sec
ABM06446	Human	sec
ABM04257	Human	sec
ABM22370	Human	sec
ABM07666	Human	sec

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247	720	100.0	720	6	ABM33166	ABM33166 Human sec	320	720	100.0	720	6	ABO35266	ABO35266 Human PRO
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249	720	100.0	720	6	ABO50252	ABO50252 Human sec	322	720	100.0	720	6	ABO47507	ABO47507 Human sec
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251	720	100.0	720	6	ABO04298	ABO04298 Human sec	324	720	100.0	720	6	ABO48422	ABO48422 Human sec
252	720	100.0	720	6	ABO05928	ABO05928 Human sec	325	720	100.0	720	6	ABO51472	ABO51472 Human PRO
253	720	100.0	720	6	ABM18468	ABM18468 Human sec	326	720	100.0	720	6	ABO51777	ABO51777 Human PRO
254	720	100.0	720	6	ADA27867	ADA27867 Human sec	327	720	100.0	720	6	ABO50557	ABO50557 Human sec
255	720	100.0	720	6	ABR97496	ABR97496 Human sec	328	720	100.0	720	6	ABR79681	ABR79681 Human sec
256	720	100.0	720	6	ABR80596	ABR80596 Human sec	329	720	100.0	720	6	ABM16943	ABM16943 Human sec
257	720	100.0	720	6	ABM01207	ABM01207 Human sec	330	720	100.0	720	6	ABO17975	ABO17975 Human sec
258	720	100.0	720	6	ABR88809	ABR88809 Human sec	331	720	100.0	720	6	ABO20927	ABO20927 Human sec
259	720	100.0	720	6	ABM13461	ABM13461 Human sec	332	720	100.0	720	6	ABR96886	ABR96886 Human sec
260	720	100.0	720	6	ABM20845	ABM20845 Human sec	333	720	100.0	720	6	ADA38672	ADA38672 Human sec
261	720	100.0	720	6	ABO41976	ABO41976 Human sec	334	720	100.0	720	6	ABM12241	ABM12241 Human sec
262	720	100.0	720	6	ABO42586	ABO42586 Human sec	335	720	100.0	720	6	ABM16333	ABM16333 Human sec
263	720	100.0	720	6	ABM10106	ABM10106 Human sec	336	720	100.0	720	6	ABM24200	ABM24200 Human sec
264	720	100.0	720	6	ABO38621	ABO38621 Human sec	337	720	100.0	720	6	ABM14681	ABM14681 Human sec
265	720	100.0	720	6	ABM32861	ABM32861 Human sec	338	720	100.0	720	6	ABM04562	ABM04562 Human sec
266	720	100.0	720	6	ABM2875	ABM2875 Human sec	339	720	100.0	720	6	ABM06751	ABM06751 Human sec
267	720	100.0	720	6	ABM74886	ABM74886 Human sec	340	720	100.0	720	6	ABM09191	ABM09191 Human sec
268	720	100.0	720	6	ADA79714	ADA79714 Human sec	341	720	100.0	720	6	ABO39231	ABO39231 Human sec
269	720	100.0	720	6	ABR96276	ABR96276 Human sec	342	720	100.0	720	6	ABM75496	ABM75496 Human sec
270	720	100.0	720	6	ABM02427	ABM02427 Human sec	343	720	100.0	720	6	ABM25420	ABM25420 Human sec
271	720	100.0	720	6	ABR86369	ABR86369 Human sec	344	720	100.0	720	6	ABM19930	ABM19930 Human sec
272	720	100.0	720	6	ABR86674	ABR86674 Human sec	345	720	100.0	720	6	ABO46836	ABO46836 Human PRO
273	720	100.0	720	6	ABM16638	ABM16638 Human sec	346	720	100.0	720	6	ABO47141	ABO47141 Human PRO
274	720	100.0	720	6	ABM29690	ABM29690 Human sec	347	720	100.0	720	6	ADAB8239	ADAB8239 Human sec
275	720	100.0	720	6	ABO29114	ABO29114 Human sec	348	720	100.0	720	6	ABR71572	ABR71572 Human sec
276	720	100.0	720	6	ABM23895	ABM23895 Human sec	349	720	100.0	720	6	ABR72182	ABR72182 Human sec
277	720	100.0	720	6	ABM23285	ABM23285 Human sec	350	720	100.0	720	6	ABR98521	ABR98521 Human sec
278	720	100.0	720	6	ABM22065	ABM22065 Human sec	351	720	100.0	720	6	ABO06891	ABO06891 Human sec
279	720	100.0	720	6	ABO37706	ABO37706 Human sec	352	720	100.0	720	6	ABR84844	ABR84844 Human sec
280	720	100.0	720	6	ABM28470	ABM28470 Human sec	353	720	100.0	720	6	ABR73402	ABR73402 Human sec
281	720	100.0	720	6	ABM28775	ABM28775 Human sec	354	720	100.0	720	6	ABR76496	ABR76496 Human sec
282	720	100.0	720	6	ABM66419	ABM66419 Human sec	355	720	100.0	720	6	ABR73097	ABR73097 Human sec
283	720	100.0	720	6	ABM75801	ABM75801 Human sec	356	720	100.0	720	6	ABM18163	ABM18163 Human sec
284	720	100.0	720	6	ABM34081	ABM34081 Human sec	357	720	100.0	720	6	ABO20622	ABO20622 Human PRO
285	720	100.0	720	6	ABM34386	ABM34386 Human sec	358	720	100.0	720	6	ABO25365	ABO25365 Human PRO
286	720	100.0	720	6	ABO20317	ABO20317 Human sec	359	720	100.0	720	6	ABO25670	ABO25670 Human PRO
287	720	100.0	720	6	ABO21232	ABO21232 Human sec	360	720	100.0	720	6	ABR94079	ABR94079 Human sec
288	720	100.0	720	6	ABO22147	ABO22147 Human sec	361	720	100.0	720	6	ADA92793	ADA92793 Human sec
289	720	100.0	720	6	ADA20072	ADA20072 Novel hum	362	720	100.0	720	6	ABR79986	ABR79986 Human sec
290	720	100.0	720	6	ABO34185	ABO34185 Human sec	363	720	100.0	720	6	ABM11326	ABM11326 Human sec
291	720	100.0	720	6	ABR96581	ABR96581 Human sec	364	720	100.0	720	6	ABO32933	ABO32933 Human PRO
292	720	100.0	720	6	ADA94447	ADA94447 Human sec	365	720	100.0	720	6	ABO30639	ABO30639 Human sec
293	720	100.0	720	6	ABR85759	ABR85759 Human sec	366	720	100.0	720	6	ABO30944	ABO30944 Human sec
294	720	100.0	720	6	ABR9741	ABR9741 Human sec	367	720	100.0	720	6	ABM27250	ABM27250 Human sec
295	720	100.0	720	6	ABM00597	ABM00597 Human sec	368	720	100.0	720	6	ABM29995	ABM29995 Human sec
296	720	100.0	720	6	ABM00292	ABM00292 Human sec	369	720	100.0	720	6	ABM05531	ABM05531 Human sec
297	720	100.0	720	6	ABO29724	ABO29724 Human sec	370	720	100.0	720	6	ABM15596	ABM15596 Human sec
298	720	100.0	720	6	ABM23590	ABM23590 Human sec	371	720	100.0	720	6	ABM05881	ABM05881 Human sec
299	720	100.0	720	6	ABO29385	ABO29385 Human sec	372	720	100.0	720	6	ABO42281	ABO42281 Human sec
300	720	100.0	720	6	ABO38316	ABO38316 Human sec	373	720	100.0	720	6	ABO38011	ABO38011 Human sec
301	720	100.0	720	6	ABO45616	ABO45616 Human PRO	374	720	100.0	720	6	ABO45921	ABO45921 Human PRO
302	720	100.0	720	6	ABM20540	ABM20540 Human sec	375	720	100.0	720	6	ABM66724	ABM66724 Human sec
303	720	100.0	720	6	ADA81441	ADA81441 Human sec	376	720	100.0	720	6	ADB20282	ADB20282 Human sec
304	720	100.0	720	6	ABO16654	ABO16654 Human sec	377	720	100.0	720	6	ABM19625	ABM19625 Human sec
305	720	100.0	720	6	ABO18280	ABO18280 Human sec	378	720	100.0	720	6	ABO49337	ABO49337 Human sec
306	720	100.0	720	6	ABO22707	ABO22707 Human PRO	379	720	100.0	720	6	ADA78534	ADA78534 Human sec
307	720	100.0	720	6	ABO23012	ABO23012 Human PRO	380	720	100.0	720	6	ABR88199	ABR88199 Human sec
308	720	100.0	720	6	ABR92554	ABR92554 Human sec	381	720	100.0	720	6	ADA00369	ADA00369 Human sec
309	720	100.0	720	6	ABR81511	ABR81511 Human sec	382	720	100.0	720	6	ABM25945	ABM25945 Human sec
310	720	100.0	720	6	ABM77935	ABM77935 Human sec	383	720	100.0	720	6	ABM03342	ABM03342 Human sec
311	720	100.0	720	6	ABR89724	ABR89724 Human sec	384	720	100.0	720	6	ABO39841	ABO39841 Human sec
312	720	100.0	720	6	ABM26640	ABM26640 Human sec	385	720	100.0	720	6	ABO49947	ABO49947 Human sec
313	720	100.0	720	6	ABM13766	ABM13766 Human sec	386	720	100.0	720	7	ABO50862	ABO50862 Human sec
314	720	100.0	720	6	ABO28504	ABO28504 Human sec	387	720	100.0	720	7	ABO05318	ABO05318 Human sec
315	720	100.0	720	6	ABO30334	ABO30334 Human sec	388	720	100.0	720	7	ABR74622	ABR74622 Human sec
316	720	100.0	720	6	ABM07351	ABM07351 Human sec	389	720	100.0	720	7	ABR77101	ABR77101 Human sec
317	720	100.0	720	6	ABM03952	ABM03952 Human sec	390	720	100.0	720	7		

391	720	100.0	720	7	ABM17858	Human	sec	464	720	100.0	720	7	ABM14986	Abm14986	Human	sec
392	720	100.0	720	7	ABR95909	Human	sec	465	720	100.0	720	7	ABO41061	AbO41061	Human	sec
393	720	100.0	720	7	ABO21842	Human	sec	466	720	100.0	720	7	ABO36791	AbO36791	Human	sec
394	720	100.0	720	7	ABO20012	Human	sec	467	720	100.0	720	7	ABO37401	AbO37401	Human	sec
395	720	100.0	720	7	ABO24315	Human	sec	468	720	100.0	720	7	ABM75191	AbM75191	Human	sec
396	720	100.0	720	7	ABR86064	Human	sec	469	720	100.0	720	7	ABM33471	AbM33471	Human	sec
397	720	100.0	720	7	ABM10716	Human	sec	470	720	100.0	720	7	ABO46526	AbO46526	Human	sec
398	720	100.0	720	7	ABM75715	Human	sec	471	720	100.0	720	7	ADA82605	AdA82605	Human	sec
399	720	100.0	720	7	ABR89419	Human	sec	472	720	100.0	720	7	ADA85611	AdA85611	Human	sec
400	720	100.0	720	7	ABM12546	Human	sec	473	720	100.0	720	7	ADB96239	AdB96239	Human	sec
401	720	100.0	720	7	ABM05836	Human	sec	474	720	100.0	720	7	ABM31825	AbM31825	Human	sec
402	720	100.0	720	7	ABO34961	Human	sec	475	720	100.0	720	7	ABM31215	AbM31215	Human	sec
403	720	100.0	720	7	ABM03037	Human	sec	476	720	100.0	720	7	ADB85913	AdB85913	Human	sec
404	720	100.0	720	7	ABM19015	Human	sec	477	720	100.0	720	7	ABM32130	AbM32130	Human	sec
405	720	100.0	720	7	ABM19320	Human	sec	478	720	100.0	720	7	ABM32435	AbM32435	Human	sec
406	720	100.0	720	7	ABO46531	Human	PRO	479	720	100.0	720	7	ADB68290	AdB68290	Human	PRO
407	720	100.0	720	7	ABO49032	Human	sec	480	720	100.0	720	7	ADB68097	AdB68097	Human	PRO
408	720	100.0	720	7	ABR69075	Human	sec	481	720	100.0	720	7	ABM31520	AbM31520	Human	sec
409	720	100.0	720	7	ABR89114	Human	sec	482	720	100.0	720	7	ABM30910	AbM30910	Human	sec
410	720	100.0	720	7	ABR72487	Human	sec	483	720	100.0	720	7	ADB90914	AdB90914	Human	sec
411	720	100.0	720	7	ABR74317	Human	sec	484	720	100.0	720	7	ADC57711	AdC57711	Human	PRO
412	720	100.0	720	7	ABO18585	Human	sec	485	720	100.0	720	7	ADC55075	AdC55075	Human	PRO
413	720	100.0	720	7	ABR80291	Human	sec	486	720	100.0	720	7	ADC11942	AdC11942	Human	sec
414	720	100.0	720	7	ABM01512	Human	sec	487	720	100.0	720	7	ADC06994	AdC06994	Human	PRO
415	720	100.0	720	7	ABM02122	Human	sec	488	720	100.0	720	7	ADC56364	AdC56364	Human	PRO
416	720	100.0	720	7	ABR87284	Human	sec	489	720	100.0	720	7	ADC17173	AdC17173	Human	PRO
417	720	100.0	720	7	ABM12851	Human	sec	490	720	100.0	720	7	ADC07419	AdC07419	Human	sec
418	720	100.0	720	7	ABM3605	Human	sec	491	720	100.0	720	7	ADC11409	AdC11409	Human	sec
419	720	100.0	720	7	ABM24505	Human	sec	492	720	100.0	720	7	ADC14871	AdC14871	Human	sec
420	720	100.0	720	7	ABO29419	Human	sec	493	720	100.0	720	7	ADC52366	AdC52366	Human	sec
421	720	100.0	720	7	ABO31249	Human	sec	494	720	100.0	720	7	ADC14531	AdC14531	Human	sec
422	720	100.0	720	7	ABM14376	Human	sec	495	720	100.0	720	7	ADC08063	AdC08063	Human	PRO
423	720	100.0	720	7	ABM09801	Human	sec	496	720	100.0	720	7	ADC81988	AdC81988	Human	PRO
424	720	100.0	720	7	ABO38926	Human	sec	497	720	100.0	720	7	ADC07530	AdC07530	Human	sec
425	720	100.0	720	7	ABM34691	Human	sec	498	720	100.0	720	7	ADC82421	AdC82421	Human	PRO
426	720	100.0	720	7	ABO51167	Human	sec	499	720	100.0	720	7	ADC05643	AdC05643	Human	sec
427	720	100.0	720	7	ABO03993	Human	sec	500	720	100.0	720	7	ADC08601	AdC08601	Human	sec
428	720	100.0	720	7	ABO10463	Human	PRO	501	720	100.0	720	7	ADC06680	AdC06680	Human	PRO
429	720	100.0	720	7	ABO53170	Human	sec	502	720	100.0	720	7	ADC83097	AdC83097	Human	PRO
430	720	100.0	720	7	ABR77706	Human	sec	503	720	100.0	720	7	ADC55204	AdC55204	Human	PRO
431	720	100.0	720	7	ABR78916	Human	sec	504	720	100.0	720	7	ADC36042	AdC36042	Human	sec
432	720	100.0	720	7	ABO24010	Human	sec	505	720	100.0	720	7	ADC56162	AdC56162	Human	PRO
433	720	100.0	720	7	ABR93774	Human	sec	506	720	100.0	720	7	ADC54600	AdC54600	Human	PRO
434	720	100.0	720	7	ABM01817	Human	sec	507	720	100.0	720	7	ADC52754	AdC52754	Human	sec
435	720	100.0	720	7	ABM78240	Human	sec	508	720	100.0	720	7	ADC56221	AdC56221	Human	sec
436	720	100.0	720	7	ABR90029	Human	sec	509	720	100.0	720	7	ADC52176	AdC52176	Human	sec
437	720	100.0	720	7	ADA22354	Human	sec	510	720	100.0	720	7	ADC74307	AdC74307	Human	sec
438	720	100.0	720	7	ABM27555	Human	sec	511	720	100.0	720	7	ADC74919	AdC74919	Human	sec
439	720	100.0	720	7	ABM13156	Human	sec	512	720	100.0	720	7	ADC70531	AdC70531	Human	PRO
440	720	100.0	720	7	ABO31859	Human	sec	513	720	100.0	720	7	ADC82880	AdC82880	Human	PRO
441	720	100.0	720	7	ABM14071	Human	sec	514	720	100.0	720	7	ADC70532	AdC70532	Human	PRO
442	720	100.0	720	7	ABM08276	Human	sec	515	720	100.0	720	7	ADC00401	AdC00401	Human	sec
443	720	100.0	720	7	ABO40146	Human	sec	516	720	100.0	720	7	ADC41706	AdC41706	Human	PRO
444	720	100.0	720	7	ABM74581	Human	sec	517	720	100.0	720	7	ADC85891	AdC85891	Human	PRO
445	720	100.0	720	7	ABM33776	Human	sec	518	720	100.0	720	7	ADC83670	AdC83670	Human	PRO
446	720	100.0	720	7	ABM20235	Human	sec	519	720	100.0	720	7	ADC85893	AdC85893	Human	PRO
447	720	100.0	720	7	ABO48727	Human	sec	520	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
448	720	100.0	720	7	ABO22540	Human	sec	521	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
449	720	100.0	720	7	ABR72792	Human	sec	522	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
450	720	100.0	720	7	ABO15434	Human	sec	523	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
451	720	100.0	720	7	ABR85149	Human	sec	524	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
452	720	100.0	720	7	ABO15129	Human	sec	525	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
453	720	100.0	720	7	ABO17264	Human	sec	526	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
454	720	100.0	720	7	ABM17553	Human	sec	527	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
455	720	100.0	720	7	ADA06520	Human	sec	528	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
456	720	100.0	720	7	ADA39213	Human	sec	529	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
457	720	100.0	720	7	ABR85454	Human	sec	530	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
458	720	100.0	720	7	ABM77020	Human	sec	531	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
459	720	100.0	720	7	ABO28199	Human	sec	532	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
460	720	100.0	720	7	ABM22980	Human	sec	533	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
461	720	100.0	720	7	ABM30300	Human	sec	534	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
462	720	100.0	720	7	ABM21760	Human	sec	535	720	100.0	720	7	ADC81980	AdC81980	Human	PRO
463	720	100.0	720	7	ABM21455	Human	sec	536	720	100.0	720	7	ADC81980	AdC81980	Human	PRO

537	9	1.2	30	2	AA076945	AA076945	UK-t-PA h	610	7	1.0	76	4	AA067610	AA067610	Proponitb
538	9	1.2	30	2	AA093590	AA093590	UK t-PA h	611	7	1.0	76	6	AA062991	AA062991	Proponitb
539	9	1.2	30	2	AA093593	AA093593	UK t-PA h	612	7	1.0	76	6	AA064129	AA064129	Proponitb
540	9	1.2	30	2	AA093588	AA093588	UK t-PA h	613	7	1.0	79	5	AA062081	AA062081	Human gen
541	9	1.2	101	2	AA082896	AA082896	CUB domai	614	7	1.0	79	5	AA064651	AA064651	Human ald
542	9	1.2	110	2	AA027043	AA027043	Amino aci	615	7	1.0	81	6	AA064695	AA064695	Proponitb
543	9	1.2	730	1	AA080618	AA080618	Human Bon	616	7	1.0	103	3	AA030800	AA030800	Human sec
544	9	1.2	730	2	AA013669	AA013669	C-protein	617	7	1.0	105	3	AA044590	AA044590	Nonclassa
545	9	1.2	788	2	AA075919	AA075919	C-protein	618	7	1.0	107	5	AA066753	AA066753	Human ORF
546	9	1.2	970	5	AA079188	AA079188	Human tol	619	7	1.0	108	4	AA027656	AA027656	Human pro
547	9	1.2	986	5	AA013670	AA013670	C-protein	620	7	1.0	111	2	AA099113	AA099113	Bovine ze
548	9	1.2	986	5	AA090755	AA090755	Human Tum	621	7	1.0	116	2	AA099115	AA099115	Human zet
549	9	1.2	986	5	AA054462	AA054462	Human tum	622	7	1.0	117	2	AA026790	AA026790	Zea may
550	9	1.2	992	5	AA079187	AA079187	Human tol	623	7	1.0	121	3	AA051373	AA051373	Arabidops
551	9	1.2	1015	3	AA032240	AA032240	Human tol	624	7	1.0	121	3	AA036791	AA036791	Zea may
552	9	1.2	1464	3	AA071111	AA071111	Drosophi	625	7	1.0	128	3	AA011631	AA011631	Arabidops
553	8	1.1	11	5	AA077068	AA077068	AC2885 an	626	7	1.0	128	3	AA051372	AA051372	Arabidops
554	8	1.1	50	6	AA036802	AA036802	Human epi	627	7	1.0	142	2	AA041967	AA041967	Flea seri
555	8	1.1	51	3	AA076087	AA076087	mutRI fra	628	7	1.0	144	2	AA050629	AA050629	Flea seri
556	8	1.1	51	4	AA056026	AA056026	Skin cell	629	7	1.0	144	3	AA051370	AA051370	Arabidops
557	8	1.1	51	5	AA072226	AA072226	Murine pr	630	7	1.0	148	4	AA054494	AA054494	Proponitb
558	8	1.1	88	3	AA056653	AA056653	Partial p	631	7	1.0	148	4	AA061013	AA061013	Proponitb
559	8	1.1	94	3	AA079331	AA079331	Human BGF	632	7	1.0	151	3	AA051371	AA051371	Arabidops
560	8	1.1	95	6	AA027159	AA027159	Human ger	633	7	1.0	172	6	AA039246	AA039246	Protein e
561	8	1.1	95	6	AA027158	AA027158	Human ger	634	7	1.0	172	6	AA039246	AA039246	Protein e
562	8	1.1	96	6	AA035905	AA035905	Human A10	635	7	1.0	184	3	AA051370	AA051370	Arabidops
563	8	1.1	124	4	AA030399	AA030399	Human mus	636	7	1.0	187	7	AA025597	AA025597	E. faeciu
564	8	1.1	124	4	AA012693	AA012693	Novel hum	637	7	1.0	194	4	AA025597	AA025597	Human G p
565	8	1.1	126	6	AA077064	AA077064	AC2885 an	638	7	1.0	200	4	AA029491	AA029491	Human G p
566	8	1.1	127	6	AA057370	AA057370	Antl-TPAI	639	7	1.0	200	5	AA060779	AA060779	Novel G p
567	8	1.1	128	3	AA056718	AA056718	Amino aci	640	7	1.0	202	4	AA086561	AA086561	Drosophi
568	8	1.1	152	3	AA076009	AA076009	Murine TG	641	7	1.0	209	4	AA045202	AA045202	Proponitb
569	8	1.1	152	4	AA055948	AA055948	Skin cell	642	7	1.0	209	6	AA041721	AA041721	Proponitb
570	8	1.1	152	4	AA072148	AA072148	Murine pr	643	7	1.0	210	2	AA035451	AA035451	Chlamydia
571	8	1.1	155	3	AA093714	AA093714	The kappa	644	7	1.0	210	6	AA027599	AA027599	Protein e
572	8	1.1	155	6	AA035906	AA035906	Human 2.1	645	7	1.0	211	6	AA049962	AA049962	Protein e
573	8	1.1	155	6	AA070774	AA070774	Human adi	646	7	1.0	212	4	AA044556	AA044556	E. coli c
574	8	1.1	156	6	AA079332	AA079332	Human BGF	647	7	1.0	212	6	AA031486	AA031486	Protein o
575	8	1.1	156	6	AA022131	AA022131	Protein e	648	7	1.0	212	6	AA048063	AA048063	Protein o
576	8	1.1	159	5	AA068935	AA068935	Human pol	649	7	1.0	212	6	AA045066	AA045066	Protein o
577	8	1.1	159	5	AA043394	AA043394	Singapore	650	7	1.0	212	6	AA045471	AA045471	Protein o
578	8	1.1	159	5	AA050750	AA050750	Horrethoe	651	7	1.0	213	5	AA085497	AA085497	Lactococc
579	8	1.1	159	5	AA094302	AA094302	Horrethoe	652	7	1.0	213	6	AA040559	AA040559	Protein o
580	8	1.1	159	5	AA042490	AA042490	Recombina	653	7	1.0	221	4	AA086505	AA086505	Drosophi
581	8	1.1	159	5	AA060935	AA060935	Horrethoe	654	7	1.0	227	4	AA082525	AA082525	Human pro
582	8	1.1	159	5	AA072332	AA072332	Horrethoe	655	7	1.0	227	4	AA082525	AA082525	Human pro
583	8	1.1	159	5	AA072332	AA072332	Horrethoe	656	7	1.0	227	4	AA082525	AA082525	Human pro
584	8	1.1	159	5	AA072332	AA072332	Horrethoe	657	7	1.0	227	4	AA082525	AA082525	Human pro
585	8	1.1	159	5	AA072332	AA072332	Horrethoe	658	7	1.0	227	4	AA082525	AA082525	Human pro
586	8	1.1	159	5	AA072332	AA072332	Horrethoe	659	7	1.0	227	4	AA082525	AA082525	Human pro
587	8	1.1	159	5	AA072332	AA072332	Horrethoe	660	7	1.0	227	4	AA082525	AA082525	Human pro
588	8	1.1	159	5	AA072332	AA072332	Horrethoe	661	7	1.0	227	4	AA082525	AA082525	Human pro
589	8	1.1	159	5	AA072332	AA072332	Horrethoe	662	7	1.0	227	4	AA082525	AA082525	Human pro
590	8	1.1	159	5	AA072332	AA072332	Horrethoe	663	7	1.0	227	4	AA082525	AA082525	Human pro
591	8	1.1	159	5	AA072332	AA072332	Horrethoe	664	7	1.0	227	4	AA082525	AA082525	Human pro
592	8	1.1	159	5	AA072332	AA072332	Horrethoe	665	7	1.0	227	4	AA082525	AA082525	Human pro
593	8	1.1	159	5	AA072332	AA072332	Horrethoe	666	7	1.0	227	4	AA082525	AA082525	Human pro
594	8	1.1	159	5	AA072332	AA072332	Horrethoe	667	7	1.0	227	4	AA082525	AA082525	Human pro
595	8	1.1	159	5	AA072332	AA072332	Horrethoe	668	7	1.0	227	4	AA082525	AA082525	Human pro
596	8	1.1	159	5	AA072332	AA072332	Horrethoe	669	7	1.0	227	4	AA082525	AA082525	Human pro
597	8	1.1	159	5	AA072332	AA072332	Horrethoe	670	7	1.0	227	4	AA082525	AA082525	Human pro
598	8	1.1	159	5	AA072332	AA072332	Horrethoe	671	7	1.0	227	4	AA082525	AA082525	Human pro
599	8	1.1	159	5	AA072332	AA072332	Horrethoe	672	7	1.0	227	4	AA082525	AA082525	Human pro
600	8	1.1	159	5	AA072332	AA072332	Horrethoe	673	7	1.0	227	4	AA082525	AA082525	Human pro
601	8	1.1	159	5	AA072332	AA072332	Horrethoe	674	7	1.0	227	4	AA082525	AA082525	Human pro
602	8	1.1	159	5	AA072332	AA072332	Horrethoe	675	7	1.0	227	4	AA082525	AA082525	Human pro
603	8	1.1	159	5	AA072332	AA072332	Horrethoe	676	7	1.0	227	4	AA082525	AA082525	Human pro
604	8	1.1	159	5	AA072332	AA072332	Horrethoe	677	7	1.0	227	4	AA082525	AA082525	Human pro
605	8	1.1	159	5	AA072332	AA072332	Horrethoe	678	7	1.0	227	4	AA082525	AA082525	Human pro
606	8	1.1	159	5	AA072332	AA072332	Horrethoe	679	7	1.0	227	4	AA082525	AA082525	Human pro
607	8	1.1	159	5	AA072332	AA072332	Horrethoe	680	7	1.0	227	4	AA082525	AA082525	Human pro
608	8	1.1	159	5	AA072332	AA072332	Horrethoe	681	7	1.0	227	4	AA082525	AA082525	Human pro
609	8	1.1	159	5	AA072332	AA072332	Horrethoe	682	7	1.0	227	4	AA082525	AA082525	Human pro

683	7	1.0	280	6	ABM57940	Abm57940	Propionib
684	7	1.0	284	3	AAy82700	Aay82700	Tick deri
685	7	1.0	295	2	AAr74778	AAr74778	Mutant ch
686	7	1.0	295	2	AAr76033	AAr76033	Mutant ch
687	7	1.0	295	2	AAr74776	AAr74776	Mutant ch
688	7	1.0	295	2	AAr76038	AAr76038	Mutant ch
689	7	1.0	295	2	AAr76039	AAr76039	Mutant ch
690	7	1.0	295	2	AAr74779	AAr74779	Mutant ch
691	7	1.0	295	2	AAr76035	AAr76035	Mutant ch
692	7	1.0	295	2	AAr74775	AAr74775	Wild-type
693	7	1.0	295	2	AAr74780	AAr74780	Mutant ch
694	7	1.0	295	2	AAr76036	AAr76036	Mutant ch
695	7	1.0	295	2	AAr74777	AAr74777	Mutant ch
696	7	1.0	295	2	AAr76034	AAr76034	Mutant ch
697	7	1.0	295	2	AAr76040	AAr76040	Mutant ch
698	7	1.0	295	2	AAr76037	AAr76037	Mutant ch
699	7	1.0	295	2	AAW22892	AAW22892	Human mat
700	7	1.0	295	3	AAH08633	AAH08633	Amino aci

ALIGNMENTS

RESULT 1

AAV66695 standard; protein; 720 AA.

ID	AAV66695	standard; protein; 720 AA.
AC	AAV66695	
XX	05-APR-2000	(first entry)
XX	05-APR-2000	
DE	Membrane-bound protein PRO1344.	
XX	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;	
XX	pharmaceutical; receptor immunoadhesin; gene mapping.	
XX	Homo sapiens.	
PN	MO9963088-A2.	
XX	09-DEC-1999.	
XX	02-JUN-1999;	99MO-US012252.
XX	02-JUN-1998;	98US-0087607P.
PR	02-JUN-1998;	98US-0087609P.
PR	02-JUN-1998;	98US-0087759P.
PR	03-JUN-1998;	98US-0088021P.
PR	04-JUN-1998;	98US-0088025P.
PR	04-JUN-1998;	98US-0088028P.
PR	04-JUN-1998;	98US-0088029P.
PR	04-JUN-1998;	98US-0088030P.
PR	04-JUN-1998;	98US-0088033P.
PR	04-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088167P.
PR	05-JUN-1998;	98US-0088202P.
PR	05-JUN-1998;	98US-0088212P.
PR	05-JUN-1998;	98US-0088217P.
PR	05-JUN-1998;	98US-0088655P.
PR	09-JUN-1998;	98US-0088722P.
PR	10-JUN-1998;	98US-0088730P.
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PR	10-JUN-1998;	98US-0088738P.
PR	10-JUN-1998;	98US-0088740P.
PR	10-JUN-1998;	98US-0088741P.
PR	10-JUN-1998;	98US-0088742P.
PR	10-JUN-1998;	98US-0088810P.
PR	10-JUN-1998;	98US-0088811P.
PR	10-JUN-1998;	98US-0088824P.
PR	10-JUN-1998;	98US-0088825P.
PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088858P.

PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088863P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089090P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089440P.
PR	16-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
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PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089599P.
PR	17-JUN-1998;	98US-0089600P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089801P.
PR	18-JUN-1998;	98US-0089907P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089947P.
PR	19-JUN-1998;	98US-0089948P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090246P.
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PR	22-JUN-1998;	98US-0090254P.
PR	23-JUN-1998;	98US-0090349P.
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PR	24-JUN-1998;	98US-0090432P.
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PR	24-JUN-1998;	98US-0090435P.
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PR	24-JUN-1998;	98US-0090540P.
PR	25-JUN-1998;	98US-0090557P.
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PR	25-JUN-1998;	98US-0090688P.
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PR	25-JUN-1998;	98US-0090691P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	01-JUL-1998;	98US-0091358P.
PR	01-JUL-1998;	98US-0091360P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091519P.
PR	02-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091633P.
PR	02-JUL-1998;	98US-0091646P.
PR	02-JUL-1998;	98US-0091673P.
PR	07-JUL-1998;	98US-0091738P.
PR	07-JUL-1998;	98US-0091982P.
PR	09-JUL-1998;	98US-0092182P.
PR	10-JUL-1998;	98US-0092472P.
PR	20-JUL-1998;	98US-0093139P.
PR	30-JUL-1998;	98US-0094651P.
PR	04-AUG-1998;	98US-0095282P.
PR	04-AUG-1998;	98US-0095285P.
PR	04-AUG-1998;	98US-0095301P.
PR	04-AUG-1998;	98US-0095302P.
PR	04-AUG-1998;	98US-0095318P.
PR	04-AUG-1998;	98US-0095321P.
PR	04-AUG-1998;	98US-0095325P.
PR	10-AUG-1998;	98US-0095916P.
PR	10-AUG-1998;	98US-0095929P.
PR	10-AUG-1998;	98US-0096012P.

PR 11-AUG-1998; 98US-0096143P.
 PR 11-AUG-1998; 98US-0096146P.
 PR 12-AUG-1998; 98US-0096329P.
 PR 17-AUG-1998; 98US-0096757P.
 PR 17-AUG-1998; 98US-0096766P.
 PR 17-AUG-1998; 98US-0096768P.
 PR 17-AUG-1998; 98US-0096773P.
 PR 17-AUG-1998; 98US-0096791P.
 PR 17-AUG-1998; 98US-0096867P.
 PR 17-AUG-1998; 98US-0096891P.
 PR 17-AUG-1998; 98US-0096894P.
 PR 17-AUG-1998; 98US-0096895P.
 PR 17-AUG-1998; 98US-0096897P.
 PR 18-AUG-1998; 98US-0096949P.
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 PR 18-AUG-1998; 98US-0096959P.
 PR 18-AUG-1998; 98US-0096960P.
 PR 18-AUG-1998; 98US-0097022P.
 PR 19-AUG-1998; 98US-0097141P.
 PR 20-AUG-1998; 98US-0097218P.
 PR 24-AUG-1998; 98US-0097661P.
 PR 26-AUG-1998; 98US-0097951P.
 PR 26-AUG-1998; 98US-0097952P.
 PR 26-AUG-1998; 98US-0097954P.
 PR 26-AUG-1998; 98US-0097955P.
 PR 26-AUG-1998; 98US-0097971P.
 PR 26-AUG-1998; 98US-0097974P.
 PR 26-AUG-1998; 98US-0097978P.
 PR 26-AUG-1998; 98US-0097979P.
 PR 26-AUG-1998; 98US-0097986P.
 PR 26-AUG-1998; 98US-0098014P.
 PR 31-AUG-1998; 98US-0098525P.
 PR 16-SEP-1998; 98US-0100634P.
 PR 12-JAN-1999; 99US-0115565P.
 XX (GETH) GENENTECH INC.
 PA Baker K, Chen J, Goddard A, Gurney AU, Smith V, Watanabe CK;
 PI Wood W, Yuan J;
 XX WPI, 2000-072883/06.
 DR N-PSDB; AAZ65034.
 XX
 PT Membrane-bound proteins and related nucleotide sequences.
 PS Claim 12, Fig 159; 822BP; English.
 XX
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIR
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes, in chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
 CC also be useful for the preparation of PRO polypeptides, especially by
 CC recombinant techniques
 XX
 XX Sequence 720 AA;

Query Match 100.0%; Score 720; DB 3; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MELGCMTOLGTLTLLTLLTSSLPREYTVINBACPGAENINMRECCEYDQIEVCQPKRE 60
 DB 1 MELGCMTOLGTLTLLTLLTSSLPREYTVINBACPGAENINMRECCEYDQIEVCQPKRE 60
 OY 61 VVGTTIPCCRNEMENEDSCLIHPGCTIFENCKSCRNMGWGLTDDFYVKGFFYCAECRAGW 120

DB 61 VVGTTIPCCRNEMENEDSCLIHPGCTIFENCKSCRNMGWGLTDDFYVKGFFYCAECRAGW 120
 OY 121 YGGDCMRGCGVTLAPAPGQILLESYPINAHCEWTTHAKPGVITLQRYMLSLEFDYMCQYD 180
 DB 121 YGGDCMRGCGVTLAPAPGQILLESYPINAHCEWTTHAKPGVITLQRYMLSLEFDYMCQYD 180
 OY 181 YVEVRDGDNDGQITKRVCGNERPAPLOSIGSSLHYLPHSDGSKNPFQFAIYEETPACS 240
 DB 181 YVEVRDGDNDGQITKRVCGNERPAPLOSIGSSLHYLPHSDGSKNPFQFAIYEETPACS 240
 OY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCEMLLEBRNCSDFGPVNGYQKITGGFGLI 300
 DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCEMLLEBRNCSDFGPVNGYQKITGGFGLI 300
 OY 301 NGRHAKIGTVASFPCNNSTYLSGNERKTCQONEMSGKOPICIKACREPKISDLVRRRLV 360
 DB 301 NGRHAKIGTVASFPCNNSTYLSGNERKTCQONEMSGKOPICIKACREPKISDLVRRRLV 360
 OY 361 PMQVSRREPLHQLYSAFQKLOSAPTKPPALPFQDLPMGYOHLHTQLQYECISPFYR 420
 DB 361 PMQVSRREPLHQLYSAFQKLOSAPTKPPALPFQDLPMGYOHLHTQLQYECISPFYR 420
 OY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRPMWQAAIYRRTSGVHDGSL 480
 DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRPMWQAAIYRRTSGVHDGSL 480
 OY 481 HKGAMFLVCSGALVNETTVVAACHCVTDLQKVMIKRADIKVYLGRKYRDDDRREKTIQS 540
 DB 481 HKGAMFLVCSGALVNETTVVAACHCVTDLQKVMIKRADIKVYLGRKYRDDDRREKTIQS 540
 OY 541 LQISAILHPNYPDILDDADIAITKLDKARISTRVOPICLAASRDISTFOESHITVAG 600
 DB 541 LQISAILHPNYPDILDDADIAITKLDKARISTRVOPICLAASRDISTFOESHITVAG 600
 OY 601 MNVLADVRSPGKNDTLRSQVSVVDSLLCEQHEHGHIPVSTDNMFCAWMEPTAPSDI 660
 DB 601 MNVLADVRSPGKNDTLRSQVSVVDSLLCEQHEHGHIPVSTDNMFCAWMEPTAPSDI 660
 OY 661 CTAFETGGTIAVSPGRASPPRWHLMGLVMSVSKTCSHRLSTFTFVLPFKDMEENMK 720
 DB 661 CTAFETGGTIAVSPGRASPPRWHLMGLVMSVSKTCSHRLSTFTFVLPFKDMEENMK 720

RESULT 2

ID AAU29108 standard; protein: 720 AA.

AC AAU29108;

DT 18-DEC-2001 (first entry)

XX Human PRO polypeptide sequence #85.

DE PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;

KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;

KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;

XX adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

OS Homo sapiens.

XX MO200168848-A2.

XX 20-SEP-2001.

XX 28-FEB-2001, 2001WO-US006520.

XX 01-MAR-2000, 2000WO-US005601.

XX 02-MAR-2000, 2000WO-US005841.

XX 03-MAR-2000, 2000US-0187202P.

XX 06-MAR-2000, 2000US-0186968P.

XX 14-MAR-2000, 2000US-0189320P.

XX 14-MAR-2000, 2000US-0189328P.

PR 15-MAR-2000; 2000MO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000MO-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 29-MAR-2000; 2000US-0193053P.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196680P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000MO-US013705.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 30-MAY-2000; 2000MO-US014941.
 PR 02-JUN-2000; 2000MO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000MO-US020710.
 PR 22-AUG-2000; 2000US-0064848.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 20-DEC-2000; 2000MO-US034956.
 XX
 PA (GETH) GENENTECH INC.
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR N-PSDB; AAS646009.
 XX
 PT WPI; 2001-602746/68.
 PT screen for modulators of the compounds.
 XX
 PS Claim 11; Fig 170; 774pp; English.
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX
 SO Sequence 720 AA;
 Query Match 100.0%; Score 720; DB 4; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MELGCTQTGLTFLQLLISSLPREYTVINBACPGAEWNIMCCECEYDQIECVCGKRE 60
 |||||||

DB 1 MELGCTQTGLTFLQLLISSLPREYTVINBACPGAEWNIMCCECEYDQIECVCGKRE 60
 QY 61 VVGTTIPCCRNENECDSCLHPGCTTIPENCKSCNNGWGTLDFFYYKGFCAECRAGW 120
 DB 61 VVGTTIPCCRNENECDSCLHPGCTTIPENCKSCNNGWGTLDFFYYKGFCAECRAGW 120
 QY 121 YGGDCMRGQVLRARKGQILLESYPLNAHCWTIAKKGFPYQLRFWMLSEFDYMCQYD 180
 DB 121 YGGDCMRGQVLRARKGQILLESYPLNAHCWTIAKKGFPYQLRFWMLSEFDYMCQYD 180
 QY 181 YVEVDGNDGDIILKRVCGNERPAPISIGSLHLVLFHSDSKXNDFPHAYIEBITACS 240
 DB 181 YVEVDGNDGDIILKRVCGNERPAPISIGSLHLVLFHSDSKXNDFPHAYIEBITACS 240
 QY 241 SSPCFHDGTCVLDKXGSKYKCAAGLYTQRCNLLLEBNCSPPGAVNGYQKITGPGIL 300
 DB 241 SSPCFHDGTCVLDKXGSKYKCAAGLYTQRCNLLLEBNCSPPGAVNGYQKITGPGIL 300
 QY 301 NGRHAKIGTVVSFFCNGSVYLSGNEKRTCOQNGEWSGKQPTICIKAREPKISDLVRRVL 360
 DB 301 NGRHAKIGTVVSFFCNGSVYLSGNEKRTCOQNGEWSGKQPTICIKAREPKISDLVRRVL 360
 QY 361 PMQVSRETPHLQLYSAAFSKOKLOSAPTKKPALEPGDLPMGYQHLHTOLQYECISPFYR 420
 DB 361 PMQVSRETPHLQLYSAAFSKOKLOSAPTKKPALEPGDLPMGYQHLHTOLQYECISPFYR 420
 QY 421 RLGSSRRCTLRGKSGRAPSCIPICGKIENITAKTQGLRPMQAAIYRRSGVHDSL 480
 DB 421 RLGSSRRCTLRGKSGRAPSCIPICGKIENITAKTQGLRPMQAAIYRRSGVHDSL 480
 QY 481 HKGAMFLVCSGALVNERTVVAHCVTDLGKWTMIKTADLKVVLGKPYRDDDRDEKTIQS 540
 DB 481 HKGAMFLVCSGALVNERTVVAHCVTDLGKWTMIKTADLKVVLGKPYRDDDRDEKTIQS 540
 QY 541 LQISAIIILHPNYDPIILLADIAIILKLDKARISTVQPICLAASDLSTSPQESHITVAG 600
 DB 541 LQISAIIILHPNYDPIILLADIAIILKLDKARISTVQPICLAASDLSTSPQESHITVAG 600
 QY 601 WNVLDVSPGPKNTLRSGVSVVDSLLCEQEHDDHGIPIVSTVNMFCASWEPAPSDI 660
 DB 601 WNVLDVSPGPKNTLRSGVSVVDSLLCEQEHDDHGIPIVSTVNMFCASWEPAPSDI 660
 QY 661 CTAETGGIAAIVSFPGRASPEPRMHLGLVSWGYDKTCSHRLSTAFKYLPRKDWIERNMK 720
 DB 661 CTAETGGIAAIVSFPGRASPEPRMHLGLVSWGYDKTCSHRLSTAFKYLPRKDWIERNMK 720
 RESULT 3
 AAB87544
 ID AAB87544 standard; protein; 720 AA.
 XX
 AC AAB87544;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Human PRO1344.
 XX
 KW Human; PRO protein; mapping.
 OS Homo sapiens.
 XX
 PN WO200116318-A2.
 XX
 PD 08-MAR-2001.
 XX
 PF 24-AUG-2000; 2000MO-US023328.
 XX
 PR 01-SEP-1999; 99MO-US020111.
 PR 15-SEP-1999; 99MO-US021090.
 PR 07-DEC-1999; 99US-0169495P.
 PR 09-DEC-1999; 99US-0170262P.
 PR 11-JAN-2000; 2000US-0175481P.
 PR 18-FEB-2000; 2000MO-US004341.

PR 18-FEB-2000; 2000MO-US004342.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 01-MAR-2000; 2000MO-US005601.
 PR 03-MAR-2000; 2000US-0187202P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 30-MAR-2000; 2000MO-US008439.
 PR 25-APR-2000; 2000US-0199397P.
 PR 22-MAY-2000; 2000MO-US014042.
 PR 05-JUN-2000; 2000US-0209832P.
 XX
 PA (GETH) GENENTECH INC.
 PI Eacon DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ,
 PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
 XX
 DR WPI: 2001-183260/18.
 DR N-PSDB; AAF92076.
 XX
 PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
 PT biology, including use as hybridization probes, and in chromosome and
 PT gene mapping.
 XX
 PS Claim 12, Fig 38; 278pp; English.
 XX
 CC The present sequence is a human PRO polypeptide (secreted and
 CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
 CC anti-PRO antibodies are useful for preparation of a medicament useful in
 CC the treatment of a condition which is responsive to the PRO protein,
 CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
 CC employed as molecular weight markers for protein electrophoresis. The PRO
 CC coding sequence has applications in molecular biology, including use as
 CC hybridisation probes, and in chromosome and gene mapping
 CC
 XX Sequence 720 AA:
 SQ
 Query Match 100.0%; Score 720; DB 4; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MELGCTWOLGTLPTQLLLISSLPREYTYINACPGAEINIMRECECEDEQIECCPGRE 60
 DB 1 MELGCTWOLGTLPTQLLLISSLPREYTYINACPGAEINIMRECECEDEQIECCPGRE 60
 QY 61 VVGTYTIPCCRNENECDSCLHPGCTIFENCKSCNWSMGGLTDFYKGFYCAECRAGW 120
 DB 61 VVGTYTIPCCRNENECDSCLHPGCTIFENCKSCNWSMGGLTDFYKGFYCAECRAGW 120
 QY 121 YGGDCMRGCVLRAPKQIILBSYPLNAHCEWTIHAKEGFIYQLRFVWLSLEFDYMCQYD 180
 DB 121 YGGDCMRGCVLRAPKQIILBSYPLNAHCEWTIHAKEGFIYQLRFVWLSLEFDYMCQYD 180
 QY 121 YGGDCMRGCVLRAPKQIILBSYPLNAHCEWTIHAKEGFIYQLRFVWLSLEFDYMCQYD 180
 DB 121 YGGDCMRGCVLRAPKQIILBSYPLNAHCEWTIHAKEGFIYQLRFVWLSLEFDYMCQYD 180
 QY 181 YVEVADGNGNRGOITIKRVCGNERPAPISIGSSILHVLPHSGSKNPFDFHAYEETNCS 240
 DB 181 YVEVADGNGNRGOITIKRVCGNERPAPISIGSSILHVLPHSGSKNPFDFHAYEETNCS 240
 QY 241 SSPCFHDTGCVLDKASGYKCAAGYTGQRCENLLEENECSDPGGPNVGYOKITGGPGLI 300
 DB 241 SSPCFHDTGCVLDKASGYKCAAGYTGQRCENLLEENECSDPGGPNVGYOKITGGPGLI 300
 QY 301 NGRNAKIGTVVSFFCNNSYVLSGNEKRTCCQNGEMSGOPICIRACREPKISDLVRRVYL 360
 DB 301 NGRNAKIGTVVSFFCNNSYVLSGNEKRTCCQNGEMSGOPICIRACREPKISDLVRRVYL 360
 QY 301 NGRNAKIGTVVSFFCNNSYVLSGNEKRTCCQNGEMSGOPICIRACREPKISDLVRRVYL 360
 DB 301 NGRNAKIGTVVSFFCNNSYVLSGNEKRTCCQNGEMSGOPICIRACREPKISDLVRRVYL 360
 QY 361 PMOVUSRETPHLQVLSAFAFSKOKLOSAPTKKPLPFGDLPMGYOHLHTQLQYECISPFYR 420
 DB 361 PMOVUSRETPHLQVLSAFAFSKOKLOSAPTKKPLPFGDLPMGYOHLHTQLQYECISPFYR 420
 QY 421 RLGSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTGSLMPWQALYRRTSGVHDSL 480
 DB 421 RLGSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTGSLMPWQALYRRTSGVHDSL 480
 QY 481 HKGAMFLVCSGALVNERTVVAHCVTLGKVTMTKTADLVVVGKFFRDDDRDEKTIQS 540
 DB 481 HKGAMFLVCSGALVNERTVVAHCVTLGKVTMTKTADLVVVGKFFRDDDRDEKTIQS 540

DB 481 HKGAMFLVCSGALVNERTVVAHCVTLGKVTMTKTADLVVVGKFFRDDDRDEKTIQS 540
 QY 541 LQISATILHNPYDPIILDADIALIKLIDKARISTRVOPICLAASRDLSFQSHITVAG 600
 DB 541 LQISATILHNPYDPIILDADIALIKLIDKARISTRVOPICLAASRDLSFQSHITVAG 600
 QY 601 MNVLADVRSPGKNDTLRSQVSVSDSLCEQHEHGHIPVSYTDNMFCAWSPEAPSIDI 660
 DB 601 MNVLADVRSPGKNDTLRSQVSVSDSLCEQHEHGHIPVSYTDNMFCAWSPEAPSIDI 660
 QY 661 CTATGTGIAAVSPFGRASPEPRNHLGLVWSYDICTSHSLSTAFKYLFPKMIERNMK 720
 DB 661 CTATGTGIAAVSPFGRASPEPRNHLGLVWSYDICTSHSLSTAFKYLFPKMIERNMK 720
 RESULT 4
 AAB65218
 ID AAB65218 standard; protein: 720 AA.
 XX
 AC AAB65218;
 XX
 DT 02-APR-2001 (first entry)
 XX
 DE Human PRO1344 (UNG699) protein sequence SEQ ID NO:231.
 XX
 KW Human; secreted and transmembrane protein; PRO; cytosolic; cell death;
 KW cancer; Chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000MO-US008439.
 XX
 PR 02-JUN-1999; 99MO-US012252.
 PR 23-JUN-1999; 99US-0141037P.
 PR 07-JUL-1999; 99US-0143048P.
 PR 20-JUL-1999; 99US-0144758P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 17-AUG-1999; 99US-0149336P.
 PR 15-SEP-1999; 99MO-US021090.
 PR 15-SEP-1999; 99MO-US021547.
 PR 08-OCT-1999; 99US-0158663P.
 PR 30-NOV-1999; 99MO-US028313.
 PR 01-DEC-1999; 99MO-US028301.
 PR 16-DEC-1999; 99MO-US030095.
 PR 20-DEC-1999; 99MO-US030911.
 PR 05-JAN-2000; 2000MO-US000219.
 PR 06-JAN-2000; 2000MO-US000376.
 PR 11-FEB-2000; 2000MO-US003565.
 PR 18-FEB-2000; 2000MO-US004341.
 PR 22-FEB-2000; 2000MO-US004414.
 PR 24-FEB-2000; 2000MO-US004914.
 PR 24-FEB-2000; 2000MO-US005004.
 PR 02-MAR-2000; 2000MO-US005841.
 PR 15-MAR-2000; 2000MO-US005884.
 PR 20-MAR-2000; 2000MO-US007377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eacon DL;
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy M, Stewart TA, Tumas D, Watanabe CK, Williams PW, Wood WI;
 PI Zhang Z;
 XX
 DR WPI: 2001-032160/04.
 DR N-PSDB; AAF44180.

PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
to cause targeted cell death.

PS Claim 12; Fig 159; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAF65154 to
CC AAF65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention

XX Sequence 720 AA:

Query Match 100.0%; Score 720; DB 4; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEIGCWTLQGLTFLQILLISLPREYVINEACGAEWNTMCBCEYDIECVCPGKRE 60
DB 1 MEIGCWTLQGLTFLQILLISLPREYVINEACGAEWNTMCBCEYDIECVCPGKRE 60
QY 61 VVGVTTCPCNENECSCLIHPGCTIFENCKSCRNMGWGLDPPVYKFGACGRAG 120
DB 61 VVGVTTCPCNENECSCLIHPGCTIFENCKSCRNMGWGLDPPVYKFGACGRAG 120
QY 121 YGGDCNRGCVLAPKQIILLESYPLNACGWTIHAKPGFVIGLRFVMSLEPDYMCQYD 180
DB 121 YGGDCNRGCVLAPKQIILLESYPLNACGWTIHAKPGFVIGLRFVMSLEPDYMCQYD 180
QY 181 YVEVRDGDNDGQIKRVCGNERPAPQISGSSHLVPHSDGSKNFGFAITERTTACS 240
DB 181 YVEVRDGDNDGQIKRVCGNERPAPQISGSSHLVPHSDGSKNFGFAITERTTACS 240
QY 241 SSPCFHDTGCVLDKAGSYKCAAGYGRCEMLERNSDPSGPNVGYOKITGGPGLI 300
DB 241 SSPCFHDTGCVLDKAGSYKCAAGYGRCEMLERNSDPSGPNVGYOKITGGPGLI 300
QY 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKOPICIKACREPKISDLVRRVL 360
DB 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOQNGEWSGKOPICIKACREPKISDLVRRVL 360
QY 361 PMOVQSEFTLHOUYSAFSGKQLOSAPTKKPALPFDLPMGOHLHTOLQYECISPFYR 420
DB 361 PMOVQSEFTLHOUYSAFSGKQLOSAPTKKPALPFDLPMGOHLHTOLQYECISPFYR 420
QY 421 RLSSRRRTCLRTGKWSGRAPSCIPICGKINENITAPKQGLRWPQALYRTSGVHDSL 480
DB 421 RLSSRRRTCLRTGKWSGRAPSCIPICGKINENITAPKQGLRWPQALYRTSGVHDSL 480
QY 481 HKGAMPLVCGALVNERTVVAHCVTDLGKVTMIKTADLKVVLGKRYRDDDDDEKTIQS 540
DB 481 HKGAMPLVCGALVNERTVVAHCVTDLGKVTMIKTADLKVVLGKRYRDDDDDEKTIQS 540
QY 541 LQISAILLHNPYDILLADDAIATKLDKARISTRVOPICLAASRDSTSFQSHITVAG 600
DB 541 LQISAILLHNPYDILLADDAIATKLDKARISTRVOPICLAASRDSTSFQSHITVAG 600
QY 601 MNVLADVRSGPKNDLRSQVSVYDLSLCEQHEHDSIPVSVYDNNFCASWEPTASDI 660
DB 601 MNVLADVRSGPKNDLRSQVSVYDLSLCEQHEHDSIPVSVYDNNFCASWEPTASDI 660
QY 661 CTATGTGIIAIVSPFGRASPEPRHMLGLVMSYKTSLSLSTAFVLPFKMIERNMK 720
DB 661 CTATGTGIIAIVSPFGRASPEPRHMLGLVMSYKTSLSLSTAFVLPFKMIERNMK 720

DB 661 CTATGTGIIAIVSPFGRASPEPRHMLGLVMSYKTSLSLSTAFVLPFKMIERNMK 720
RESULT 5
ID ABG95869 standard; protein; 720 AA.
XX ABG95869;
AC
XX
XX 10-DEC-2002 (first entry)
DT
XX
XX Human secreted/transmembrane protein PRO1344.
DE
XX
XX Human; secreted protein; transmembrane protein; arthritic;
KW antirheumatic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
OS Homo sapiens.
XX
XX US2002119130-A1.
XX
XX
XX 29-AUG-2002.
XX
XX
XX 06-DEC-2001; 2001US-00006867.
PF
XX
XX 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085759P.
PR 02-JUN-1998; 98US-0087559P.
PR 04-JUN-1998; 98US-0088021P.
PR 04-JUN-1998; 98US-0088029P.
PR 04-JUN-1998; 98US-0088030P.
PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 11-JUN-1998; 98US-0088863P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 19-JUN-1998; 98US-0089552P.
PR 22-JUN-1998; 98US-0090246P.
PR 24-JUN-1998; 98US-0090444P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-0090862P.
PR 02-JUL-1998; 98US-0091628P.
PR 10-AUG-1998; 98US-0096012P.
PR 17-AUG-1998; 98US-0096577P.
PR 18-AUG-1998; 98US-0096549P.
PR 18-AUG-1998; 98US-0096599P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097979P.
PR 01-SEP-1998; 98US-0098749P.
PR 10-SEP-1998; 98US-0098741P.
PR 10-SEP-1998; 98US-0098763P.
PR 10-SEP-1998; 98US-0098792P.
PR 10-SEP-1998; 98US-00998112P.
PR 10-SEP-1998; 98US-0099815P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-01019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100930P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101475P.
PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101743P.

XX 15-APR-2003 (first entry)
DT Human PRO polypeptide #85.
XX
DE Human PRO polypeptide #85.
XX
KW Human; PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;
dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KM antibody-dependent enzyme mediated prodrug therapy.
XX
OS Homo sapiens.
XX
PN US2003027272-A1.
XX
PD 06-FEB-2003.
XX
PF 21-JUN-2002; 2002US-00176492.
XX
PR 18-SEP-1997; 97US-0059263P.
PR 18-SEP-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
PR 28-OCT-1997; 97US-0063541P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063545P.
PR 29-OCT-1997; 97US-0063734P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 13-NOV-1997; 97US-0065311P.
PR 21-NOV-1997; 97US-0066120P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066772P.
PR 11-DEC-1997; 97US-0069335P.
PR 12-DEC-1997; 97US-0069425P.
PR 17-DEC-1997; 97US-0069870P.
PR 18-DEC-1997; 97US-0068017P.
PR 10-MAR-1998; 98US-0077450P.
PR 11-MAR-1998; 98US-0077632P.
PR 11-MAR-1998; 98US-0077649P.
PR 20-MAR-1998; 98US-0078886P.
PR 20-MAR-1998; 98US-0078939P.
PR 27-MAR-1998; 98US-0079664P.
PR 27-MAR-1998; 98US-0079786P.
PR 31-MAR-1998; 98US-0080107P.
PR 31-MAR-1998; 98US-0080194P.
PR 01-APR-1998; 98US-0080327P.
PR 01-APR-1998; 98US-0080333P.
PR 08-APR-1998; 98US-0081049P.
PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0083222P.
PR 28-APR-1998; 98US-0083495P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083496P.
PR 29-APR-1998; 98US-0083499P.
PR 29-APR-1998; 98US-0083559P.
PR 05-MAY-1998; 98US-0084366P.
PR 06-MAY-1998; 98US-0084414P.
PR 07-MAY-1998; 98US-0084639P.
PR 07-MAY-1998; 98US-0084640P.
PR 07-MAY-1998; 98US-0084643P.
PR 15-MAY-1998; 98US-0085579P.
PR 15-MAY-1998; 98US-0085580P.
PR 15-MAY-1998; 98US-0085582P.
PR 15-MAY-1998; 98US-0085700P.
PR 18-MAY-1998; 98US-0086023P.
PR 22-MAY-1998; 98US-0086392P.
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PR 28-MAY-1998; 98US-0087098P.
PR 28-MAY-1998; 98US-0087208P.
PR 02-JUN-1998; 98US-0087509P.
PR 02-JUN-1998; 98US-0087759P.
PR 03-JUN-1998; 98US-0087827P.
PR 04-JUN-1998; 98US-0088025P.
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PR 04-JUN-1998; 98US-0088033P.
PR 04-JUN-1998; 98US-0088326P.
PR 05-JUN-1998; 98US-0088167P.
PR 05-JUN-1998; 98US-0088202P.
PR 05-JUN-1998; 98US-0088212P.
PR 05-JUN-1998; 98US-0088217P.
PR 09-JUN-1998; 98US-0088655P.
PR 10-JUN-1998; 98US-0088722P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088740P.
PR 10-JUN-1998; 98US-0088811P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088863P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089090P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089908P.
PR 19-JUN-1998; 98US-0089952P.
PR 22-JUN-1998; 98US-0090246P.
PR 22-JUN-1998; 98US-0090252P.
PR 22-JUN-1998; 98US-0090254P.
PR 24-JUN-1998; 98US-0090435P.
PR 24-JUN-1998; 98US-0090444P.
PR 24-JUN-1998; 98US-0090461P.
PR 24-JUN-1998; 98US-0090535P.
PR 24-JUN-1998; 98US-0090540P.
PR 25-JUN-1998; 98US-0090676P.
PR 25-JUN-1998; 98US-0090678P.
PR 25-JUN-1998; 98US-0090688P.
PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
PR 25-JUN-1998; 98US-0090695P.
PR 25-JUN-1998; 98US-0090696P.
PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
PR 26-JUN-1998; 98US-0090863P.
PR 26-JUN-1998; 98US-0091010P.
PR 01-JUL-1998; 98US-0091159P.
PR 01-JUL-1998; 98US-0091544P.
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ABUS8032; (first entry)

07-JUL-2003 (first entry)

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Homo sapiens.

US2003032127-A1.

13-FEB-2003.

26-JUN-2002; 2002US-00183012.

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MELGCTOGLTFLQLLLISLPRETYVINEACPGAEKNNIMCECEYDIECVCKGRE 60
QY 61 VVGYYTTPCCRNENEDSCLIHPGCTIFENCKSCRNNGSGTDDPYVNGFYCAEGRAGW 120
61 VVGYYTTPCCRNENEDSCLIHPGCTIFENCKSCRNNGSGTDDPYVNGFYCAEGRAGW 120
DB 61 VVGYYTTPCCRNENEDSCLIHPGCTIFENCKSCRNNGSGTDDPYVNGFYCAEGRAGW 120
QY 121 YGGDCRCQGVLAAPKQOILLESYPUNAHCWTHAKPGFVQLRPMVLSLEFDYMCQYD 180
121 YGGDCRCQGVLAAPKQOILLESYPUNAHCWTHAKPGFVQLRPMVLSLEFDYMCQYD 180
DB 121 YGGDCRCQGVLAAPKQOILLESYPUNAHCWTHAKPGFVQLRPMVLSLEFDYMCQYD 180
QY 181 YVEVRDGNRDGQIRVCGNERPAPISIGSLHVLPHSDSKNDFHAYIEETIACS 240
181 YVEVRDGNRDGQIRVCGNERPAPISIGSLHVLPHSDSKNDFHAYIEETIACS 240
DB 181 YVEVRDGNRDGQIRVCGNERPAPISIGSLHVLPHSDSKNDFHAYIEETIACS 240
QY 241 SSPCFHDGTCVLDKAGSYKACIAGYTGRCENTLEERNCSDPGCVNGYOKITGGPGIL 300
241 SSPCFHDGTCVLDKAGSYKACIAGYTGRCENTLEERNCSDPGCVNGYOKITGGPGIL 300
DB 241 SSPCFHDGTCVLDKAGSYKACIAGYTGRCENTLEERNCSDPGCVNGYOKITGGPGIL 300
QY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGEMSGKOPICIKACREPKISLVRRVYL 360
301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGEMSGKOPICIKACREPKISLVRRVYL 360
DB 301 NGRHAKIGTVVSFFCNNSYVLSGNEKRTCOQNGEMSGKOPICIKACREPKISLVRRVYL 360
QY 361 PMOVOSRETPHLQVLAASKOKLOSAPTKKPALPFGDLPNGYQHLHTOLOVECISPFYR 420
361 PMOVOSRETPHLQVLAASKOKLOSAPTKKPALPFGDLPNGYQHLHTOLOVECISPFYR 420
DB 361 PMOVOSRETPHLQVLAASKOKLOSAPTKKPALPFGDLPNGYQHLHTOLOVECISPFYR 420
QY 421 RLGSRRRTCLRTGKMSGRAPSCIPICQKIENTITAPKTOGLRPMWQNAIYRRTSGVHDSI 480
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DB 421 RLGSRRRTCLRTGKMSGRAPSCIPICQKIENTITAPKTOGLRPMWQNAIYRRTSGVHDSI 480
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QY 541 LQISATILHPNYPILDDADIALIKLDDKARISTRVQPICLAASRLDSTFSQESHITVAG 600
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QY 661 CTAETGGIAAVSPRGASPEPRWHLMGLVSWSDTKCSHRLSTAFYKVLPMKIMERNMK 720
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RESULT 10
ABR65611
ID ABR65611 standard; protein; 720 AA.

XX AC ABR65611;
XX 05-AUG-2003 (first entry)
XX DE Human secreted polypeptide PRO1344, SEQ ID NO:170.
XX XX
XX Human; PRO: secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX chondrocyte; proliferation; differentiation; cartilage disorder;
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX liver; drug screening; transgenic animal; genetic analysis;
XX antarthritic; vulnery; gene therapy.
XX
XX Homo sapiens.
XX OS
XX US2003036159-A1.
XX PD 20-FEB-2003.
XX PF 02-JUL-2002; 2002US-00188773.
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Query Match 100.0%; Score 720; DB 6; Length 720;
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DB 61 VVGTYIPCCRNENECDSCLHPGCTTFENCKSCRNCSWGSLTDFYVKGFFYCAECRAGW 120
QY 121 YGGGCMRCGQVTLAPKQIILLESYPLNACHCWTTHAKRGFTYQIRFWLSEFPYMCQYD 180
DB 121 YGGGCMRCGQVTLAPKQIILLESYPLNACHCWTTHAKRGFTYQIRFWLSEFPYMCQYD 180
QY 181 YVEVRDGNRDGOIIRKVCNERNAPAPISIGSSILHVLPHSGSKNFGFPAIYEITRACS 240
DB 181 YVEVRDGNRDGOIIRKVCNERNAPAPISIGSSILHVLPHSGSKNFGFPAIYEITRACS 240

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QY 301 NGRHAKIGTVSPFCNNSYVLSGNERRTCOQNGWSGKOPICIKACREPKISDLVRRVL 360
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QY 361 PMQVOSRETPPLHOLYSAASKQLOSAPTKRALPFGDLPNGYQHHTLOQYECISPFYR 420
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RESULT 11
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 AC ABU99551;
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 DT 09-AUG-2003 (first entry)
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 DE Human secreted and transmembrane protein (PRO); TNF-alpha;
 KM Human necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 KW tissue typing.
 OS Homo sapiens.
 XX
 XX US2003040070-A1.
 PN
 XX
 PD 27-FEB-2003.
 XX
 XX 27-JUN-2002; 2002US-00184627.
 PF
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 Best Local Similarity 100.0%; Pired. No. 0;
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 DB 61 VVGTTIICCRNEBECSCLIHPCCTIFENCKSCRNMGWGTLDLDFYKGFYCAECRAG 120
 QY 121 YGGGCMGCGOVLRAKGOIILLESYPLNAHCWTHAKRGFIOLRFYMLSLERPYNQYD 180
 DB 121 YGGGCMGCGOVLRAKGOIILLESYPLNAHCWTHAKRGFIOLRFYMLSLERPYNQYD 180
 QY 181 YVEVRDNDNRDGOIIRKVCGERPAPLOSIGSSHLVLFHSDGSKNPDGFALYEEITACS 240
 DB 181 YVEVRDNDNRDGOIIRKVCGERPAPLOSIGSSHLVLFHSDGSKNPDGFALYEEITACS 240
 QY 241 SSPFHGTGCVLDKAGSYKCACTAGYTGRCENILBERNCSDPGPNVGYOKITGGGLI 300
 DB 241 SSPFHGTGCVLDKAGSYKCACTAGYTGRCENILBERNCSDPGPNVGYOKITGGGLI 300
 QY 301 NGRAKIGTVVFFCNSYVLGNEKRTCOQNGEMSGKOPICIAACEPKISDLVRRLV 360
 DB 301 NGRAKIGTVVFFCNSYVLGNEKRTCOQNGEMSGKOPICIAACEPKISDLVRRLV 360
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 QY 421 RLGSRRCTCLATGKMSGRAPSCIPICGKIENITAPKTQGLRWPQOALYRTSGVHGS 480
 DB 421 RLGSRRCTCLATGKMSGRAPSCIPICGKIENITAPKTQGLRWPQOALYRTSGVHGS 480
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 DB 661 CTAETGGIAAVSPGRASPEPRMHLMLGVSVSYDKTCSHRLSTAFTYKLPKDMIEBMMK 720

RESULT 12
 ABUS8033

ID ABUS8033 standard; protein; 720 AA.
 XX AC ABUS8033;
 XX 14-APR-2003 (first entry)
 DT XX
 XX Human PRO polypeptide #65.
 DE XX
 XX Human; PRO; cytosolic; tumour; cancer; breast; lung; stomach; liver;
 KW horse; dog; cat; sheep; pig; goat; rabbit; ADAPT;
 KW antibody-dependent enzyme mediated produg therapy.
 OS Homo sapiens.
 XX
 XX US2003027163-A1.
 XX
 XX 06-FEB-2003.
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 PF 15-NOV-2001; 2001US-00997666.
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Query Match 100.0%; Score 720; DB 6; Length 720;
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DB 61 VVGTTIPCCRNENECOSCLTHPGCTTIFENCKSCRNGSGTLDLDFYKGFYCAECRA 120
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 Db 661 CTAETGGIAAVSPGRASPEPRMIMGLVSVYDKTCSHRLSTAFTVLPFKMWERMK 720
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RESULT 13

ABUS9111
 ID ABUS9111 standard; protein; 720 AA.

AC ABUS9111;
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DT 28-APR-2003 (first entry)
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DE Novel human secreted or transmembrane protein PRO1344.
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KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-Fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disease;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.

OS Homo sapiens.
 XX

PN US2002132252-A1.
 XX

PD 19-SEP-2002.
 XX

PF 14-NOV-2001; 2001US-00990442.
 XX

PR 15-JUN-1997; 97US-0049787P.
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 PR 16-SEP-1998; 98WO-US01330.
 PR 17-SEP-1998; 98WO-US019437.
 PR 07-OCT-1998; 98WO-US021141.
 PR 01-DEC-1998; 98WO-US025108.
 PR 05-JAN-1999; 99WO-US000106.
 PR 08-MAR-1999; 99WO-US005028.
 PR 02-JUN-1999; 99WO-US01252.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 30-NOV-1999; 99WO-US028313.
 PR 01-DEC-1999; 99WO-US028301.
 PR 01-DEC-1999; 99WO-US028634.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 06-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US003565.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 15-MAY-2000; 2000WO-US013358.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.

PR 11-AUG-2000; 2000MO-US022031.
 PR 23-AUG-2000; 2000MO-US023522.
 PR 24-AUG-2000; 2000MO-US023328.
 PR 08-NOV-2000; 2000MO-US030952.
 PR 01-DEC-2000; 2000MO-US032678.
 PR 28-FEB-2001; 2001MO-US006520.
 PR 01-JUN-2001; 2001MO-US017800.
 PR 20-JUN-2001; 2001MO-US019692.
 PR 29-JUN-2001; 2001MO-US021066.
 PR 09-JUL-2001; 2001MO-US021735.
 PR 28-AUG-2001; 2001US-00941992.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gebber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gunney AL, Kljavin IJ, Napier MA, Pan U, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX
 DR WPI: 2003-247083/24.
 DR N-PSDB: ABX80270.
 XX
 PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 PT are therapeutically useful for enhancing immune response and in cancer
 PT treatments.
 XX
 PS Claim 12, Fig 159; 648bp; English.
 XX
 CC The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1346 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonists of this polypeptide are
 CC useful for treating cancerous tumors. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO1068 or PRO1132 enhance survival/proliferation of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 CC and PRO1106 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO110, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and are
 CC thus useful for treating sports injuries, and arthritis. This is the
 CC amino acid sequence of a novel human PRO protein
 XX
 SQ Sequence 720 AA;
 Query Match 100.0%; Score 720; DB 6; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 121 YGDDCKRCGQVLAAPKQIILLESYPLNACSWTIHAKPGFVILQRFVYMLSLBEDYMCQYD 180
 QY 181 YVEVRDNDNDGGQITKRVCGNERPAPIQSIGSSLHLVLFHSDGSKNFGFHAIVEITACS 240
 DB 181 YVEVRDNDNDGGQITKRVCGNERPAPIQSIGSSLHLVLFHSDGSKNFGFHAIVEITACS 240
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 DB 301 NGRHAKIGTVSFFCNNSVYLSGNEKRTCOONGEWSGKQPICIKACREPKISDLVRRVL 360
 QY 361 PMOVQSRFPLHQLYSAFSPKQLQSAFTKPKALPFQDLPMGQHLHTOLQYECISPFYR 420
 DB 361 PMOVQSRFPLHQLYSAFSPKQLQSAFTKPKALPFQDLPMGQHLHTOLQYECISPFYR 420
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 DB 421 RLSSRRRTCLRTGKSGRASCIPICGKIENITAPKTQGLRMPQOALYRTSGVHDSGL 480
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 DB 481 HKGAMFLVCSGALVNEKTVVVAACVTDLGKVTWIKTADLKVVGKFRDDEKTIQS 540
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 DB 541 LQSAIILHNPYDPLLDADIAIILKLDKARISRRVOPICLAASRDISTFQESHITVAG 600
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 DB 661 CTATGGAIVSFFGRASPBRWMLMGLVMSYDKTCSHRLSTAFYVLPFKMNIERNMK 720
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 ID ABU82623 standard; protein; 720 AA.
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 AC ABU82623;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Human secreted/transmembrane protein PRO1344.
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 KW Human; PRO; secreted protein; transmembrane protein;
 KW cardiac insufficiency disorders; angiogenesis; wound healing;
 KW cancerous tumour; immune response; retinal disorder; sight loss;
 KW retinitis pigmentosa; age-related macular degeneration; AMD;
 KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;
 KW Crohn's disease; sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2003032023-A1.
 XX
 PD 13-FEB-2003.
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 PF 14-NOV-2001; 2001US-00990711.
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 PR 16-JUN-1997; 97US-0049787P.
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 PR 05-NOV-1997; 97MO-US02006P.
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PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
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PR 30-NOV-1999; 99WO-US028313.
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 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 06-JAN-2000; 2000WO-US000376.
 PR 11-FEB-2000; 2000WO-US003565.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US004914.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 10-MAR-2000; 2000WO-US006319.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 20-MAR-2000; 2000WO-US007377.
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 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-JUN-2000; 2000US-0213637P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 11-AUG-2000; 2000WO-US022031.

Query Match 100.0%; Score 720; DB 6; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 VVGCTTTPCCGNEBNECDSCIHGCTTIFENCKSCRGSGWGTDDYVVGFGFYCAERAW 120
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 DB 121 YGSDCKRCGQVLAAPKQIILLESYPLNAHCEWTHAKPGFVIOLEFVMSLEEDYICQYD 180
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 DB 181 YVEVDGDNNDGQIIRKVCNEBPAPISIGSSHLVLFHSDGSKNPDGFHAIYEETIACS 240
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 DB 421 RLSSSRRTCLRTKMSGRAPSCPIGCKIENITAPKTQGRMWOAIYRRISGVHDGSL 480
 QY 481 HKGAMFLVSGALVNERTVVAHVAAHCVTDLGKVTMIKTADLVKVLGFRYDDDEDEKTIQS 540
 DB 481 HKGAMFLVSGALVNERTVVAHVAAHCVTDLGKVTMIKTADLVKVLGFRYDDDEDEKTIQS 540
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 DB 541 LQISAILHPNYPILIDADIALKLDKRISTRVQPICTLAASRLDLSFQESHITVAG 600
 QY 601 WNTLADVRSPGKNDTLRSGVSVVDSILCEBOHEHDGIPVSTLDMNFCASWEPTAPSDI 660
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QY 661 CTAETGIAAVSPQCRASPEPRMHLMLGLVSNYDKTCSHRLSTAFFTKVLPKDWIERNMK 720
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RESULT 15
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 DT 27-JUN-2003 (first entry)
 XX
 DE Human PRO polypeptide #85.
 XX
 KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;
 KW chromosome mapping; gene mapping; cytostatic.
 OS Homo sapiens.
 XX
 PN US2003032113-A1.
 PD 13-FEB-2003.
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 PF 20-JUN-2002; 2002US-00176911.
 XX
 PR 18-SEP-1997; 97US-0059263P.
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 PR 17-OCT-1997; 97US-0062250P.
 PR 21-OCT-1997; 97US-0063486P.
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Query Match 100.0%; Score 720; DB 6; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: August 18, 2004, 16:32:15
Job time : 74 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:20:53 ; Search time 42 Seconds
(without alignments)
5408.883 Million cell updates/sec

Title: US-10-063-546-38
Perfect score: 3945
Sequence: 1 MELGCMCTQGLTFQLLLIS.....LSPTFTKVLPEKDMIRBNMK 720

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 700 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP_organelle:*
9: SP_phage:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriap:*
17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	3921.5	99.4	737 4 Q96JW2	Q96JW2 homo sapien
2	3612	91.6	720 11 Q8K2B8	Q8K2B8 mus musculu
3	3612	91.6	720 11 Q8B0Z5	Q8B0Z5 mus musculu
4	949	24.1	181 4 Q9Y432	Q9Y432 homo sapien
5	678	17.2	1019 5 Q8T9A1	Q8T9A1 tachyplesu
6	665	16.9	1083 5 Q264Z3	Q264Z3 carcinoscor
7	608.5	15.4	680 5 Q868H7	Q868H7 branchiosto
8	604	15.3	680 5 Q868H5	Q868H5 branchiosto
9	597	15.1	688 5 Q868H6	Q868H6 branchiosto
10	576.5	14.6	698 5 Q868H4	Q868H4 branchiosto
11	489.5	12.4	698 13 Q9PU71	Q9PU71 xenopus lae
12	483	12.2	701 11 Q9JUS9	Q9JUS9 rattus norv
13	482.5	12.2	703 11 Q8CHN8	Q8CHN8 rattus norv
14	482	12.2	717 13 Q8AXR1	Q8AXR1 xenopus lae
15	468	11.9	728 4 Q96RS4	Q96RS4 homo sapien
16	467	11.8	697 11 Q8CG43	Q8CG43 rattus norv

17	466	11.8	717 13 Q8AXR0	Q8AXR0 xenopus lae
18	459	11.6	733 11 Q8CDZ7	Q8CDZ7 mus musculu
19	457	11.6	719 13 Q9PVY2	Q9PVY2 triakis acy
20	452	11.5	733 11 Q920S0	Q920S0 mus musculu
21	448	11.4	745 13 Q9PVY3	Q9PVY3 cyprinus ca
22	436.5	11.1	681 13 Q7ZT70	Q7ZT70 lampetra ja
23	429	10.9	707 11 Q9ET60	Q9ET60 mus musculu
24	428	10.8	707 11 Q99K16	Q99K16 mus musculu
25	428	10.8	707 11 Q8CG16	Q8CG16 mus musculu
26	424	10.7	678 11 Q9JUS8	Q9JUS8 rattus norv
27	421.5	10.7	688 13 Q9PVY4	Q9PVY4 xenopus lae
28	420	10.6	643 11 Q9QX84	Q9QX84 rattus norv
29	417	10.6	685 11 Q91WPO	Q91WPO mus musculu
30	416.5	10.6	706 11 Q8CF59	Q8CF59 mus musculu
31	412	10.4	685 11 Q923J8	Q923J8 mus musculu
32	401.5	10.2	496 11 Q8CHP7	Q8CHP7 cavia porce
33	401.5	10.2	746 5 Q81AD8	Q81AD8 halocynthia
34	400.5	10.2	746 5 Q01654	Q01654 halocynthia
35	398.5	10.1	686 13 Q9DGC2	Q9DGC2 cyprinus ca
36	395	10.0	721 13 Q7ZT69	Q7ZT69 lampetra ja
37	384	9.7	688 11 Q8CFG8	Q8CFG8 mus musculu
38	382.5	9.7	752 5 Q01655	Q01655 halocynthia
39	382	9.7	722 13 Q8AW90	Q8AW90 lampetra ja
40	381	9.7	722 13 Q9PSZ5	Q9PSZ5 lampetra ja
41	376	9.5	623 11 Q9JJP3	Q9JJP3 rattus norv
42	372.5	9.4	752 5 Q81AD7	Q81AD7 halocynthia
43	371.5	9.4	541 11 Q9QX90	Q9QX90 rattus norv
44	370	9.4	688 11 Q8CG14	Q8CG14 mus musculu
45	369	9.4	694 11 Q8B0C4	Q8B0C4 mus musculu
46	368	9.3	685 13 Q9DGC1	Q9DGC1 cyprinus ca
47	366	9.3	685 13 Q9DGC0	Q9DGC0 cyprinus ca
48	364	9.2	688 11 Q8CH28	Q8CH28 mus musculu
49	364	9.2	694 11 Q8BVY4	Q8BVY4 mus musculu
50	354	9.0	1524 13 Q91674	Q91674 xenopus lae
51	342	8.7	694 11 Q8B099	Q8B099 mus musculu
52	340.5	8.6	449 4 Q8U012	Q8U012 homo sapien
53	340.5	8.6	694 11 Q70542	Q70542 rattus norv
54	334	8.5	503 13 Q8AYE4	Q8AYE4 brachydanio
55	329.5	8.4	3389 4 Q96Q09	Q96Q09 homo sapien
56	329.5	8.4	3566 4 Q96RM4	Q96RM4 homo sapien
57	329	8.3	3564 11 Q923L3	Q923L3 mus musculu
58	318	8.1	3467 4 Q7Z408	Q7Z408 homo sapien
59	316.5	8.0	460 11 Q99PC6	Q99PC6 mus musculu
60	316.5	8.0	460 11 Q91WN8	Q91WN8 mus musculu
61	313	7.9	855 11 Q9JUI7	Q9JUI7 rattus norv
62	311	7.9	446 11 Q8K3U6	Q8K3U6 rattus norv
63	310.5	7.9	434 13 Q7N3B6	Q7N3B6 brachydanio
64	305	7.7	456 6 Q9TTR0	Q9TTR0 canis famli
65	301.5	7.6	433 13 Q8JHD0	Q8JHD0 brachydanio
66	300.5	7.6	446 11 Q61109	Q61109 mus musculu
67	299	7.6	1111 11 Q80YN4	Q80YN4 rattus norv
68	298.5	7.6	433 13 Q90YK1	Q90YK1 brachydanio
69	297.5	7.5	777 11 Q8CAN9	Q8CAN9 mus musculu
70	295.5	7.5	336 11 Q8CIR9	Q8CIR9 mus musculu
71	295.5	7.5	441 13 Q804X2	Q804X2 fugu rubrip
72	295	7.5	425 13 Q804X7	Q804X7 gallus gall
73	293	7.4	430 13 Q804X0	Q804X0 fugu rubrip
74	291.5	7.4	516 4 Q9BU99	Q9BU99 homo sapien
75	291	7.4	475 13 Q804W9	Q804W9 fugu rubrip
76	284	7.2	974 13 Q9NWD8	Q9NWD8 buto japoni
77	283.5	7.2	482 11 Q63207	Q63207 rattus norv
78	282.5	7.2	320 11 Q63207	Q63207 rattus norv
79	282	7.1	469 6 Q9GMD9	Q9GMD9 ornithorhyn
80	282	7.1	1466 13 Q7Z241	Q7Z241 brachydanio
81	281	7.1	481 11 Q99L32	Q99L32 mus musculu
82	281	7.1	481 11 Q8B947	Q8B947 mus musculu
83	280.5	7.1	269 4 Q81WMO	Q81WMO homo sapien
84	280	7.1	562 4 Q86YK8	Q86YK8 homo sapien
85	278	7.0	408 5 Q9VW19	Q9VW19 drosophiila
86	278	7.0	433 13 Q804X5	Q804X5 gallus gall
87	276.5	7.0	679 4 Q96P08	Q96P08 homo sapien
88	276	7.0	481 11 Q54740	Q54740 mus musculu
89	274.5	7.0	3501 4 Q7Z407	Q7Z407 homo sapien

90	273.5	6.9	443	13	Q8H9C9	Q8h9c brachydanio	163	242.5	6.1	574	5	Q86RL8	Q86rl8 llyanasea o
91	273.5	6.9	517	11	Q8K0D2	Q8k0d mus musculu	164	242.5	6.1	691	13	Q57658	Q57658 gallus gall
92	273	6.9	366	11	Q9OX85	Q9ox8 rattus norv	165	242.5	6.1	1019	13	Q57382	Q57382 xenopus lae
93	273	6.9	560	4	Q14520	Q14520 homo sapien	166	241.5	6.1	279	11	Q99MS4	Q99ms4 mus musculu
94	273	6.9	2796	11	Q80T79	Q80t79 mus musculu	167	241.5	6.1	416	4	Q86T26	Q86t26 homo sapien
95	271	6.9	433	6	Q8M1LO	Q8m1l oryctolagus	168	241	6.1	1415	6	Q8MJ16	Q8mj16 bos taurus
96	271	6.9	433	6	Q8MHY7	Q8mhy7 oryctolagus	169	240.5	6.1	238	13	Q8WVQ6	Q8wvq6 paralicthys
97	269	6.8	643	6	Q97506	Q97506 sus scrofa	170	240.5	6.1	422	4	Q8WVCI	Q8wvc1 homo sapien
98	269	6.8	833	5	Q96442	Q96442 strongyloce	171	240	6.1	242	13	Q92099	Q92099 parasciothe
99	267	6.8	339	11	Q9QX91	Q9qx91 rattus norv	172	240	6.1	1059	4	Q72411	Q72411 homo sapien
100	267	6.8	435	13	Q7SY86	Q7sy86 xenopus lae	173	239.5	6.1	240	13	Q98TH0	Q98th0 engraulis j
101	267	6.8	868	5	Q9Y1V3	Q9y1v3 polyandroc	174	239.5	6.1	926	4	Q9UQ00	Q9uq00 homo sapien
102	265.5	6.7	250	5	Q9V514	Q9v514 drosophila	175	239.5	6.1	1015	4	Q9Y6L7	Q9y6l7 homo sapien
103	263.5	6.7	263	13	Q7SX97	Q7sxc97 brachydanio	176	239.5	6.1	3567	11	Q9SE77	Q9se77 mus musculu
104	263	6.7	653	11	Q8VCS4	Q8vcs4 mus musculu	177	239	6.1	977	13	Q91925	Q91925 xenopus lae
105	262.5	6.7	300	5	Q819P4	Q819p4 aurelia aur	178	238.5	6.0	268	5	Q46151	Q46151 pacifastacu
106	262.5	6.7	461	6	Q9SND7	Q9snd7 pan troglod	179	238.5	6.0	946	4	Q96QJ3	Q96qj3 homo sapien
107	261.5	6.6	284	13	Q8AX08	Q8axq8 xenopus lae	180	238	6.0	435	5	Q9NFX2	Q9nfx2 anopheles g
108	260.5	6.6	264	11	Q9EQZ8	Q9eqz8 rattus norv	181	238	6.0	767	13	Q9DGR2	Q9dgr2 xenopus lae
109	260.5	6.6	456	11	Q7TT43	Q7tt43 mus musculu	182	237.5	6.0	735	13	Q57381	Q57381 xenopus lae
110	259	6.6	474	13	Q8THC8	Q8thc8 brachydanio	183	237	6.0	237	13	Q91515	Q91515 fugu rubrip
111	259	6.6	581	5	Q9XZM7	Q9xzm7 strongyloce	184	235	6.0	761	11	Q93YC8	Q93yc8 rattus norv
112	258.5	6.6	683	5	Q8MRH5	Q8mrh5 drosophila	185	235.5	6.0	1013	11	Q92381	Q92381 mus musculu
113	258.5	6.6	787	5	Q9VEY6	Q9vey6 drosophila	186	235.5	6.0	260	13	Q9W7Q3	Q9w7q3 paralicthys
114	258	6.5	263	13	Q9PMQ6	Q9pmq6 gadus morhu	187	235.5	6.0	453	11	Q812A6	Q812a6 mus musculu
115	258	6.5	612	13	Q804W7	Q804w7 fugu rubrip	188	235	6.0	524	6	Q28800	Q28800 pan troglod
116	257.5	6.5	1004	13	P79953	P79953 xenopus lae	189	235	6.0	812	11	Q9R0W3	Q9r0w3 brachydanio
117	256.5	6.5	264	11	Q9D7P8	Q9d7p8 mus musculu	190	235	6.0	395	4	Q9BZW1	Q9bzw1 homo sapien
118	256.5	6.5	264	11	Q9ER05	Q9er05 mus musculu	191	234.5	5.9	624	11	Q9D4T3	Q9d4t3 mus musculu
119	255.5	6.5	763	7	Q31430	Q31430 lampetra ja	192	234.5	5.9	575	5	Q81R88	Q81rb8 drosophila
120	255	6.5	325	5	Q15944	Q15944 sarcophaga	193	234	5.9	267	13	Q7S251	Q7s251 brachydanio
121	254.5	6.5	315	11	Q7TT44	Q7tt44 mus musculu	194	233.5	5.9	420	13	Q90504	Q90504 eplatretus
122	254.5	6.5	461	6	Q9SND6	Q9snd6 pan troglod	195	233.5	5.9	273	6	Q9XSM1	Q9xsm1 ovis aries
123	254	6.4	314	4	Q9VR15	Q9vr15 drosophila	196	233	5.9	445	11	Q8CJ17	Q8cj17 rattus norv
124	253.5	6.4	487	4	Q9NZP8	Q9nzp8 homo sapien	197	233	5.9	936	5	Q81FX2	Q81fx2 caesostrea
125	253.5	6.4	1048	4	Q9VEP7	Q9ver7 drosophila	198	232.5	5.9	1013	4	Q9NQ84	Q9nq84 homo sapien
126	253.5	6.4	628	4	Q96PZ6	Q96p27 homo sapien	199	232.5	5.9	200	13	Q43897	Q43897 homo sapien
127	253	6.4	471	13	Q804X6	Q804x6 gallus gall	200	232.5	5.9	270	13	Q91039	Q91039 gadus morhu
128	253	6.4	616	6	Q97507	Q97507 sus scrofa	201	231.5	5.9	371	11	Q8CJ16	Q8cj16 rattus norv
129	253	6.4	1070	5	P91972	P91972 aplysia cal	202	231.5	5.9	483	5	Q8TRX4	Q8trx4 drosophila
130	251	6.4	295	11	Q8C1P7	Q8c1p7 rattus norv	203	231.5	5.9	483	5	Q9VK10	Q9vkl0 drosophila
131	251	6.4	537	13	Q804W8	Q804w8 fugu rubrip	204	231.5	5.9	624	6	Q95ME7	Q95me7 oryctolagus
132	250	6.3	562	6	Q8EQ23	Q8eq23 sus scrofa	205	231.5	5.9	242	13	Q93266	Q93266 pseudopleur
133	250	6.3	1379	5	Q9VAN6	Q9van6 drosophila	206	231	5.9	1008	11	Q9WY65	Q9wyt6 gallus gall
134	249.5	6.3	400	5	Q27081	Q27081 tachyleus	207	231	5.9	231	13	Q9DER7	Q9der7 gallus gall
135	249	6.3	263	11	Q9CR35	Q9cr35 mus musculu	208	231	5.9	1012	11	Q9WM65	Q9wm65 mus musculu
136	248	6.3	261	13	Q9W7Q4	Q9w7q4 paralicthys	209	230	5.8	244	13	Q8QCM3	Q8qcm3 anguilla ja
137	248	6.3	540	13	Q800Y7	Q800y7 melagris g	210	230	5.8	265	5	Q9VVT3	Q9vvt3 drosophila
138	248	6.3	764	6	Q864W0	Q864w0 pan troglod	211	230	5.8	372	5	Q9Y1K6	Q9y1k6 anopheles g
139	247.5	6.3	307	11	Q7TML0	Q7tml0 mus musculu	212	230	5.8	607	13	Q91001	Q91001 gallus gall
140	247.5	6.3	311	5	Q9W2C2	Q9w2c2 drosophila	213	229.5	5.8	374	5	Q9VUC2	Q9vuc2 drosophila
141	247	6.3	235	6	Q28731	Q28731 oryctolagus	214	229.5	5.8	624	11	Q9BK47	Q9bk47 mus musculu
142	247	6.3	364	5	Q917V4	Q917v4 drosophila	215	229	5.8	267	5	Q9BK47	Q9bk47 luidia foli
143	247	6.3	386	5	Q81924	Q81924 bombix mori	216	229	5.8	274	11	Q924N9	Q924n9 mus musculu
144	246.5	6.2	235	13	Q90387	Q90387 cyrops pyrr	217	229	5.8	733	5	Q9VTRX	Q9vtrx drosophila
145	246.5	6.2	264	11	Q9D960	Q9d960 mus musculu	218	229	5.8	845	13	Q9DGR1	Q9dgr1 xenopus lae
146	246.5	6.2	297	11	Q88781	Q88781 rattus ratl	219	228.5	5.8	347	11	Q63927	Q63927 mus sp. hap
147	246.5	6.2	323	4	Q96QG4	Q96qg4 homo sapien	220	228.5	5.8	600	5	Q17480	Q17480 anopheles g
148	246.5	6.2	622	4	Q727P3	Q727p3 homo sapien	221	228.5	5.8	1084	5	Q9BP40	Q9bp40 halocynthia
149	246	6.2	263	11	Q9D8X8	Q9d8x8 mus musculu	222	228.5	5.8	2516	11	Q7TQ52	Q7tq52 mus musculu
150	246	6.2	764	6	Q864V9	Q864v9 gorilla gor	223	228.5	5.8	2526	11	Q7TQ51	Q7tq51 mus musculu
151	245.5	6.2	265	13	Q804G1	Q804g1 brachydanio	224	228.5	5.8	2531	11	Q8K428	Q8k428 mus musculu
152	245.5	6.2	467	5	Q967X8	Q967x8 panulirus a	225	228.5	5.8	3687	5	Q9M132	Q9m132 mus musculu
153	245	6.2	638	11	Q8R0P5	Q8r0p5 mus musculu	226	228	5.8	235	13	Q91004	Q91004 gecko gecko
154	244.5	6.2	608	13	Q9PTW7	Q9ptw7 struthio ca	227	227.5	5.8	349	6	Q28802	Q28802 pan troglod
155	244	6.2	263	11	Q9DC86	Q9dc86 mus musculu	228	227.5	5.8	385	4	Q92659	Q92659 homo sapien
156	244	6.2	322	11	Q920S2	Q920s2 mus musculu	229	227.5	5.8	263	13	Q7S954	Q7s954 xenopus lae
157	243.5	6.2	285	11	Q8CG42	Q8cg42 rattus norv	230	227	5.8	275	6	Q7YS62	Q7ys62 equus cabal
158	243.5	6.2	435	5	Q9VFZ7	Q9vfz7 drosophila	231	227	5.8	336	11	Q80YD8	Q80yd8 mus musculu
159	243	6.2	764	6	Q864W1	Q864w1 pongo pygma	232	227	5.8	417	11	Q8BZ10	Q8bz10 mus musculu
160	243	6.2	282	11	Q9PD413	Q9pd413 mus musculu	233	227	5.8	488	5	Q9TYH4	Q9tyh4 echiscosoma
161	243	6.1	442	13	Q804X1	Q804x1 fugu rubrip	234	227	5.8	1464	5	Q23995	Q23995 drosophila
162	242.5	6.1	564	6	Q8MKB1	Q8mbk1 oryctolagus	235	227	5.8				

236	227	5.8	1464	5	Q9VC47	Q9VC47 drosophila	309	215	5.4	1116	11	Q7TP05	Q7TP05 rattus norv
237	237	5.8	1464	5	Q24132	Q24132 drosophila	310	214.5	5.4	195	5	Q819P3	Q819P3 aurelia aur
238	226.5	5.7	257	11	Q8B204	Q8B204 mus musculus	311	214.5	5.4	366	11	Q70170	Q70170 mus musculus
239	226.5	5.7	371	5	Q8MS52	Q8MS52 drosophila	312	214.5	5.4	505	5	Q966V4	Q966V4 halocynthia
240	226.5	5.7	855	4	Q72410	Q72410 homo sapien	313	214.5	5.4	1322	5	Q9NAT0	Q9NAT0 anopheles g
241	226	5.7	405	4	Q96E86	Q96E86 homo sapien	314	214	5.4	810	4	Q15146	Q15146 homo sapien
242	225.5	5.7	418	5	Q8SKX2	Q8SKX2 drosophila	315	213.5	5.4	241	13	Q98T99	Q98T99 engraulis j
243	225.5	5.7	418	5	Q9VA87	Q9VA87 drosophila	316	213.5	5.4	248	5	Q9VOT8	Q9VOT8 drosophila
244	225.5	5.7	429	13	Q8AVB0	Q8AVB0 brachydanto	317	213.5	5.4	423	11	Q8BM10	Q8BM10 mus musculus
245	225	5.7	328	11	Q80Z40	Q80Z40 rattus norv	318	213.5	5.4	2352	5	Q61240	Q61240 halocynthia
246	225	5.7	387	5	Q9XY57	Q9XY57 ctenocephal	319	213	5.4	355	5	Q9NFT1	Q9NFT1 anopheles g
247	225	5.7	455	11	Q8CDR0	Q8CDR0 mus musculus	320	213	5.4	394	5	P91817	P91817 tachyples
248	225	5.7	490	11	Q920X3	Q920X3 rattus norv	321	213	5.4	615	5	Q81Z25	Q81Z25 homo sapien
249	225	5.7	490	11	Q7TN04	Q7TN04 mus musculus	322	212.5	5.4	327	4	Q8N171	Q8N171 homo sapien
250	224.5	5.7	266	11	Q8B301	Q8B301 mus musculus	323	212.5	5.4	339	11	Q91L44	Q91L44 mus musculus
251	224.5	5.7	251	11	Q54854	Q54854 rattus norv	324	212.5	5.4	778	5	Q9V519	Q9V519 drosophila
252	224.5	5.7	251	11	Q54854	Q54854 rattus norv	325	212	5.4	340	11	Q8BVT6	Q8BVT6 mus musculus
253	224.5	5.7	1437	11	Q91Y82	Q91Y82 mus musculus	326	212	5.4	1322	5	Q9NUS5	Q9NUS5 anopheles g
254	224	5.7	1237	11	Q8V1B7	Q8V1B7 mesocricetu	327	211	5.3	237	6	Q29464	Q29464 bos tauru
255	224	5.7	242	13	Q8AV11	Q8AV11 oncorhynch	328	211	5.3	2447	13	Q13149	Q13149 fuigu rubrip
256	224	5.7	242	13	Q7T1R8	Q7T1R8 pangasius h	329	210.5	5.3	360	5	Q9W1X6	Q9W1X6 drosophila
257	224	5.7	174	5	Q9VTR4	Q9VTR4 drosophila	330	210.5	5.3	505	4	Q8N963	Q8N963 homo sapien
258	223.5	5.7	234	13	Q90244	Q90244 acipenser c	331	210.5	5.3	754	6	Q28290	Q28290 canis famli
259	223.5	5.7	266	13	Q9W7Q0	Q9W7Q0 parailichthy	332	209.5	5.3	313	5	Q81N51	Q81N51 drosophila
260	223.5	5.7	1599	5	Q9V513	Q9V513 drosophila	333	209.5	5.3	321	4	Q9ERZ8	Q9ERZ8 homo sapien
261	223.5	5.7	1674	5	Q8SY35	Q8SY35 drosophila	334	209.5	5.3	1441	4	Q723G3	Q723G3 homo sapien
262	222.5	5.6	412	13	Q9W7Q7	Q9W7Q7 parailichthy	335	209	5.3	384	13	Q9W630	Q9W630 cyprinus ca
263	222.5	5.6	273	5	Q9VUP0	Q9VUP0 drosophila	336	208.5	5.3	236	5	Q9YTH3	Q9YTH3 schistosoma
264	222	5.6	267	5	Q9V940	Q9V940 drosophila	337	208.5	5.3	258	6	Q28B03	Q28B03 pan troglod
265	222	5.6	273	11	Q9V940	Q9V940 drosophila	338	208.5	5.3	279	11	Q7TNX3	Q7TNX3 mus musculus
266	222	5.6	275	4	Q8ETM8	Q8ETM8 homo sapien	339	208.5	5.3	311	11	Q80XV3	Q80XV3 rattus norv
267	222	5.6	276	4	Q8EUM5	Q8EUM5 homo sapien	340	208.5	5.3	417	11	Q8VDM1	Q8VDM1 mus musculus
268	221.5	5.6	271	13	Q803Z4	Q803Z4 brachydanto	341	208.5	5.3	417	11	Q8VHK8	Q8VHK8 mus musculus
269	221.5	5.6	3620	6	Q9TUS3	Q9TUS3 canis famli	342	208.5	5.3	444	5	Q9V4W6	Q9V4W6 mus musculus
270	221	5.6	258	5	Q97399	Q97399 phaeton coc	343	208.5	5.3	471	11	Q8CPR0	Q8CPR0 mus musculus
271	221	5.6	258	5	P91658	P91658 drosophila	344	208	5.3	256	5	Q25082	Q25082 hypoderma 1
272	220.5	5.6	242	11	Q80VS4	Q80VS4 mus musculus	345	208	5.3	271	6	Q8H1J2	Q8H1J2 bos tauru
273	220.5	5.6	250	11	Q8CGR5	Q8CGR5 mus musculus	346	208	5.3	275	4	Q81XD7	Q81XD7 homo sapien
274	220.5	5.6	277	11	Q80MM7	Q80MM7 mus musculus	347	208	5.3	558	4	Q8NFM6	Q8NFM6 homo sapien
275	220.5	5.6	360	5	Q17489	Q17489 anopheles g	348	207.5	5.3	195	4	Q8U006	Q8U006 homo sapien
276	220.5	5.6	408	5	Q9UDG3	Q9UDG3 pacifiaacu	349	207.5	5.3	239	13	Q91218	Q91218 oncorhynch
277	220.5	5.6	488	5	Q7YU36	Q7YU36 drosophila	350	207.5	5.3	266	13	Q20277	Q20277 gadus morhu
278	220	5.6	260	13	Q9W7P9	Q9W7P9 parailichthy	351	207.5	5.3	298	5	Q9NHO6	Q9NHO6 heliothis z
279	220	5.6	261	5	Q962G7	Q962G7 culx pipie	352	207.5	5.3	1282	5	Q8TER0	Q8TER0 homo sapien
280	220	5.6	331	11	Q8B1A5	Q8B1A5 mus musculus	353	207	5.2	240	13	Q7SYO8	Q7SYO8 mus musculus
281	220	5.6	331	11	Q80X17	Q80X17 mus musculus	354	206.5	5.2	269	4	Q96C0V5	Q96C0V5 homo sapien
282	219.5	5.6	228	13	Q7S2T1	Q7S2T1 xenopus lae	355	206.5	5.2	269	5	Q9Y929	Q9Y929 drosophila
283	219.5	5.6	255	5	Q961Y0	Q961Y0 galleria me	356	206.5	5.2	270	5	Q27824	Q27824 uca pugilic
284	219	5.6	318	11	Q80UR4	Q80UR4 mus musculus	357	206.5	5.2	284	4	Q8NFM6	Q8NFM6 homo sapien
285	219	5.5	365	5	Q97366	Q97366 holotrichia	358	206.5	5.2	467	4	Q86WX2	Q86WX2 homo sapien
286	218.5	5.5	374	5	Q81862	Q81862 dermacentor	359	206.5	5.2	573	5	Q9V516	Q9V516 drosophila
287	218.5	5.5	375	5	Q817W8	Q817W8 dermacentor	360	206.5	5.2	1065	11	Q810H2	Q810H2 agrotis ips
288	218.5	5.5	1007	13	Q8U128	Q8U128 xenopus lae	361	206	5.2	263	5	Q9N892	Q9N892 chironomus
289	218	5.5	242	13	Q78X90	Q78X90 brachydanto	362	206	5.2	492	5	Q72155	Q72155 chironomus
290	218	5.5	271	2	Q54213	Q54213 streptomyc	363	205.5	5.2	374	11	Q80YD5	Q80YD5 mus musculus
291	217	5.5	275	4	Q96RZ6	Q96RZ6 homo sapien	364	205.5	5.2	416	11	Q8B230	Q8B230 mus musculus
292	217	5.5	597	11	Q35727	Q35727 mus musculus	365	205.5	5.2	416	11	Q8B213	Q8B213 mus musculus
293	216.5	5.5	277	5	Q96899	Q96899 scolopendra	366	205	5.2	264	5	Q02569	Q02569 culx quing
294	216.5	5.5	346	6	Q28801	Q28801 pan troglod	367	205	5.2	492	4	Q96T73	Q96T73 homo sapien
295	216.5	5.5	2528	13	Q8AXP0	Q8AXP0 cynops pyr	368	205	5.2	814	5	Q810G6	Q810G6 drosophila
296	216.5	5.5	2616	5	Q9V8P5	Q9V8P5 drosophila	369	204.5	5.2	216	11	Q9QX63	Q9QX63 rattus norv
297	216	5.5	255	11	Q7TNI0	Q7TNI0 mus musculus	370	204.5	5.2	247	11	Q9D7Y7	Q9D7Y7 mus musculus
298	216	5.5	269	11	Q9D7T9	Q9D7T9 mus musculus	371	204.5	5.2	247	11	Q9CPN9	Q9CPN9 mus musculus
299	216	5.5	269	11	Q9C052	Q9C052 mus musculus	372	204.5	5.2	281	5	Q46137	Q46137 lumbricus r
300	215.5	5.5	243	5	Q9TXD8	Q9TXD8 agelenopsis	373	204.5	5.2	367	11	Q70169	Q70169 mus musculus
301	215.5	5.5	254	11	Q8CGR4	Q8CGR4 mus musculus	374	204.5	5.2	449	5	Q9SRA3	Q9SRA3 drosophila
302	215.5	5.5	321	11	Q80Y38	Q80Y38 mus musculus	375	204.5	5.2	510	4	Q9H4V1	Q9H4V1 homo sapien
303	215.5	5.5	326	11	Q9D9M0	Q9D9M0 mus musculus	376	204.5	5.2	752	6	Q8SQ75	Q8SQ75 pongo pygma
304	215	5.4	256	5	Q25081	Q25081 hypoderma 1	377	204.5	5.2	1497	4	Q8NBT9	Q8NBT9 homo sapien
305	215	5.4	609	13	Q9PVX7	Q9PVX7 xenopus lae	378	204	5.2	367	11	Q9QXD2	Q9QXD2 mus musculus
306	215	5.4	609	11	Q80YC5	Q80YC5 mus musculus	379	204	5.2	417	11	Q8VHU4	Q8VHU4 rattus norv
307	215	5.4	749	13	Q9YGE8	Q9YGE8 oncorhynch	380	203.5	5.2	195	4	Q81XB4	Q81XB4 homo sapien
308	215	5.4	760	13	Q8JG08	Q8JG08 tetraodon n	381	203.5	5.2	261	4	Q7Z5F3	Q7Z5F3 homo sapien

382	203.5	5.2	309	5	Q27083	Q27083 tachyleus	455	195.5	5.0	752	6	Q8S074	Q8eq74 pan troglod
383	203.5	5.2	335	11	Q8VIF2	Q8vif2 mus musculu	456	195	4.9	262	5	Q7Z0C3	Q7z0c3 phlebotomus
384	203.5	5.2	664	13	Q8IAT6	Q8iat6 brachydantio	457	195	4.9	276	4	Q8BRH3	Q8brh3 homo sapien
385	203.5	5.2	750	13	Q8W633	Q8w633 cyprinus ca	458	194.5	4.9	246	11	Q9ROT7	Q9rot7 mus musculu
386	203.5	5.2	1123	4	Q7Z387	Q7z387 homo sapien	459	194.5	4.9	261	4	Q7Z5F4	Q7z5f4 homo sapien
387	203.5	5.2	1332	11	Q9J866	Q9j866 rattus norv	460	194.5	4.9	283	5	Q9SV22	Q9sv22 lumbricus b
388	203.5	5.2	3623	4	Q6O494	Q6o494 homo sapien	461	194.5	4.9	1374	5	Q9VUS0	Q9vu0 drosophila
389	203	5.1	177	11	Q9OX86	Q9ox86 rattus norv	462	194.5	4.9	1449	5	Q9UI12	Q9ui12 drosophila
390	203	5.1	185	11	Q9OX88	Q9ox88 rattus norv	463	194.5	4.9	1450	5	Q8IOQ8	Q8iod8 drosophila
391	203	5.1	185	11	Q9OX84	Q9ox84 mus musculu	464	194.5	4.9	1462	5	Q9UI13	Q9ui13 drosophila
392	203	5.1	186	11	Q9OXD4	Q9oxd4 rattus norv	465	194.5	4.9	2382	5	Q9BII9	Q9bi19 drosophila
393	203	5.1	370	5	Q9VA44	Q9va44 drosophila	466	194.5	4.9	2409	5	Q9B0G6	Q9b0g6 drosophila
394	203	5.1	403	16	Q9XS06	Q9xsg6 vibrio chol	467	194.5	4.9	2428	5	Q8I6X6	Q8i6x6 boophilus m
395	203	5.1	537	4	Q9BVE1	Q9bve1 homo sapien	468	194.5	4.9	2786	5	Q9SVU2	Q9svu2 drosophila
396	203	5.1	581	4	Q9BYE2	Q9bye2 homo sapien	469	194	4.9	245	13	Q42160	Q42160 drosophila
397	203	5.1	833	13	Q9YIC5	Q9yic5 cyrinus ca	470	194	4.9	253	5	Q9VAG3	Q9vag3 petromyzon
398	202.5	5.1	239	4	Q8NIC9	Q8nic9 homo sapien	471	194	4.9	514	4	Q9EPZ3	Q9epz3 homo sapien
399	202.5	5.1	274	5	Q8I133	Q8i133 anopheles s	472	194	4.9	556	13	Q8O3D5	Q8o3d5 brachydantio
400	202.5	5.1	372	5	Q9W2C8	Q9w2c8 drosophila	473	194	4.9	806	6	Q18783	Q18783 macropus eu
401	202	5.1	190	11	Q9QXD5	Q9qxd5 mus musculu	474	193.5	4.9	246	11	Q9OUK9	Q9ouk9 mus musculu
402	202	5.1	488	13	Q8IUV8	Q8iuv8 homo sapien	475	193.5	4.9	247	13	Q9W7O5	Q9w7o5 paralicthy
403	202	5.1	743	13	Q9YGE7	Q9yge7 oncorhynch	476	193.5	4.9	256	5	Q27540	Q27540 charitomeu
404	201.5	5.1	195	4	Q8U008	Q8u008 homo sapien	477	193.5	4.9	267	5	Q9V3X7	Q9v3x7 drosophila
405	201.5	5.1	195	4	Q8U007	Q8u007 homo sapien	478	193.5	4.9	317	13	Q9DGR3	Q9dgr3 xenopus lae
406	201.5	5.1	320	13	Q7TOX2	Q7tox2 xenopus lae	479	193.5	4.9	830	4	Q8IVD1	Q8ivd1 homo sapien
407	201	5.1	247	13	Q8I6O8	Q8i6o8 homo sapien	480	193.5	4.9	790	4	Q8IT3A0	Q8it3a0 clones infes
408	201	5.1	260	4	Q8IM69	Q8im69 homo sapien	481	193.5	4.9	258	6	Q86780	Q86780 canis famli
409	201	5.1	351	5	Q8I6K0	Q8i6k0 holotrichia	482	193	4.9	268	5	Q86780	Q86780 canis famli
410	201	5.1	392	5	Q9VMZ3	Q9vmz3 drosophila	483	193	4.9	268	5	Q9X156	Q9x156 ctenocephal
411	200.5	5.1	175	4	Q9UMV3	Q9umv3 homo sapien	484	193	4.9	269	6	Q9SKW7	Q9skw7 bos taurus
412	200.5	5.1	249	13	Q9W7Q1	Q9w7q1 paralicthy	485	193	4.9	423	13	Q57433	Q57433 figu rubrip
413	200.5	5.1	358	13	Q57434	Q57434 figu rubrip	486	193	4.9	481	4	Q9H284	Q9h284 homo sapien
414	200.5	5.1	951	5	Q9UKZ9	Q9ukz9 homo sapien	487	193	4.9	962	11	Q8C420	Q8c420 mus musculu
415	200.5	5.1	951	5	Q20176	Q20176 caenothabi	488	192.5	4.9	178	13	Q93594	Q93594 dicentrarch
416	200	5.1	247	13	Q421E8	Q421e8 petromyzon	489	192.5	4.9	232	5	Q94508	Q94508 dermatophag
417	200	5.1	504	6	Q4E506	Q4e506 papio hamad	490	192.5	4.9	246	11	Q9Z1R9	Q9z1r9 mus musculu
418	200	5.1	545	5	Q9VFM0	Q9vfm0 drosophila	491	192.5	4.9	247	4	Q8NHM4	Q8nhm4 homo sapien
419	199.5	5.1	223	5	Q9VBV4	Q9vbv4 drosophila	492	192.5	4.9	249	11	Q9OYN4	Q9oyn4 mus musculu
420	199.5	5.1	258	6	Q28508	Q28508 macaca mula	493	192.5	4.9	276	11	Q9OYN3	Q9oyn3 m hippocas
421	199.5	5.1	348	4	Q8KWS5	Q8kws5 homo sapien	494	192.5	4.9	381	5	Q8MOY4	Q8moy4 drosophila
422	199.5	5.1	378	13	Q9OWP0	Q9owp0 trachemys s	495	192.5	4.9	438	4	Q8H804	Q8h804 homo sapien
423	199.5	5.1	1193	13	Q20819	Q20819 gallus gall	496	192.5	4.9	754	13	F79816	F79816 oryzias lat
424	199.5	5.1	1175	11	Q9PPW0	Q9ppw0 rattus norv	497	192	4.9	244	13	Q42159	Q42159 petromyzon
425	199.5	5.1	253	5	Q25253	Q25253 lucilia cup	498	192	4.9	246	5	Q9BL17	Q9bl17 lumbricus r
426	199	5.0	263	5	Q6Z562	Q6z562 penaeus van	499	192	4.9	254	5	Q9XYX0	Q9xyx0 rhyzopercha
427	199	5.0	264	13	Q8QGF6	Q8qgf6 xenopus lae	500	192	4.9	380	5	Q9YIK5	Q9yik5 anopheles g
428	199	5.0	441	5	Q9XXV0	Q9xxv0 bombyx mori	501	192	4.9	383	5	Q77102	Q77102 manduca rex
429	198.5	5.0	181	4	Q9ULC7	Q9ulc7 homo sapien	502	191.5	4.9	247	5	Q77039	Q77039 anopheles g
430	198.5	5.0	237	5	Q17035	Q17035 anopheles g	503	191.5	4.9	281	5	Q76898	Q76898 drosophila
431	198.5	5.0	260	13	Q7SZC3	Q7szc3 gallus gall	504	191.5	4.9	284	5	Q8IRX5	Q8irx5 drosophila
432	198.5	5.0	279	11	Q9QZ74	Q9qz74 rattus norv	505	191.5	4.9	360	5	Q8SX54	Q8sx54 drosophila
433	198.5	5.0	364	5	Q9NNS9	Q9nas9 anopheles g	506	191.5	4.9	385	5	Q8SX54	Q8sx54 drosophila
434	198.5	5.0	388	5	Q44330	Q44330 manduca rex	507	191.5	4.9	579	4	Q96D09	Q96d09 drosophila
435	198.5	5.0	461	5	Q8T4N2	Q8t4n2 rhipicephal	508	191.5	4.9	713	11	Q8D0F0	Q8d0f0 homo sapien
436	198.5	5.0	752	6	Q8E3A0	Q8e3a0 xenopus lae	509	191.5	4.9	2468	13	Q8MOE4	Q8moe4 brachydantio
437	198.5	5.0	1214	13	Q9OYD2	Q9oyd2 anopheles g	510	191.5	4.9	3396	5	Q9VMS5	Q9vms5 drosophila
438	197.5	5.0	255	4	Q9ER00	Q9er00 homo sapien	511	191	4.8	255	5	Q25227	Q25227 lucilia cup
439	197.5	5.0	258	6	Q28805	Q28805 pan troglod	512	191	4.8	256	5	Q8I8B5	Q8i8b5 ochlerotatu
440	197	5.0	222	11	Q9IWM0	Q9iwm0 rattus norv	513	191	4.8	277	5	Q8IOJ0	Q8ioj0 drosophila
441	197	5.0	236	4	Q9H4V7	Q9h4v7 homo sapien	514	191	4.8	317	11	Q8K4D1	Q8k4d1 mus musculu
442	197	5.0	261	5	Q9VXC7	Q9vxc7 drosophila	515	191	4.8	317	11	Q8K4I7	Q8k4i7 mus musculu
443	197	5.0	421	5	Q9SR86	Q9s86 drosophila	516	191	4.8	415	5	Q9GRW0	Q9grw0 holotrichia
444	197	5.0	585	5	Q9U0E2	Q9u0e2 ciribolium c	517	191	4.8	646	6	Q29097	Q29097 sus scrofa
445	197	5.0	745	13	Q9I701	Q9i701 xenopus lae	518	190.5	4.8	579	4	Q8I8B3	Q8i8b3 aedes polyn
446	197	5.0	760	11	Q7O350	Q7o350 mus musculu	519	190.5	4.8	579	4	Q9BY79	Q9by79 homo sapien
447	196.5	5.0	219	13	Q9I036	Q9i036 gadus morhu	520	190.5	4.8	762	13	Q9YIC6	Q9yic6 cyprinus ca
448	196.5	5.0	259	5	Q8IRB0	Q8irb0 drosophila	521	190	4.8	243	4	Q86VU5	Q86v5 homo sapien
449	196.5	5.0	298	5	Q8T4N4	Q8t4n4 rhipicephal	522	190	4.8	253	4	Q8W2B4	Q8w2b4 homo sapien
450	196	5.0	400	5	Q9GRG2	Q9grg2 tenebrio mo	523	190	4.8	277	6	Q8SQ44	Q8sq44 sus scrofa
451	196	5.0	3623	11	Q7O244	Q7o244 rattus norv	524	190	4.8	282	5	Q25395	Q25395 lumbricus r
452	195.5	5.0	267	5	Q9GP27	Q9gp27 drosophila	525	190	4.8	334	6	Q46507	Q46507 papio hamad
453	195.5	5.0	274	5	Q17086	Q17086 anopheles s	526	190	4.8	378	5	Q8SV50	Q8sv50 drosophila
454	195.5	5.0	276	5	Q18443	Q18443 helicoverpa	527	190	4.8	414	11	Q8R4W6	Q8r4w6 mus musculu

528	189.5	4.8	241	11	Q92135	Q92135 rattus norv	601	182.5	4.6	257	5	Q81883	Q81883 aedes albop
529	189.5	4.8	255	3	Q9Y7A9	Q9Y7A9 metarhizium	602	182.5	4.6	274	5	Q9VRS7	Q9VRS7 dirosophila
530	189.5	4.8	257	5	Q27440	Q27440 aedes aegy	603	182.5	4.6	295	5	Q9NRC6	Q9NRC6 heliothis z
531	189.5	4.8	258	6	Q28804	Q28804 pan troglod	604	182.5	4.6	297	5	Q86M89	Q86M89 spodoptera
532	189.5	4.8	263	5	Q9Y116	Q9Y116 penaeus van	605	182.5	4.6	310	11	Q9QY29	Q9QY29 mus musculu
533	189.5	4.8	263	5	Q02570	Q02570 cullex quin	606	182.5	4.6	327	5	Q8MS77	Q8MS77 dirosophila
534	189.5	4.8	266	5	Q27761	Q27761 penaeus van	607	182.5	4.6	371	5	Q8MR93	Q8MR93 dirosophila
535	189.5	4.8	271	5	Q9VRS6	Q9VRS6 dirosophila	608	182.5	4.6	482	6	Q28982	Q28982 sus scrofa
536	189.5	4.8	281	5	Q8SYB5	Q8SYB5 dirosophila	609	182.5	4.6	520	5	Q8ING0	Q8ING0 dirosophila
537	189.5	4.8	381	5	Q9VRS6	Q9VRS6 dirosophila	610	182.5	4.6	1551	5	Q9NGV4	Q9NGV4 dirosophila
538	189.5	4.8	385	13	Q9VRS2	Q9VRS2 elaphie sp.	611	182.5	4.6	2531	5	Q16004	Q16004 lytechinus
539	189.5	4.8	470	5	Q8T3A1	Q8T3A1 cioma intes	612	182	4.6	240	5	Q9SC03	Q9SC03 biophalari
540	189.5	4.8	572	11	Q8B1K6	Q8B1K6 oryctolagus	613	182	4.6	241	5	Q917L2	Q917L2 dirosophila
541	189.5	4.8	649	6	Q28597	Q28597 oryctolagus	614	182	4.6	254	5	Q18434	Q18434 heliocoverpa
542	189.5	4.8	1737	4	Q75097	Q75097 homo sapien	615	182	4.6	280	5	Q9VRS8	Q9VRS8 dirosophila
543	189.5	4.8	2386	4	Q727M0	Q727M0 homo sapien	616	182	4.6	391	5	Q9V322	Q9V322 dirosophila
544	189	4.8	181	5	Q9GSM5	Q9GSM5 chrysomya b	617	182	4.6	836	13	Q8AM87	Q8AM87 cymops pyrr
545	189	4.8	245	5	Q9BL18	Q9BL18 lumbricus r	618	181.5	4.6	284	5	Q9C089	Q9C089 haemaphysal
546	189	4.8	246	11	Q7TT42	Q7TT42 mus musculu	619	181.5	4.6	295	5	Q9NM07	Q9NM07 heliothis z
547	189	4.8	414	11	Q9CX06	Q9CX06 mus musculu	620	181.5	4.6	450	13	Q7SY99	Q7SY99 xenopus lae
548	189	4.8	758	11	Q8CIP8	Q8CIP8 rattus norv	621	181.5	4.6	487	13	Q7ZMR8	Q7ZMR8 xenopus lae
549	188.5	4.8	382	13	Q90MT4	Q90MT4 crocodylus	622	181.5	4.6	754	13	Q98U16	Q98U16 cyprinus ca
550	188.5	4.8	713	5	Q962W9	Q962W9 podocoryne	623	181	4.6	254	5	Q18436	Q18436 heliocoverpa
551	188	4.8	235	4	Q8N4E0	Q8N4E0 homo sapien	624	181	4.6	254	5	Q76934	Q76934 lacnobia o
552	188	4.8	253	4	Q8N5N9	Q8N5N9 homo sapien	625	181	4.6	255	13	Q34289	Q34289 salvelinus
553	188	4.8	266	5	Q8MR10	Q8MR10 parailithode	626	181	4.6	270	5	Q819P2	Q819P2 aplisyne fl
554	188	4.8	271	5	Q18487	Q18487 penaeus van	627	181	4.6	405	5	Q8MQS8	Q8MQS8 apis mellif
555	188	4.8	276	5	Q9VXP8	Q9VXP8 dirosophila	628	181	4.6	412	13	Q7SYT3	Q7SYT3 xenopus lae
556	187.5	4.8	250	5	Q17036	Q17036 anopheles g	629	181	4.6	840	4	Q9VUD7	Q9VUD7 dirosophila
557	187.5	4.8	251	4	Q8N2U3	Q8N2U3 homo sapien	630	181	4.6	840	4	Q9UD45	Q9UD45 homo sapien
558	187.5	4.8	257	5	Q9NBA9	Q9NBA9 aedes aegy	631	180.5	4.6	1229	5	Q9EMB0	Q9EMB0 caenorhabd1
559	187.5	4.8	283	5	Q25394	Q25394 lumbricus r	632	180.5	4.6	264	5	Q62561	Q62561 penaeus van
560	187.5	4.8	283	5	Q8ITU7	Q8ITU7 lumbricus r	633	180.5	4.6	266	5	Q81916	Q81916 blomla trop
561	187.5	4.8	1216	13	Q90V55	Q90V55 brachydantio	634	180.5	4.6	293	4	Q725A4	Q725A4 homo sapien
562	187	4.7	256	5	Q18439	Q18439 heliocoverpa	635	180.5	4.6	390	5	Q8MP08	Q8MP08 bombyx mori
563	187	4.7	261	6	Q29474	Q29474 canis famli	636	180.5	4.6	520	5	Q8S933	Q8S933 dirosophila
564	187	4.7	291	5	Q25510	Q25510 manduca sex	637	180.5	4.6	717	13	P70006	Q9N076 xenopus lae
565	186.5	4.7	235	5	Q9GTR7	Q9GTR7 aedes albop	638	180	4.6	203	5	Q9NBT7	Q9NBT7 heliothis z
566	186.5	4.7	250	13	Q93265	Q93265 pseudopleur	639	180	4.6	234	11	Q9CV76	Q9CV76 mus musculu
567	186.5	4.7	257	5	Q81BE2	Q81BE2 aedes trise	640	180	4.6	254	3	Q01136	Q01136 metarhizium
568	186.5	4.7	287	5	Q9VTV2	Q9VTV2 dirosophila	641	180	4.6	256	3	Q9Y842	Q9Y842 metarhizium
569	186.5	4.7	397	5	Q9W314	Q9W314 dirosophila	642	180	4.6	511	5	Q9VZHS	Q9VZHS dirosophila
570	186	4.7	181	5	Q9GSM1	Q9GSM1 chrysomya b	643	180	4.6	546	5	Q8SXG6	Q8SXG6 dirosophila
571	186	4.7	249	13	Q92046	Q92046 disosotichu	644	179.5	4.6	354	5	Q9U611	Q9U611 dirosophila
572	186	4.7	449	5	Q9VDU8	Q9VDU8 cryocollagus	645	179.5	4.6	581	5	Q96015	Q96015 dirosophila
573	185	4.7	1594	6	Q95218	Q95218 cryocollagus	646	179.5	4.6	728	13	Q90656	Q90656 gallus gall
574	185.5	4.7	211	4	Q8U009	Q8U009 homo sapien	647	179.5	4.6	1047	5	Q24019	Q24019 dirosophila
575	185.5	4.7	256	5	Q9XYS1	Q9XYS1 ctenocepal	648	179.5	4.6	1047	5	Q9VZM2	Q9VZM2 dirosophila
576	185.5	4.7	292	5	Q18438	Q18438 heliocoverpa	649	179	4.5	270	5	Q8MR11	Q8MR11 parailithode
577	185.5	4.7	310	11	Q91XC4	Q91XC4 mus musculu	650	179	4.5	282	5	Q18655	Q18655 plodia inte
578	185.5	4.7	439	11	Q8BHM9	Q8BHM9 mus musculu	651	179	4.5	384	5	Q9XY63	Q9XY63 ctenocepal
579	185.5	4.7	1254	13	Q90YU2	Q90YU2 brachydantio	652	179	4.5	440	5	Q8MRFF	Q8MRFF dirosophila
580	185.5	4.7	1254	13	Q90YU6	Q90YU6 brachydantio	653	179	4.5	606	11	P70412	P70412 mus musculu
581	185	4.7	287	5	Q9NH10	Q9NH10 agrotis ips	654	179	4.5	675	13	Q9M6J8	Q9M6J8 disosotichu
582	185	4.7	508	16	Q8DA23	Q8DA23 vibrio vuln	655	179	4.5	905	13	Q8UVR0	Q8UVR0 gallus gall
583	185	4.7	709	13	Q7ZTN9	Q7ZTN9 xenopus lae	656	179	4.5	919	13	Q8UVR0	Q8UVR0 gallus gall
584	184.5	4.7	295	5	Q18450	Q18450 heliocoverpa	657	179	4.5	936	13	Q8UVR0	Q8UVR0 gallus gall
585	184.5	4.7	295	5	Q18450	Q18450 heliocoverpa	658	179	4.5	2898	5	Q9VLT6	Q9VLT6 dirosophila
586	184.5	4.7	427	11	Q8BQH6	Q8BQH6 mus musculu	659	178.5	4.5	292	13	Q7S206	Q7S206 xenopus lae
587	184	4.7	246	5	Q817P0	Q817P0 lumbricus b	660	178.5	4.5	300	5	Q9NM08	Q9NM08 agrotis ips
588	184	4.7	381	11	Q7TP23	Q7TP23 rattus norv	661	178.5	4.5	300	5	Q9NRC3	Q9NRC3 dirosophila
589	184	4.7	405	5	Q8S260	Q8S260 dirosophila	662	178.5	4.5	400	5	Q9NRC3	Q9NRC3 dirosophila
590	184	4.7	745	13	Q9OWF9	Q9OWF9 triaklis scy	663	178	4.5	212	11	Q09020	Q09020 rattus norv
591	184	4.7	988	4	Q81WY4	Q81WY4 homo sapien	664	178	4.5	256	5	Q18599	Q18599 dirosophila
592	183.5	4.7	247	11	Q9CNP7	Q9CNP7 mus musculu	665	178	4.5	289	5	Q8MR67	Q8MR67 dirosophila
593	183.5	4.7	257	5	Q86P18	Q86P18 aedes aegy	666	178	4.5	290	5	Q9VRS7	Q9VRS7 dirosophila
594	183.5	4.7	329	13	Q42272	Q42272 caenorhabd1	667	178	4.5	434	5	Q8TD25	Q8TD25 homo sapien
595	183.5	4.7	1372	5	P91526	P91526 caenorhabd1	668	178	4.5	936	4	Q8TD25	Q8TD25 homo sapien
596	183	4.6	257	6	Q19023	Q19023 macaca mula	669	177.5	4.5	1212	13	Q42347	Q42347 gallus gall
597	183	4.6	267	6	Q9MZ26	Q9MZ26 stomoxys ca	670	177.5	4.5	261	3	Q00344	Q00344 cochliobolu
598	183	4.6	267	6	Q9MZ26	Q9MZ26 macaca fasc	671	177.5	4.5	267	5	Q9VLF5	Q9VLF5 dirosophila
599	183	4.6	272	5	Q9VXK6	Q9VXK6 dirosophila	672	177	4.5	2524	5	Q9GP45	Q9GP45 branchiostoc
600	183	4.6	752	13	Q42374	Q42374 brachydantio	673	177	4.5	233	4	Q96R27	Q96R27 homo sapien

674 177 4.5 258 5 Q9WSU8
675 177 4.5 328 11 Q9BUB6
676 177 4.5 385 5 Q2S101
677 177 4.5 425 5 Q9W1Q9
678 177 4.5 737 13 Q90422
679 177 4.5 747 13 Q91900
680 176.5 4.5 267 5 Q9VRU0
681 176.5 4.5 413 13 Q7S925
682 176.5 4.5 716 13 Q91691
683 176.5 4.5 926 11 Q9Q2Y7
684 176 4.5 243 13 Q8AV83
685 176 4.5 260 5 Q8TAP5
686 176 4.5 270 4 Q96GL8
687 176 4.5 389 5 Q9V517
688 176 4.5 575 5 Q22328
689 176 4.5 584 11 Q8K480
690 176 4.5 891 5 Q9VV38
691 175.5 4.4 257 5 Q818B4
692 175.5 4.4 272 5 Q9VRS3
693 175.5 4.4 459 5 Q9V4W7
694 175.5 4.4 522 5 Q8MQM9
695 175.5 4.4 617 13 Q801S1
696 175.5 4.4 677 5 Q9VVC7
697 175.5 4.4 921 11 Q9QX38
698 175.5 4.4 1316 4 Q96JU7
699 175 4.4 260 5 Q8TAP6
700 175 4.4 261 5 Q62598

ALIGNMENTS

PRELIMINARY; PRT; 737 AA.

RESULT 1
Q96JW2
ID Q96JW2
AC Q96JW2; 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DR 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Hypothetical protein FLJ14935.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_Taxid=9606;
[1]
RN
RP
SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isoeai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,
RA Watanabe M., Hosokawa T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Matanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto U., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
RA Niimiya K., Iwayanagi T.;
RT "NEO human cDNA sequencing project."
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL AK027841. BAB55404.1.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00084; sushi; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00020; Tryp_Spe; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; EGF; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
KW Hypothetical protein; EGF-like domain; Hydrolase; Protease;
KW Serine protease.
SQ SEQUENCE 737 AA; 81952 MW; 4F51689C5EB2B44 CMC64;

Query Match 99.4%; Score 3921.5; DB 4; Length 737;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 719; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

QY 1 MELGCTQLGLTPQLQLISSLPREYVYINACPGAEWNIMCECEYDOIECVCPGARE 60
DB 1 MELGCTQLGLTPQLQLISSLPREYVYINACPGAEWNIMCECEYDOIECVCPGARE 60
QY 61 VGYTIPCCRNENECDCLIPGCTIFENCKSCRNMGWGLTDFYKGFYCAECRAAG 120
DB 61 VGYTIPCCRNENECDCLIPGCTIFENCKSCRNMGWGLTDFYKGFYCAECRAAG 120
QY 121 YGDCMRCGQVLRAPKQIILLESYPLNACWMTIHAKEGPIQLRFVNLSEFDWQCYD 180
DB 121 YGDCMRCGQVLRAPKQIILLESYPLNACWMTIHAKEGPIQLRFVNLSEFDWQCYD 180
QY 181 YVEVADGNRPGQIIRKVCNERPAPISIGSSLPVLPHSDGSKNFDFAHAYEITACS 240
DB 181 YVEVADGNRPGQIIRKVCNERPAPISIGSSLPVLPHSDGSKNFDFAHAYEITACS 240
QY 241 SSPCFHDTGCVLDKAGSYKCACLAAGYTGRCENT-----LEERNCSDP 283
DB 241 SSPCFHDTGCVLDKAGSYKCACLAAGYTGRCENT-----LEERNCSDP 283
QY 284 GPPVNGYKQITGPGPLINGRAKIGTIVSFFCNNSYVLSGNEKRCQNGESGKOPICI 343
DB 284 GPPVNGYKQITGPGPLINGRAKIGTIVSFFCNNSYVLSGNEKRCQNGESGKOPICI 343
QY 301 GPPVNGYKQITGPGPLINGRAKIGTIVSFFCNNSYVLSGNEKRCQNGESGKOPICI 360
DB 301 GPPVNGYKQITGPGPLINGRAKIGTIVSFFCNNSYVLSGNEKRCQNGESGKOPICI 360
QY 344 KACREPKISDLVRRRVLPVQVSRETPLHQVLSAFAFSKQKQSAPTKKPALPFGDLPNGY 403
DB 344 KACREPKISDLVRRRVLPVQVSRETPLHQVLSAFAFSKQKQSAPTKKPALPFGDLPNGY 403
QY 361 KACREPKISDLVRRRVLPVQVSRETPLHQVLSAFAFSKQKQSAPTKKPALPFGDLPNGY 420
DB 361 KACREPKISDLVRRRVLPVQVSRETPLHQVLSAFAFSKQKQSAPTKKPALPFGDLPNGY 420
QY 404 QHLHTQLQYECISPPYRRLSSRRCTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMP 463
DB 404 QHLHTQLQYECISPPYRRLSSRRCTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMP 463
QY 421 QHLHTQLQYECISPPYRRLSSRRCTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMP 480
DB 421 QHLHTQLQYECISPPYRRLSSRRCTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMP 480
QY 464 WQALVRRRTSGVHGSGLHKGMPLVCSGALVNERVVVAACVTDLGVVTMIKTADLVV 523
DB 464 WQALVRRRTSGVHGSGLHKGMPLVCSGALVNERVVVAACVTDLGVVTMIKTADLVV 523
QY 481 WQALVRRRTSGVHGSGLHKGMPLVCSGALVNERVVVAACVTDLGVVTMIKTADLVV 540
DB 481 WQALVRRRTSGVHGSGLHKGMPLVCSGALVNERVVVAACVTDLGVVTMIKTADLVV 540
QY 524 LKGFYRDDRDREKTIQSLSAIIIPVYDPIILDADIAIKLIDKARISTRVOPICLAA 583
DB 524 LKGFYRDDRDREKTIQSLSAIIIPVYDPIILDADIAIKLIDKARISTRVOPICLAA 583
QY 541 LKGFYRDDRDREKTIQSLSAIIIPVYDPIILDADIAIKLIDKARISTRVOPICLAA 600
DB 541 LKGFYRDDRDREKTIQSLSAIIIPVYDPIILDADIAIKLIDKARISTRVOPICLAA 600
QY 584 SRDLSTQSESHITVAGNNVLADVRSPEFKNDTLRSQVSVYVDSLLCEQHEDHGIPIVS 643
DB 584 SRDLSTQSESHITVAGNNVLADVRSPEFKNDTLRSQVSVYVDSLLCEQHEDHGIPIVS 643
QY 601 SRDLSTQSESHITVAGNNVLADVRSPEFKNDTLRSQVSVYVDSLLCEQHEDHGIPIVS 660
DB 601 SRDLSTQSESHITVAGNNVLADVRSPEFKNDTLRSQVSVYVDSLLCEQHEDHGIPIVS 660
QY 644 TDNNECASMEPTAPSDICTAETGGLAASVPGRASPEPRMMLGLVSVYKTCSHRLST 703
DB 644 TDNNECASMEPTAPSDICTAETGGLAASVPGRASPEPRMMLGLVSVYKTCSHRLST 703
QY 661 TDNNECASMEPTAPSDICTAETGGLAASVPGRASPEPRMMLGLVSVYKTCSHRLST 720
DB 661 TDNNECASMEPTAPSDICTAETGGLAASVPGRASPEPRMMLGLVSVYKTCSHRLST 720
QY 704 AFTKVLPEKDWIERNMK 720
DB 704 AFTKVLPEKDWIERNMK 720
QY 721 AFTKVLPEKDWIERNMK 737
DB 721 AFTKVLPEKDWIERNMK 737

RESULT 2

ID	Q8K2B8	PRELIMINARY;	PRT;	720 AA.
AC	Q8K2B8:			
DT	01-OCT-2002 (TREMBLrel. 22, Created)			
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Similar to DKFZP568121.25 protein.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Strausberg R.;			
RL	Submitted (JUN-2002) to the EMBL/Genbank/DBJP databases.			
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.			
CC	EMBL; BC031841; AAH1841.1; .			
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.			
DR	GO; GO:0008233; F:peptidase activity; IEA.			
DR	GO; GO:0004295; F:trypsin activity; IEA.			
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPR000859; CUB.			
DR	InterPro; IPR009003; Cys_Ser_trypsin.			
DR	InterPro; IPR006209; EGF-like.			
DR	InterPro; IPR006210; IEGF.			
DR	InterPro; IPR001354; Peptidase_S1.			
DR	InterPro; IPR001314; Sush1_SCR_CCP.			
DR	Pfam; PF00431; CUB; 1.			
DR	Pfam; PF00008; EGF; 1.			
DR	Pfam; PF00084; Sush1; 2.			
DR	Pfam; PF00089; trypsin; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	SMART; SM00032; CCP; 2.			
DR	SMART; SM00042; CUB; 1.			
DR	SMART; SM00181; EGF; 2.			
DR	SMART; SM00020; TRYP_SPC; 1.			
DR	PROSITE; PS01180; CUB; 1.			
DR	PROSITE; PS00022; EGF_1; 1.			
DR	PROSITE; PS01186; EGF_2; 1.			
DR	PROSITE; PS0240; TRYPSIN_DOM; 1.			
KW	EGF-like domain; Hydrolase; Protease; Serine protease.			
KW	SEQUENCE 720 AA; 80377 MW; 7172B7F1E690FD0E CRC64;			
SQL				
Query Match	91.6%; Score 3612; DB 11; Length 720;			
Best Local Similarity	90.1%; Pred. No. 0;			
Matches 649;	Conservative 33; Mismatches 38; Indels 0; Gaps 0			
QY	1 MELGCMTQGLTFLQLLLISSLPREYTVNEACPGAENNMNRCCEYDQIECVCPGRKE 60			
DB	1 MELDMNAQGLVFLQLLLISSLPREYTVINEACPGAENNMNRCCEYDQIECLCPGKKE 60			
QY	61 VVGYYTIPCCRNENEEDCSCLIHPGCTIFPNCKSCRNGSWGTLDPFYKGFCAECRAGW 120			
DB	61 VVGYYTIPCCRNEDNECDSCLIHPGCTIFENCKSCRNGSWGTLDPFYVGFYCECRAGW 120			
QY	121 YGGDCMRGCGVLRARPGQILLHSYPLNAHCENTITAKKPEFVQLRFVMSLEFDVMCOYD 180			
DB	121 YGGDCMRGCGVLRARPGQILLHSYPLNAHCENTITAKKPEFVQLRFVMSLEFDVMCOYD 180			
QY	181 YVEVRDGDNRDQIILKRVCGNERPAPITQSIGSLHLVLFPSDSSKNFDFGHAYEEITACS 240			
DB	181 YVEVRDGDNRDQIILKRVCGNERPAPITQSIGSLHLVLFPSDSSKNFDFGHAYEEITACS 240			
QY	241 SSPCHFDGTCVLDKAGSYCALAGTITGRCENLLERKCSPPGCPVNGYQKITGSPGLI 300			
DB	241 SSPCHFDGTCVLDITGSGFRCCALAGTYGRCENLLERKCSDLGCPVNGYKKITGSPGLI 300			
QY	301 NRRHAKITGVVFFPCNNSYVLSGNERKTQONGEMSGKQPICTIKACREBKIDLVARRYL 360			
DB	301 NRRHAKITGVVFFPCNNGSYVLSGNERKTQONGEMSGKQPVCMKACREKIDLVARRYL 360			

Oy		36	PMOVGEREPFLHQLVSAFSSKQICQASAPTKKPALPFGDLPWGVOHTLQAYECISPFYR	420
Dd		361	SMOVGEREPFLHQLVSTAFSSKQIKODASTKKPALPFGDLPPGYOHLTLQVYELCISPFYR	420
Oy		421	RUGSSRRTCIRTGKWSGRAPSCIPICGIENITPAKTGLRWPMQAIIYRTSGVHDGSL	480
Dd		421	RUGSSRRTCIRTGKWSGRAPSCIPICGIESTSPSKTGTWRMPQAIIYRTSGVHDGCL	480
Oy		481	HKGAMFLVCSGALVNERTVVAACHCVTLDGKYTMILKPADLKVLGKRYRDDDDREKTIOS	540
Dd		481	HKGAMFLVCSGALVNERTVVAACHCVTELGAQTIIKPADLVVIGKEYYRDDDRDKSION	540
Oy		541	LOLSAIIHPNDPLILDADIAILLKLDPKARISTRVOPICLAARDLSTFSOSHITVAG	600
Dd		541	LRLVSAILIHPNDPLILDADIAVLLKLDPKAISTRVOPICLATRDISTFSOSHITVAG	600
Oy		601	MNVLAIVRSPEGFKNLTRSRGVSVVDSSLCEBOEHDHGIPVSYTDNMFCAWSPEABSDI	660
Dd		601	MNLIVAVRSPEGFKNDTLIHGVRVVYDPMLCBEGQHEDHGIPIVSYTDNMFCAKDSPTSDI	660
Oy		661	CIAETGGIAIVSFPGRASPPEPRMHLMGVLSNSYDKTGSHRLSTFTYLPRKDMIEENMK	720
Dd		661	CTAETGGIAIALSPGRASPEPRMHLVGLVSNYSYDKTGSHRLSTFTYLPRKDMIEENMK	720
RESULT 3				
OQB25				
ID	OQB25	PRELIMINARY;	PRT; 720 AA.	
AC	OQB25;			
DT	01-MAR-2003 (TEMBLrel_23, Created)			
DT	01-MAR-2003 (TEMBLrel_23, Last sequence update)			
DT	01-OCT-2003 (TEMBLrel_25, Last annotation update)			
DE	Hypothetical EGF-like domain.			
GN	E430002G05RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=NOD; TISSUE=Thymus;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	the PANTOM Consortium,			
RA	The RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-73(2002).			
DR	EMBL; AK088017; BAC740098.1; -			
DR	WGD; MG1:2445082; E430002G05RIK.			
DR	GO; GO:0005509; F:calcium ion binding; IEA.			
DR	GO; GO:0004263; F:cytoskeleton activity; IEA.			
DR	GO; GO:0004295; F:protein activity; IEA.			
DR	GO; GO:0005608; P:proteolysis and peptidolysis; IEA.			
DR	InterPro; IPRO00858; CUB.			
DR	InterPro; IPRO00903; Cys_Set_trypsin.			
DR	InterPro; IPRO01881; EGF Ca.			
DR	InterPro; IPRO06209; EGF like.			
DR	InterPro; IPRO06210; EGF.			
DR	InterPro; IPRO01254; peptidase S1.			
DR	InterPro; IPRO01314; peptidase_S1A.			
DR	InterPro; IPRO00436; Sushi_SCR_CCP.			
DR	pfam; PF00431; CUB; 1.			
DR	pfam; PF00008; EGF; 1.			
DR	pfam; PF00084; sushi; 2.			
DR	pfam; PF00089; trypsin; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	SMART; SM00032; CCP; 2.			
DR	SMART; SM00042; CUB; 1.			
DR	SMART; SM00181; EGF; 2.			
DR	SMART; SM00179; EGF CA; 1.			
DR	SMART; SM00020; Tryp_Spc; 1.			
DR	PROSITE; PS01180; CUB; 1.			
DR	PROSITE; PS00022; EGF_1; 1.			

DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF03815; LCCU; 1.
 DR Pfam; PF00059; Lectin_C; 1.
 DR Pfam; PF00084; Sushi_5.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 5.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00603; LCCU; 1.
 DR SMART; SM00020; tryp; 1.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PROSITE; PS50820; LCCU; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR HydroLase; Protease; Serine protease; Signal.
 PT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 1019 FACTOR C.
 SQ SEQUENCE 1019 AA; 112248 MW; B0B51730A559593 CRC64;

Query Match 17.2%; Score 678; DB 5; Length 1019;
 Best Local Similarity 25.6%; Pred. No. 8,1e-54;
 Matches 223; Conservative 117; Mismatches 308; Indels 222; Gaps 37;

QY 34 PGAWNMIM---CRECEYDQIE--CYCPGRKREVTGTTCCNNEHCSCLIHQCT 86
 DB 184 PNGQWSSPPKPCIRECAKVSPEHGKVTAPSGNMIEGATL-----PHYLT 233
 QY 87 IFENKSCR-NGSGWGLT----- 103
 DB 234 IGGETLTQSGNGSGQIPCKKLVFCDDLPVNAHENVKIVGQKKGQPGQTEVYTT 293
 QY 104 --DDPYVKGFCACR--AGVYGG--DCMR-----CGVLR--APKG 137
 DB 294 CSGNYFLMGFTLCKNLDSWSGSPSCVVADEVDSCRAVDLVDVGEFVHICPAG 353
 QY 138 QILLES-----YPLNAHEWTHA---KPGFV----- 163
 DB 354 CSLTAGVTGTAIVHELSVCRAAIHAGKLPNSGGAHVNNGSPFLSGDLNGIKSEE 413
 QY 164 LRFVWLSLEPYM-----CQDYVEYVD-----GDRDGOITKRVCGN--ERRAP 206
 DB 414 LKSLARSRFPYVSSSTAGSGCDDGMEVEVENCVVYTSKRAERAGVCTMAALAV 473
 QY 207 IQS--IGSSLHLVLFHSDG-SKNPFGF-----AIYEITACSSSPCF 245
 DB 474 LDKVIVPESLLEALRGKGLTTWTGILHRLDAEKFVWELMDRSVVINDNLTFWASGEPG 533
 QY 246 HDGTCV-LDKAGS---YKCACLAGYTCQRENLEEN---CSDPGPNVGYKTIQGP 297
 DB 534 NETNCVYLDIRDQLOPVWKTKSCFQPSSEFAQMDLSDNNKAKCDPSSLGHTLHGQS 593
 QY 298 GLINGRAHAKITGVVFPCCNNSVYLSGNEKRTCCQNGSGEKOPICIK--ACREPKIDLV 355
 DB 594 --LDGFYA--GSSIRYSCVLAHYSGETETVCTTNGTMSAKPRCIVKTCQNPVSYG 649
 QY 356 RRRVLPVMOVQSGREFPLHQLVSAFSSKQLO--SAPYKPLPRGD-----LP 400
 DB 650 SVEIKP---PRTNISIRVSGPFLRLPLPLRLAARAPPKPRSSGPSTVDLASKVLP 706
 QY 401 MGQHLHTQLOVEICISPYRRLGSSRRCTATGKMSGAPSCIPICKIENITAP----- 455
 DB 707 EGHRTVSGRAIYTESRYELLGSGRRCDNSNGMSGPACIPVCGSDSPRSPFTWNG 766
 QY 456 -KTQGLRPMQAAIYRRTSGVHDSLHGAWFLVCSGALVNERVVAHAACVTDLGKVTM 514
 DB 767 NSTEIGQWPMQAGISRWLA-----DHNMFLLCGGSLNKKVIVAAHCVTYSATAEI 819
 QY 515 IKTADLVKVLGKFRDDDRDEKTIQSLQISAIILHPNYPDLLADDAIILKLDKARIST 574

DB 820 IDSQFIYLGKYYRDSRDDYQVREALEIHVNNPNYDGNLFDIALIQLKTPVLT 879
 QY 575 RVQPICLAARDISTFQESH-----TYAGNNVLADVRSPFGKNDTLRSGVSVVDSL 628
 DB 880 RVQPICLPT--DIT--REHLEGTIAVVTGNG---LNNNTYSMTQOAVLPVVAAS 930
 QY 629 LCEEHEDHGIPIVVDNMFCAEWEPTASDICTAETGIAAVSPGRASPEPRMLMGL 688
 DB 931 TCEGKREKDLPLTVEENMFCAQYK-KGRYDACSQSGG--PLVPFADDSRTERRWLEGI 987
 QY 689 VSWSYDTKCSH-RLSTAFTKLPFKDMIER 717
 DB 988 VSWSGSPGCGKANQYGFYVNFVLSMIRQ 1017

RESULT 6
 Q26423
 ID Q26423 PRELIMINARY; PRT; 1083 AA.

AC Q26423; (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Factor C.
 GN Factor C.
 OS Carthoscorpius rotundicauda (Southeast Asian horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OC Limulidae; Carthoscorpius.
 OX NCBI_TaxId=6848;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95268506; PubMed=7536401;
 RA Ding J.L., Navas M.A.3rd, Ho B.;
 RT "Molecular cloning and sequence analysis of factor C cDNA from the
 RL Singapore horseshoe crab, Carthoscorpius rotundicauda.";
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 DR EMBL; S77064; AAB34362.1; -.
 DR HSP; P00763; IDPO.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0005529; F:sugar binding; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR003066; IG_MHC.
 DR InterPro; IPR004043; LCCU_dom.
 DR InterPro; IPR001304; Lectin_C.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF03815; LCCU; 1.
 DR Pfam; PF00059; Lectin_C; 1.
 DR Pfam; PF00084; Sushi_5.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 5.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00603; LCCU; 1.
 DR SMART; SM00020; tryp; 1.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR PROSITE; PS50820; LCCU; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR HydroLase; Protease; Serine protease.
 SQ SEQUENCE 1083 AA; 120228 MW; C82CC45A5C9FCB7 CRC64;

Query Match 16.9%; Score 665; DB 5; Length 1083;

Best Local Similarity 25.4%; Pred. No. 1.5e-52;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

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QY 34 PGAEINIMRECEYQIEVCCEPKRE-----VGTITPCCNRENECDCLIH 82
DB 248 PNGQSNFPKICR-----SCAMVSPDHKVNALSGDMLEGATL-----RPSCD5--- 293
QY 83 PGCTIENKCSGR-NGSWGTL----- 103
DB 294 FYTLLIGETLTCQNGQNGQIPQCKNLVFCPELDVNAEHKVKIGVEQKYGPPQCTE 353
QY 104 -----DFFVKGFCACGR--AGWYG--DCMR-----CGQVLR-- 133
DB 354 VVYTGSGNFMGFDLTLCNPDQSGSGSPSCYKAVDREVDGSKAVDFLDVGEVRLH 413
QY 134 ARKQQLLES-----YPLNACHTIHA-----KPGVVI----- 162
DB 414 CPAGCSLTAGTWTGTAIYHLSVCRALHAGKLPNSGAVVNVNNGPYSDFLGDLNGI 473
QY 163 -----QLRFVWLSLEFDY-----CQDYVEVRD-----GDNRDQILIRVCGN--E 202
DB 474 KSEELKSLARSPFDVSSSTAGKSGCPDGMFEVDENCVYTSKQAMERAGVCTNMAA 533
QY 203 RPAPIQS--IGSLHVLHFSHG-SKNPDPFH-----AIYEETACSS 241
DB 534 RLAVLDKDVIPNSLTETLTKGGLTTWIGLHRLDAEKFPIWELMDRSNVVLDNLTWMS 593
QY 242 SECFHDGTCVL-----DKAGS--YKACLAGYTGRCNLLBERN---CSPGPGVNGYQKI 293
DB 594 GEPGETNCVVDIQQQLQSVWTKSCFPPSPACMMDDSDRKAACDDPGGLENGHATL 653
QY 294 TGGPGLINGRAKIGTVSFFCNNSVLSGNEKRTQONGEMSGKOPICR--ACBPKI 351
DB 654 HGOS--IDGFYA--GSIIRYSCVHLHLSGTETVCTTNGTMSAPRRCIKYITCONPVP 709
QY 352 SOLVRRRLVPMOVQSETPHQLYSAFSGKQLQ--SAPTKKPALPGD----- 398
DB 710 PSYGSVEIKP--PSRTNISRYGSPFLRLPLRLPLABAKPPKPRSSQPTVDLASK 766
QY 399 --LPMQYQHLHQLQYECTSPYRRLGSSRRCTLRGKMSGAPGCTIPCGKINENTAP- 455
DB 767 VKLPBEGHYVVGSAIYATCSRYELLGSGRCDSNGNNSGSPASCTIPCGSDSRSPF 826
QY 456 -----KTQGLRMPWQAIYRTSGVADGSLHKAMFVLSGALVNERVVAHAQCVTDIG 510
DB 827 INNGNSTELGQMPWQAGISRMLA-----DNNMVLQCGSLNEMKIVTAAHCVTYSA 879
QY 511 KVTMIKTADLVKLVGKFRDDDEKTIQSLQISLIIHPNYDPILLADIALKLIDKA 570
DB 880 TAEIIPNPFKMYLKGKYRDDSDDDYQVREALIHNPNYDPGNLFDIALIQLKTPV 939
QY 571 RSTRVOPICLAASRLSTSPQESH-----TVAGMNLAVYRSGFKNDLRSGVSYV 624
DB 940 TLTTRVOPICLPT--DITT--REHLKEGTAVVYWG--LNENNYSETTIOQAVLPV 990
QY 625 VDSLCEOEHDHGLPVSTYDMNFCASMEPTAPSDICTAETGIAAASPAGASPEPRMH 684
DB 991 VAASTCEBYKADLPLVTBNNFCAGYK--KGRYDSCGSDSG--PLVYADSRTERRV 1047
QY 685 LMGVLSWSTDKTCSH--RLSTAFKVLPRKWIET 717
DB 1048 LEGIVSWGSPSGCGKANQYGFYKVVVFWIRQ 1081

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OS Branchiostoma belcheri (Amphioxus).
OC Euteleostei; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OK NCBI_TaxID=7741;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Notochord;
RX MEDLINE=22593355; PubMed=12707349;
RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matsushita A., Takahashi M.,
RA Matsushita M., Fujita T.,
RT "Origin of Mannose-Binding Lectin-Associated Serine Protease (MASP)-1
RT and MASP-3 involved in the Lectin Complement Pathway Traced Back to
RT the Invertebrate, Amphioxus."
RL J. Immunol. 170:4701-4707(2003).
DR EMBL: AB089267; BAC75866.1;
DR GO:GO:0005509; F:calcium ion binding; IEA.
DR GO:GO:0004263; F:chymotrypsin activity; IEA.
DR GO:GO:0008233; F:peptidase activity; IEA.
DR GO:GO:0005529; F:sugar binding; IEA.
DR GO:GO:0004295; F:trypsin activity; IEA.
DR GO:GO:0007157; P:heterophilic cell adhesion; IEA.
DR GO:GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR00152; Asx_Hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR009003; Cys_ser_trypsin.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR001254; peptidase_S1.
DR InterPro: IPR001314; peptidase_S1A.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00084; suah1; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00032; CCP; 2.
DR SMART: SM00042; CUB; 2.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00179; EGF_Ca; 1.
DR SMART: SM00020; Tryp_Spc; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 1.
DR PROSITE: PS01180; CUB; 2.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS01187; EGF_Ca; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Lectin; Protease.
SQ SEQUENCE 680 AA; 75871 MW; 496985A94A728318 CRC64;

Query Match 15.4%; Score 608.5; DB 5; Length 680;
Best Local Similarity 26.3%; Pred. No. 1.4e-47;
Matches 195; Conservative 92; Mismatches 239; Indels 215; Gaps 35;

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0688H6 ID 0688H6 PRELIMINARY: PRT: 688 AA.
AC 0688H6:
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Manose-binding lectin associated serine protease-3.
GN MASP-3.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Notochord;
RX MEDLINE=22593355; PubMed=12707349;
RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matusita A., Takahashi M.,
RA Matushita M., Fujita T.;
RT "Origin of Manose-Binding Lectin-Associated Serine Protease (MASP)-1
RT and MASP-3 involved in the Lectin Complement Pathway Traced Back to
RT the Invertebrate, Amphioxus."
RT J. Immunol. 170:4701-4707(2003).
DR EMBL; AB089268; BAC75887.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_5.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; TYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR KEGG; K01135; trypsin; 1.
DR KEGG; K01135; trypsin; 1.
SQ SEQUENCE 688 AA; 76890 MW; 14B3AD8215BD4D15 CRC64;

Query Match 15.1%; Score 597; DB 5; Length 688;
Best Local Similarity 26.6%; Pred. No. 1.7e-46;
Matches 197; Conservative 88; Mismatches 244; Indels 212; Gaps 36;

46 CEYDQIECV-----CPGKREV-----VGYT 65
DB 84 CEYDVKKWEKDKLVGLFCTEDTDTDEQVGDVISTGSLFKSPDNADRKAFRA 143
QY 66 IPCRNEBNEBSCSLHPGCTITENCKSCNWSGGTLDFFYKGYCAECRAG-WYGD 124
DB 144 VHYRVVDRECC-AVNGGCHHF-----CHN-----YISGYCS-CRAGYIMXD 185
QY 125 ---C-WRCG-QVLRAPGQILSS---YPLNHCETIHKAGFYIOLRFVWLSLEFPD- 174
DB 186 RETCKGCGKGVLTUKLSGTISPEYPLKPKVLDCKKIVGEPYVTTLOF---DDFDV 242

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QY 175 -----YMCQDYVEVRDGNDRDGOIKRVCGNERPAPIQSIGSSLHVLPHSGSKNFDGF 229
DB 243 EQHEVESCPIYHLKAKGADCKP-----YCGKTPPTITSDHNMVHFPHSDGSEKNGF 298
QY 220 HAIYEETACSSSPCFHDGTCVLDKAGSYKACLAGYTGRCENILLEERNCSDPGVPNG 289
DB 229 RATYFT-----TARPEAL-----SAP----- 315
QY 220 YOKITGPGLINGRHAKIGTVVSPFCNNSTYLSGNEKRTCCQNGWSGKOPICIRACREP 349
DB 316 -----AVGTMEGSPFTYSQKVSFACGEGYLDGPDHVCADPSGSGVQPTC----- 362
QY 350 KISDLVRRRLVPMQVOSRETPHLQLYSAPFSKQKLOSAPTKKPALPFGDLPMGYOHLHTQ 409
DB 353 ---ELVNGCPLE-NISNIEIVDGNFS-----YADINL----- 391
QY 410 LQYECISPPYRRLGSSRPTCLRTGKWSGRAPSCIPICGI-----ENIT--APKTQGLRW 462
DB 392 ---YRC-DQFYEMAGCGTRFCAGGKMTGNEPSCPKICGESSFPSRDRIVGGGPKKG-AW 447
QY 463 PMQAIYRTSGVHDGSLHKAMFL---VCSGALVNEHTVVAACVTDLGKVTMKTAD 519
DB 448 PMQANV-----IHQAPRIKPKPCGALVDKAMITLAAHCV---GENDILPTGY 493
QY 520 LKVVLGKFEYRDDDRDEKTIQSLQISAILAHNPYDPIILDADIAIKLIDKARISTRVQPI 579
DB 494 FNVSLGLHKRKEPDNVVFP--EYERVIRHPDMDNDNDSDIALLEBEVDLTGYIRPV 551
QY 560 CLAAAS--RDLSTFQESH-I-TVAGNVLADYRSPGKNDTIRSGVSVYDLSLCEQHED 636
DB 552 CLQSGRGRSAQDVQEGRAGVVTGWRGTSNLF--GSEANTLOEVEVPVVDDECCSAVAG 609
QY 637 HGIPVSYDNNMFCASWEPTASDICTAETGGIAANSPFGRAFPBRMILMGVSYDXT 696
DB 610 ---DYPTVGNMLCAGLR-IGKSDSCDSDSGGPLEFQDDPT---KFYAGLVNSGEPSE 661
QY 697 CSH-RLSTAFTVLPFKDMIE 716
DB 662 CGRAKRGVAVRVENFVQMIK 682

RESULT 10
0688H4 ID 0688H4 PRELIMINARY: PRT: 688 AA.
AC 0688H4:
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Manose-binding lectin associated serine protease-3.
GN MASP1/3.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Notochord;
RX MEDLINE=22593355; PubMed=12707349;
RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Matusita A., Takahashi M.,
RA Matushita M., Fujita T.;
RT "Origin of Manose-Binding Lectin-Associated Serine Protease (MASP)-1
RT and MASP-3 involved in the Lectin Complement Pathway Traced Back to
RT the Invertebrate, Amphioxus."
RT J. Immunol. 170:4701-4707(2003).
DR EMBL; AB089507; BAC75889.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_5.

```

DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sush1_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00084; sush1; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_Spec; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Lectin; Protease.
SQ SEQUENCE 688 AA; 76890 MW; 39D62C0C038A78EB CRC64;

Query Match 14.6%; Score 576.5; DB 5; Length 688;

Best Local Similarity 27.4%; Pred. No. 1.4e-44;

Matches 185; Conservative 79; Mismatches 231; Indels 181; Gaps 34;

DR 77 DSCLI-HPGCTIFENCKSCRNMGWGLDDPYVKGFGYCAEGRAG-WYGGD--C-MRGC-129
DB 152 DECAVDNGGCHNF-----CHN-----YISGYCS-CRAGYIMKDKETCKFGGR 195
QY 130 QVLPAKPGQILLES---YPLNAHCWTIAHKPGFVIQLRFVMLSLEFD-----YWCQY 179
DB 196 QVLQLSGTISSEPEYRLYPKVLCDWKIQVEPGYVVLQF---DDPDVQGHPEVSCPY 252
QY 180 DYVAVRQDNDNDGQIKRVCGNERPAPIQSIGSLHVLFHSDGSKNFGFAIYEITAC 239
DB 253 DHLKIQADEXKYP---CCGKTVPPTITSDNNRVRVHSDDGENKGFATYFT--- 304
QY 240 SSSPCFHDGTCVLDAKAGSKACLAGYTGRCENILEERNCSDDPGPVNYQKITGPGCL 299
DB 305 -----TARPCAL-----SAP-----AYGT 319
QY 300 INGRHAKIGTVSFCNNNSYVLSGNEKRTCCQNGEMSGKQPI-C-IKACREPKISDLVARR 358
DB 320 MEGSNFTSQKVSFACGEGYLDGPDHRVCOADGWSGVQPTCELVNGCP----- 370
QY 359 VLPQOVQRETRFPHOLVLAASKQQLQSAFRTKRLPLPGDPLPMYQHLHTQLQ-YECISP 417
DB 371 -----PINSNGELEVDGNFSEYADIAIAYRC-DQ 396
QY 418 FYRRLGSSRRCTCLRTGKWSGRAPSCIPICGKI-----ENIT--APKTGLRPMQAIYR 470
DB 397 FYEMAGSETRCEADGKMTGNEPCKPICGSSSPFSRRIRYGGPSKKG-AMPQAMV-- 453
QY 471 RTSGVHDSLHKA-----WFLVCSGALVNERTVVAHAHCVTDLGKVTMIKTDLKVL 524
DB 454 -----HQGAPRIKKPF---GGLVLDKXKMLTLAHCV---GENDILPTGVFNVL 498
QY 525 GKTFYRDDRDREKTIQSLQISAILHPNYDPIILDADNILLKLDKARISTVQPICLAAS 584
DB 499 GLHKRKEPDDVVPF--QVERVIRHPDWKDNFSDILLLEKEKVDLTDIRPVCQRS 556
QY 585 --RDLSFGFQSHI-TVAGMNVLADVRSPGFKNITLRGGVSVVDYLCECHEDHGIPV 641
DB 557 GRGSAQOVQEGRAGVTVGKRTSLF--GSEANTLQVEVYVVDQECVAYEG--DY 611
QY 642 SVTDNMFCASENPITAPSDICTAETGIIAIVSPGASPEPRMHLGLVMSYDKTCSH-R 700

DB 612 PYTGNNLCAGLR-IGGKSCDSDSGGPELLFQDDPTT---RFYVAGLVSGEPSECGRAR 666
QY 701 LSTAFTKVLFPKDMIE 716
DB 667 KGVYARVENFVQMIK 682

RESULT 11

09PU71 PRELIMINARY; PRT; 698 AA.

AC 09PU71; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Mannose-binding protein-associated serine protease (Masp)

DE precursor.

GN MASP.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=99008558; PubMed=9794427;

RA Endo Y., Takahashi M., Nakao M., Saiga H., Sekine H., Matsushita M.,

RA Noraka M., Fujita T.;

RT "Two lineages of mannose-binding lectin-associated serine protease

RT (Masp) in vertebrates."

RL J. Immunol. 161:4924-4930(1998).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.

DR EMBL; D83276; BAA8669.1; -.

DR HSP; P00763; IDPO.

DR MEROPS; S01.198; -.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000152; Asx_hydroxyl_5.

DR InterPro; IPR000089; CUB.

DR InterPro; IPR009003; Cys_ser_trypsin.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR000436; Sush1_SCR_CCP.

DR Pfam; PF00431; CUB; 2.

DR Pfam; PF00084; sush1; 2.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR SMART; SM00032; CCP; 2.

DR SMART; SM00042; CUB; 2.

DR SMART; SM00179; EGF_CA; 1.

DR SMART; SM00020; Tryp_Spec; 1.

DR PROSITE; PS00010; ASX_HYDROXYL; 1.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS01186; EGF_2; 1.

DR PROSITE; PS01187; EGF_CA; 1.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

DR EGF-like domain; Hydroxylase; Protease; Serine protease; Signal.

FT SIGNAL 1 17

FT SIGNAL 17 17

SQ SEQUENCE 698 AA; 79414 MW; 79CE2FA4B77A6BB CRC64;

Query Match 12.4%; Score 489.5; DB 13; Length 698;

Best Local Similarity 25.0%; Pred. No. 1.9e-36;

Matches 183; Conservative 98; Mismatches 219; Indels 233; Gaps 38;

QY 142 ESYPLNAHCWTIAHKPGFVIQLRFVMLSLEFDYMCQYDVEVRDGNNDGQIIKRVCGN 201


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Db      345 DTQIECLKDGANSNKIPCTKIDCGVP-----AVLK 376
QY      382 QKLSAPTKKRALPFGDLPNGYOHLTQLOECISPEYRLGSSR--RTCLRTGKMSGRA 439
Db      377 HGLVTFSTRNNLTLY-----KSEIRYSCQAPYKMLHNTTGVYTCSAHGTWNEV 426
QY      440 -----PSCIPICG-----KIENITAPKTOGLMPPQALYRTSGVHDSLHKGA 484
Db      427 LKSLPCLPLVCGLPKFSRKHSIFN-GRPAQKGT-PIIAML-----SOLNGQ 474
QY      485 WFLVSGALVNERVVAHAACVTD-----LGKVTMIKTDLKVVLGKFY-RDDDRDE 535
Db      475 PF--CGSLLSGSNWVLTAAHCHLHPDPEPILHNSLSPDFKIMGMRRRSDDE 532
QY      536 KTQSLQISAIIHPNYDPLLDADIALKLDKARISTVOPICLAASDLSFGESH 595
Db      533 ---QHLYVKHIMLHPILNPSSTFENDLGLVELSESPRLNDFVMPCLPE---HPSTEGTW 585
QY      596 ITVAGNNVLDVRSFGKNDLRSQVVSVDLSLCEQHEDHGIPIVSTDNMFCAWEP 655
Db      586 VIVSGMKQFLQRLP---ENLMEIEIPVYHTCOEAYPLG--KKTVDMLCAG-EKE 638
QY      656 APSDICTAETGIAAASFPGRASPEPRMHLMLGLVMSYDTCSHRLSTAFKVLFPKDWI 715
Db      639 GGDACAGDSGSPVNT---KDAERDQWLVGVVSWGDCGKKDRYG-VYSIYIPNDWI 693
QY      716 ER 717
Db      694 QR 695

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RESULT 13

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Q8CHN8 PRELIMINARY; PRT; 703 AA.
AC Q8CHN8;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Mannose-binding protein associated serine protease-1.
GN MASP-1/3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP STRAIN=Sprague Dawley;
RA Stover C.M., Lynch N.J., Dahl M.R., Hanson S., Frankenberger M.,
RA Ziegler-Heitbrock L., Thiel S., Schwaeble W.J.;
RT "The rat homologues of MASP-1 and MASP-3, components of the lectin
RT activation pathway of Complement."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ457084; CAD29746.1;
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0004235; F:peptidase activity; IEA.
DR GO: GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro: IPR00152; AaX_hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR009003; Cys_ser_trypsin.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR000436; Sushi_SCR_CCP.
DR Pfam: PF00431; CUB; 2.
DR Pfam: PF00084; sushi; 2.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00424; CUB; 2.

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DR SMART; SM00179; EGF CA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF CA; 1.
DR PROSITE; PS01187; EGF CA; 2.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PROTEASE.
SQ SEQUENCE 703 AA; 80049 MW; 8E4CFA6413020F18 CRC64;

Query Match 12.2%; Score 482.5; DB 11; Length 703;
Best Local Similarity 22.9%; Pred. No. 8,5e-36;
Matches 193; Conservative 108; Mismatches 259; Indels 281; Gaps 44;

QY 11 LTFLOLL-----ISSLPREYVINE-----ACPG-----AEWIMCRE---- 44
Db 4 LSFRRLLVHVLCLTLEVSAAHVEINEMFGQIQSGYDPSYSDSEVTNITVPEFRVQ 63
QY 45 -----CCEYDOIE-----CVC-----PGKREV----- 61
Db 64 LYFMHNLSSYLCEYDVKVEDEQVLTATFCGRETTTEQTPGQEVLSPSFSVTR 123
QY 62 -----VGTYIPCCRNENECDCILHPCTIFENCKSGNSWGGLTD 105
Db 124 SDFSNERFTGPDANMAVDVDECKERDELSCHY-----CHN----- 163
QY 106 FYVKGFFCAECRAGY---GGDC-MRC-GQVLRAPKQIIL---ESYPLAHCEWTH 155
Db 164 -YIGGYCS-CRFGYILHTDNRCTRCVCSGNLFTORTGTITSPDYENPYPKSECSYITD 221
QY 156 AKRGVIOIRFVWLSEFD-----YMCQDYVAVDGDNRDQGIKRCGNRPAPIOS 209
Db 222 LSEGFWVTLHFEDI---FIEDHPEVPCPYDIKIKAGSKWGP---CGEKSPPIST 274
QY 210 ISSSLVLFHSDGSKNFDFHAIYEITACSSSPCFHDTCVLDKAGSYKACLAGYTSQ 269
Db 275 QSHSIIILPRSDMSGNRMRL-----SYRAA-----GN 303
QY 270 RCENLLEKNCSDPGPVPNGYOKITGGPGLNGRAKIGTVVSFFCNMY-VLSGNE--- 325
Db 304 ECPKL-----QP--PV--YGIKIPSOAVSFQKQ---VLISCDTYKVLKDEVND 347
QY 326 --KRTQNGENSGKQPIG-ICACREPKISDLVRRRLVPMQVSRETPHQLYSAFASK 382
Db 348 TFOIECLKDGANSNKIPCTKIDCGVP-----AVLK 379
QY 383 KLSAPTKKRALPFGDLPNGYOHLTQLOECISPEYRLGSSR--RTCLRTGKMSGRA 439
Db 380 GLVTFSTRNNLTLY-----KSEIRYSCQAPYKMLHNTTGVYTCSAHGTWNEV 429
QY 440 -----PSCIPICG-----KIENITAPKTOGLMPPQALYRTSGVHDSLHKGA 485
Db 430 KSLPCLPLVCGLPKFSRKHSIFN-GRPAQKGT-PIIAML-----SOLNGQ 477
QY 486 FLVCSGALVNERVVAHAACVTD-----LGKVTMIKTDLKVVLGKFY-RDDDRDE 536
Db 478 F--CGSLLSGSNWVLTAAHCHLHPDPEPILHNSLSPDFKIMGMRRRSDDE- 534
QY 537 KTQSLQISAIIHPNYDPLLDADIALKLDKARISTVOPICLAASDLSFGESH 596
Db 535 ---QHLYVKHIMLHPILNPSSTFENDLGLVELSESPRLNDFVMPCLPE---HPSTEGTW 588
QY 597 TVAGNNVLDVRSFGKNDLRSQVVSVDLSLCEQHEDHGIPIVSTDNMFCAWEP 655
Db 589 IYSGMKQFLQRLP---ENLMEIEIPVYHTCOEAYPLG--KKTVDMLCAG-EKEG 641
QY 657 PSDICTAETGIAAASFPGRASPEPRMHLMLGLVMSYDTCSHRLSTAFKVLFPKDWI 716
Db 642 GGDACAGDSGSPVNT---KDAERDQWLVGVVSWGDCGKKDRYG-VYSIYIPNDWI 696
QY 717 R 717

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Db 697 R 697

RESULT 14

ID Q8AXR1 PRELIMINARY; PRT; 717 AA.

AC Q8AXR1; 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 GN Manose-binding lectin-associated serine protease-3a.
 GN MASP-3a.
 OC Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Endo Y., Nonaka M., Saiga H., Kakinuma Y., Takahashi M.,
 RA Matsushita M., Fujita T.
 RT "Ancient origin and extensive distribution of manose-binding lectin-
 RT associated serine protease-3 in vertebrate lineage."
 RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB076636; BAC41339.1; -.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:000529; F:sugar binding; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007157; P:heterophilic cell adhesion; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR000152; Asx_hydroxyl_S.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR009003; Cys_Ser_trypsin.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF_Like.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR000436; Sushi_SCR_CCP.
 DR Pfam: PF00431; CUB; 2.
 DR Pfam: PF00084; sushi; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPsin.
 DR SMART: SM00032; CCP; 2.
 DR SMART: SM00042; CUB; 2.
 DR SMART: SM00181; EGF; 1.
 DR SMART: SM00179; EGF_Ca; 1.
 DR SMART: SM00020; Tryp_SPC; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS01180; CUB; 2.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_Ca; 1.
 DR PROSITE: PS02040; TRYPsin DOM; 1.
 DR PROSITE: PS00135; TRYPsin_SER; 1.
 KM lectin; Protease.
 SQ SEQUENCE 717 AA; 80959 MW; 5130CAF3CBEBBA0 CRC64;

Query Match 12.2%; Score 482; DB 13; Length 717;
 Best Local Similarity 25.4%; Pred. No. 9, 7e-36;
 Matches 180; Conservative 100; Mismatches 240; Indels 188; Gaps 36;

QY 69 CRNEENECBSCLHPGCTIFENCKSRNGSWGTLDDFYVKGFGYCAECRAGWY---GGD 124
 Db 141 CTKSEBDLVCDH-----CHN-----YIGGYCS-CRFGYLLHNDNT 178
 QY 125 C-MRGOVILAPK-GQILLESYP---LNAHCMTTHAKGPIQIRF---VMSLEPDY 175
 Db 179 CKVECSDNLFTRSGSLISPDYGPVAKSSDCRYRIQLBEGFVYNLHFDNFVVEHPHY 238

QY 176 MCOYDYVEVRDGDNRDQIIRKVCNERNPAPFIOGSSLHVLFFHSDSKNFDFGHAAYEE 235
 Db 239 KCPYDIKIKTKGKEPGL-----CGEKSFGRIETGNSVQILFFHSNDSNGENGRISY-- 292
 QY 236 ITACSSPCHFDGTCLDKAGSYKACLAGYTGRCENLEERNCSDPGCVNG-----Y 290
 Db 293 -----SVTGMPCPPL-----HPPMCKLEBPQ 314
 QY 291 QKITGPELNGRAHAKIGTVSPFCNNNSY-VLGSNEKR-----TCOONGESGKOPIC-I 343
 Db 315 SEYT-----FKQNVIS--CNQGYVKKNVEMESIQICRKGDTGNSNQIPQOI 362
 QY 344 KACEPKSIDLVRRRVLPVQYQSRHETPLHQLYSAFSKOKLSAPTYKPPALPFQDLPMGY 403
 Db 363 VDCKKPK-----EIENG-----FIYSTAEKRTYQSS----- 390
 QY 404 QHMTQLOLEYCISPPYRRLGSSR--RTCLRGKMS-----GRAPSCIPCGK----- 448
 Db 391 -----FNYSCEPEYMMVNPITLVYTCDSAGEWTSOEIGAKIPTCOPCGKPARPLPGI 444
 QY 449 IENITAPKT--QGLRMPQALVYRTSGVHDGS-LHKGMFLVCSGALVNERVTVAANC 505
 Db 445 VKRIIGGNAPGP-FPQVULIV-----VEDLSKVPMMKW--GGGALISDWVLTAAHN 496
 QY 506 VTDLGK--VTMIKTADLKVVLGKFRYDDDRDEKTTOSLQISAILLHPNYPILLADIA 562
 Db 497 LRSQGRDWTVPVAKHEVTYLG--LHDVASKTDAVVRTEKILILHEMFPDESYNHDA 553
 QY 553 ILKLIDKARISTROYPTL--AASRDLSTSPESHITVAGNV-----LADVRPGRFND 615
 Db 554 LVKNEKVIQVYMPVCLPFLHELEBPQNTGLVAGWISDPNITVDVSISSGKTH 613
 QY 616 T--LRSQVSVVDSLICEQHEHDGIPVSVTDNMFCSMEWETASDICTAETGIAVASF 673
 Db 614 SAILQVVLPLYVAHVACSEYSSGNSVTEMFCAGY-EGGKDTLGSQG---AF 668
 QY 674 PGRASPEPRHLMGVSWSYKTC-SHRLTAFTKVLFPKQWIERANK 720
 Db 669 IMODTDRKVAQGLVSWGPEEGSKQVGVYTKVSNFVMDNLK 716

RESULT 15

ID Q96RS4 PRELIMINARY; PRT; 728 AA.

AC Q96RS4;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Complement factor MASP-3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21378425; PubMed=11485744;
 RA Dahl M.R., Thiel S., Matsushita M., Fujita T., Willis A.C.,
 RA Christensen T., Vorup-Jensen T., Jensenius J.C.;
 RT "Masp-3 and its association with distinct complexes of the mannan-
 RT binding lectin complement activation pathway."
 RL Immunity 15:127-135(2001).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 DR EMBL; AF284421; AAK84071.1; -.
 DR HSPB; P00761; IAN1.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR000152; Asx_hydroxyl_S.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR009003; Cys_Ser_trypsin.

DR InterPro; IPR001861; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR01254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_Scr_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00084; Sushi; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR EGF-like domain; Hydrolyase; Protease; Serine protease.
SC SEQUENCE 728 AA; 81860 MW; 09B5297A6C14283A CRC64;

Query Match 11.9%; Score 468; DB 4; Length 728;

Best Local Similarity 25.0%; Pred. No. 2e-34;

Matches 180; Conservative 97; Mismatches 228; Indels 214; Gaps 39;

QY 69 CRNEBNECDCLIPGCTIFENCKSCRGSGWGLDIPYKGFYCAEGRAGWY----GGD 124
DB 143 CKEREDEELSCDHY-----CHN-----YIGYYCS-CRFGYIATDNR 180
QY 125 C-MRGGVLRAPKQGIIL-ESYPLNAHCWNTIHAKEGVIQLRPMLEFD--- 174
DB 181 CRVCSDNLFQRTGVITSPFPNPFKSSSECLYTIIEBGFVNLOPEDI--FDIEDH 237
QY 175 --YMQQDYVEVRQDNRDQIIRKVCGERPAPISIGSSLAHYLFHSDGSKNDFGFAI 232
DB 238 PEVPCPYDIKIKVGP---KVLGPFCEKAPFISTQSHVLIIFHSDNGENRGWRL- 292
QY 233 YEBITACSSPCFHDGTCLVLDKAGSYKACIAGTGORCENLBERNCSDPGPVNGYQK 292
DB 293 -----SYRAA-----GNECPPL-----QP-PVH----- 309
QY 293 ITGGPGLINGRAKIGTVVSFF-----CNSY-VLSGNEK-----TCQONGEMSKQ 339
DB 310 -----GKIEPSQAKT-----FFKQVLYVSCDTGYKVLKDNVEMDTFOIECLKDGTMSNKI 359
QY 340 PIC-IKACREPKISDLVRRVLPQVQSRETPLQLYSAFSSKQLOSAPTKKPALPFGD 398
DB 360 FTCKIVDCRAP-----GE 372
QY 399 LPMGYQHHT-----QIQYECISPFYRLGSSR--RTCLRTGKWS---GRA--PSC 442
DB 373 LEHGITEFTSTNNLTTYKSEIKYSCQEPYKMLNNTGIYTCQAQVMMNKVLRSLPTC 432
QY 443 IPIGK-----IENITAPKT--QGLRPMQAAIYRTSGVHDS--LHKGAWFLVCSG 491
DB 433 LPECGQPSRLPSLVKRIIGGRNAPGL-FPMQALIV-----VEDTSRVNDKWF--GSG 484
QY 492 ALVNERIVVAACHVTLGKVTMTKTADLVKLVGKPYRDDDRDEKTIQSLQISAILIHPN 551
DB 485 ALLSASWILTAHVRSORDTTVIPVSKHNTVYLGLHVDKSGAVNSSARVVLHPD 544
QY 552 YDPIILLDDIALLKLDKARISTVQPCICLASRLDSTSPESH--TVAGW-----NYL 604
DB 545 FNIQNTNHDIALVQIQEPVPLGPHWPCVCLPR--LEPEGPAFPHLGLVAGMGISNPVT 601
QY 605 AD-VASPEFK--NDTLRSGVSVVDSLCEQHEDHGIPVSTVDNMFCAWSEPTAPSDIC 661
DB 602 VDEILSSGTRTLSDVLYKLVPHVPAECKTSYBSRSGNYSTENMFCAGY--EGKQDTC 660
QY 662 TAETGGLAIVSFPGRASPEPRMHLMLGLYSWYDKTC-SHRLSTAFATKYLPRKDWIERNM 719
DB 661 LGDSGG-AFVIFDDLSQ--RWVVGGLVSWGPECGSKQYVGYVTKVSNYVDWVMEQM 715

Search completed: August 18, 2004, 16:25:01
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:29:15 ; Search time 44 Seconds
(without alignments)
5163.025 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 720

Sequence: 1 MELGCWTQLGLTFLQLLLIS.....LSTAFTRKVLPEKDWIRBNMK 720

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 700 summaries

Database :

1: SPTRMBL.25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvtrus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	446	61.9	737	4	Q96JW2	Q96JW2 homo sapien
2	178	24.7	181	4	Q9Y432	Q9Y432 homo sapien
3	61	8.5	720	11	Q8BU25	Q8BU25 mus musculus
4	41	5.7	720	11	Q8K2B8	Q8K2B8 mus musculus
5	9	1.2	222	11	Q91WZ0	Q91WZ0 ratius norvy
6	9	1.2	276	16	Q86553	Q86553 streptomyce
7	9	1.2	691	13	Q57658	Q57658 gallus galli
8	9	1.2	923	13	Q8QFX6	Q8QFX6 brachydanio
9	9	1.2	923	13	Q8AXP1	Q8AXP1 brachydanio
10	9	1.2	926	4	Q9U000	Q9U000 homo sapien
11	9	1.2	1015	4	Q9Y6L7	Q9Y6L7 homo sapien
12	9	1.2	1464	5	Q23395	Q23395 drosophila
13	9	1.2	1464	5	Q9VC47	Q9VC47 drosophila
14	9	1.2	1464	5	Q24132	Q24132 drosophila
15	9	1.2	2531	5	Q16004	Q16004 lytechinus
16	8	1.1	81	15	Q79204	Q79204 human immun

17	8	1.1	136	11	Q8CEX5	Q8CEX5 mus musculu
18	8	1.1	152	11	Q924X1	Q924X1 mus musculu
19	8	1.1	234	13	Q90244	Q90244 actinomor t
20	8	1.1	235	6	Q28731	Q28731 oryctolagus
21	8	1.1	240	16	Q8D223	Q8D223 yersinia pe
22	8	1.1	242	16	Q8D0T9	Q8D0T9 yersinia pe
23	8	1.1	302	5	Q9XUN6	Q9XUN6 caenorhabd
24	8	1.1	385	13	Q90WS2	Q90WS2 elaphs sp.
25	8	1.1	413	2	Q7X370	Q7X370 uncultured
26	8	1.1	556	16	Q7UX12	Q7UX12 rhodospirell
27	8	1.1	607	13	Q91001	Q91001 gallus gall
28	8	1.1	608	13	Q9PTW7	Q9PTW7 struthio ca
29	8	1.1	611	10	Q94HU9	Q94HU9 oryza sativ
30	8	1.1	611	10	Q7XG00	Q7XG00 oryza sativ
31	8	1.1	719	13	Q9PYV2	Q9PYV2 triakis bcy
32	8	1.1	737	16	Q8YTB7	Q8YTB7 anabaena sp
33	8	1.1	752	13	Q42374	Q42374 brachydantlo
34	8	1.1	764	16	Q8XTM0	Q8XTM0 raietonia s
35	8	1.1	963	5	Q44393	Q44393 pisaster oc
36	8	1.1	1019	5	Q8T9S1	Q8T9S1 tachyleus
37	8	1.1	1070	5	P91972	P91972 aplysia cal
38	8	1.1	1083	5	Q26423	Q26423 carcinocor
39	8	1.1	1238	5	Q9VCD8	Q9VCD8 drosophila
40	8	1.1	1338	5	Q9N614	Q9N614 drosophila
41	8	1.1	1316	4	Q96JW7	Q96JW7 homo sapien
42	7	1.0	36	16	Q7UL51	Q7UL51 rhodospirell
43	7	1.0	37	16	Q8F0D5	Q8F0D5 leptospira
44	7	1.0	54	16	Q8N087	Q8N087 corynebact
45	7	1.0	59	16	Q99SV1	Q99SV1 staphylococ
46	7	1.0	59	16	Q931M9	Q931M9 staphylococ
47	7	1.0	61	10	Q8GZP9	Q8GZP9 arabidopsis
48	7	1.0	61	10	Q8GZP8	Q8GZP8 arabidopsis
49	7	1.0	61	10	Q8GZP7	Q8GZP7 arabidopsis
50	7	1.0	61	10	Q8GZP6	Q8GZP6 arabidopsis
51	7	1.0	61	10	Q8GZP5	Q8GZP5 arabidopsis
52	7	1.0	61	10	Q8GZP4	Q8GZP4 arabidopsis
53	7	1.0	61	10	Q8GZP3	Q8GZP3 arabidopsis
54	7	1.0	61	10	Q8GZP2	Q8GZP2 arabidopsis
55	7	1.0	61	10	Q8GZP1	Q8GZP1 arabidopsis
56	7	1.0	71	9	Q855B3	Q855B3 mycobacteri
57	7	1.0	75	10	Q9C8F3	Q9C8F3 arabidopsis
58	7	1.0	81	12	Q9EMT8	Q9EMT8 amebaet mo
59	7	1.0	81	15	Q79303	Q79303 human immun
60	7	1.0	81	15	Q79209	Q79209 human immun
61	7	1.0	82	15	Q90D16	Q90D16 human immun
62	7	1.0	86	2	Q7X3H3	Q7X3H3 thlocapna r
63	7	1.0	91	10	Q9M9B7	Q9M9B7 arabidopsis
64	7	1.0	106	12	Q87074	Q87074 suid herpes
65	7	1.0	109	5	Q866A7	Q866A7 caenorhabd
66	7	1.0	112	5	P91967	P91967 trichinella
67	7	1.0	114	17	Q9YCI9	Q9YCI9 aeropyrum p
68	7	1.0	120	5	Q8T6A0	Q8T6A0 aplysia cal
69	7	1.0	124	16	Q8G3X3	Q8G3X3 blifidobact
70	7	1.0	124	16	Q81G20	Q81G20 bacillus ce
71	7	1.0	124	16	Q7WC39	Q7WC39 bordetella
72	7	1.0	129	16	Q87F53	Q87F53 vibrio para
73	7	1.0	132	8	Q8W697	Q8W697 apantania zo
74	7	1.0	133	16	Q9L158	Q9L158 streptomyce
75	7	1.0	143	16	Q9S9X5	Q9S9X5 arabidopsis
76	7	1.0	144	8	Q8WG98	Q8WG98 moropyche
77	7	1.0	154	2	Q50211	Q50211 mycobacteri
78	7	1.0	156	16	Q8PFF6	Q8PFF6 xanthomonas
79	7	1.0	157	5	Q95W21	Q95W21 anthomomus
80	7	1.0	158	10	Q9AY48	Q9AY48 oryza sativ
81	7	1.0	164	4	Q7RDB3	Q7RDB3 oryza sativ
82	7	1.0	164	4	Q96QK6	Q96QK6 homo sapien
83	7	1.0	168	16	Q8DUF0	Q8DUF0 synchococ
84	7	1.0	168	16	Q928J3	Q928J3 chlamydia p
85	7	1.0	169	16	Q87NKG	Q87NKG vibrio para
86	7	1.0	170	10	Q84SG4	Q84SG4 chlamydom
87	7	1.0	170	10	Q84RTE	Q84RTE chlamydom
88	7	1.0	171	2	Q9R0P0	Q9R0P0 vibrio chol
89	7	1.0	171	16	Q9K279	Q9K279 chlamydia p

90	172	13	Q9DFD1	Q9dfd1 oncorhynch	163	7	1.0	286	4	Q9H7G9	Q9h7g9 homo sapien
91	172	16	Q9C1Y6	Q9c1y6 pasteurella	164	7	1.0	291	2	Q9R9T0	Q9r9t0 pseudomonas
92	176	13	Q9PUC7	Q9puc7 gallus gall	165	7	1.0	291	16	Q9BN41	Q9bn41 pseudomonas
93	178	10	Q9LMH2	Q9lmh2 arabidopsis	166	7	1.0	299	5	Q8TRD9	Q8trd9 trypanosoma
94	181	16	Q8VNZ6	Q8vnz6 vibrio para	167	7	1.0	300	5	Q8TN70	Q8tn70 drosophila
95	185	2	Q9KWV2	Q9kwv2 salmonella	168	7	1.0	301	13	Q7ZSK7	Q7zsk7 fugu rubrip
96	187	10	Q84SJ0	Q84sj0 matricaria	169	7	1.0	304	16	Q8XXF6	Q8xxf6 ralsstonia s
97	189	10	Q84SJ0	Q84sj0 matricaria	170	7	1.0	306	10	Q8LSB0	Q8lsb0 oryza sativ
98	191	16	Q9RSA2	Q9rsa2 deinooccus	171	7	1.0	307	16	Q9KV89	Q9kv89 vibrio chol
99	191	16	Q8ILD6	Q8ild6 bacillus an	172	7	1.0	312	3	Q12125	Q12125 saccharomye
100	198	16	Q8XR75	Q8xr75 ralsstonia s	173	7	1.0	315	2	Q55220	Q55220 streptomyce
101	204	13	Q8U1S7	Q8u1s7 xenopus lae	174	7	1.0	317	2	Q9KWA7	Q9kwa7 agrobacteri
102	208	2	Q9Z315	Q9z315 bradyrhizob	175	7	1.0	324	13	Q90Z55	Q90z55 scopthalmu
103	211	16	Q8ZEH2	Q8zeh2 yerisina pe	176	7	1.0	329	16	Q89MG1	Q89mg1 bradyrhizob
104	212	16	Q8XCB6	Q8xcb6 escherichia	177	7	1.0	329	17	Q89DM3	Q89dm3 pyrococcus
105	213	16	Q9CE55	Q9ce55 lactococcus	178	7	1.0	330	2	Q30523	Q30523 vibrio shii
106	214	16	Q87K02	Q87k02 vibrio para	179	7	1.0	332	16	Q8NKT9	Q8nkt9 strephlococ
107	215	16	Q9RKP8	Q9rkp8 streptomyce	180	7	1.0	333	16	Q9K7W7	Q9k7w7 bacillus ha
108	215	16	Q8DUJ8	Q8duj8 yerisina pe	181	7	1.0	336	16	Q8PR42	Q8pr42 xanthomonas
109	221	5	Q95S24	Q95s24 drosophila	182	7	1.0	336	16	Q69510	Q69510 mycobacteri
110	221	5	Q9VWV7	Q9vwv7 drosophila	183	7	1.0	337	17	Q7WLM07	Q7wlm07 bordetella
111	222	5	Q8K0M4	Q8km4 saccharopol	184	7	1.0	337	17	Q9YDH3	Q9ydh3 aeropyrum p
112	222	3	Q871A9	Q871a9 neutrospora	185	7	1.0	338	16	Q8PE85	Q8pe85 xanthomonas
113	223	3	Q7Z724	Q7z724 inocybe sie	186	7	1.0	342	10	Q7XEE3	Q7xex3 oryza sativ
114	225	8	Q8M0X1	Q8m0x1 gynodiactyl	187	7	1.0	343	16	Q8D7G2	Q8d7g2 vibrio vuln
115	225	10	Q8W5L0	Q8w5l0 oryza sativ	188	7	1.0	344	16	Q7VV13	Q7vv13 bordetella
116	225	10	Q7XH60	Q7xh60 oryza sativ	189	7	1.0	344	10	Q84QA9	Q84qa9 oryza sativ
117	226	16	Q81KCS	Q81kcs bacillus an	190	7	1.0	344	16	Q92M18	Q92m18 rhizobium m
118	226	16	Q81EL1	Q81el1 bacillus ce	191	7	1.0	345	16	Q7W718	Q7w718 bordetella
119	227	3	Q7Z8D8	Q7z8d8 inocybe ada	192	7	1.0	349	17	Q9YBV1	Q9ybv1 aeropyrum p
120	227	16	Q88Q18	Q88q18 pseudomonas	193	7	1.0	350	5	Q18122	Q18122 caenorhabdi
121	227	17	Q29875	Q29875 archaeoglob	194	7	1.0	352	11	Q8C9H0	Q8c9h0 mus musculu
122	228	3	Q7Z8Z5	Q7z8z5 inocybe che	195	7	1.0	354	16	Q99QEO	Q99qe0 bradyrhizob
123	228	16	Q889S0	Q889s0 pseudomonas	196	7	1.0	354	16	Q99QEO	Q99qe0 bradyrhizob
124	231	16	Q9Z795	Q9z795 chlamydia p	197	7	1.0	355	2	Q99Z86	Q99z86 bradyrhizob
125	232	16	Q9HWM1	Q9hwm1 pseudomonas	198	7	1.0	355	8	Q37446	Q37446 carabus bla
126	233	3	Q7Z8Z4	Q7z8z4 inocybe che	199	7	1.0	355	8	Q99052	Q99052 carabus por
127	235	10	Q8YV63	Q8yv63 arabidopsis	200	7	1.0	355	8	Q9PM04	Q9pm04 carabus van
128	235	10	Q8LD25	Q8ld25 arabidopsis	201	7	1.0	355	8	Q9TE94	Q9te94 carabus bla
129	235	13	Q91004	Q91004 gecko gecko	202	7	1.0	355	8	Q9GBL3	Q9gb13 carabus poc
130	236	17	Q9HGG1	Q9hgg1 halobacteri	203	7	1.0	355	8	Q9B9L9	Q9b9l9 carabus hum
131	237	13	Q7ZML3	Q7zml3 xenopus lae	204	7	1.0	355	8	Q9GBK8	Q9gbk8 carabus sma
132	238	3	Q7Z7Z1	Q7z7z1 inocybe ste	205	7	1.0	355	8	Q9M1Z5	Q9m1z5 carabus lop
133	238	16	Q8CW43	Q8cw43 escherichia	206	7	1.0	355	8	Q9TEA3	Q9tea3 carabus bla
134	239	13	Q91218	Q91218 oncorhynch	207	7	1.0	355	8	Q9TE05	Q9te05 carabus can
135	239	16	Q9KOD6	Q9k0d6 vibrio chol	208	7	1.0	355	8	Q9M1Z7	Q9m1z7 carabus sma
136	240	16	Q891B3	Q891b3 bradyrhizob	209	7	1.0	355	8	Q9TE93	Q9te93 carabus bla
137	241	16	Q8FRK8	Q8frk8 corynebacte	210	7	1.0	355	8	Q9MR60	Q9mr60 carabus por
138	244	10	Q7X990	Q7x990 oryza sativ	211	7	1.0	355	8	Q9TB99	Q9tb99 carabus bla
139	247	16	Q8XGUV	Q8xguv escherichia	212	7	1.0	355	8	Q9GBN2	Q9gbn2 carabus nan
140	247	16	Q8FCQ3	Q8fcq3 escherichia	213	7	1.0	355	8	Q9TE04	Q9te04 carabus can
141	247	16	Q83PU8	Q83pu8 shigella fl	214	7	1.0	355	8	Q9TEA9	Q9tea9 carabus bla
142	248	10	Q49138	Q49138 arabidopsis	215	7	1.0	355	8	Q9MR79	Q9mr79 carabus por
143	249	11	Q8C1Q8	Q8c1q8 mus musculu	216	7	1.0	355	8	Q9TDY5	Q9tdy5 carabus cya
144	250	10	Q8ZFK6	Q8zfk6 yerisina pe	217	7	1.0	355	8	Q9B9R9	Q9b9r9 carabus lac
145	250	16	Q89UG6	Q89ug6 bradyrhizob	218	7	1.0	355	8	Q37444	Q37444 carabus bla
146	253	16	Q9Y7A9	Q9y7a9 metarhizium	219	7	1.0	355	8	Q9TEB6	Q9teb6 carabus bla
147	255	12	Q84700	Q84700 pea early b	220	7	1.0	355	8	Q9TE85	Q9te85 carabus bla
148	255	16	Q8HDL2	Q8hdl2 agrobacteri	221	7	1.0	355	8	Q47486	Q47486 carabus sic
149	265	2	Q07812	Q07812 mycobacteri	222	7	1.0	355	8	Q9B9S4	Q9b9s4 carabus kad
150	265	16	Q07181	Q07181 mycobacteri	223	7	1.0	355	8	Q9TEA5	Q9tea5 carabus bla
151	265	16	Q7U190	Q7u190 mycobacteri	224	7	1.0	355	8	Q9M1Z4	Q9m1z4 carabus gen
152	266	12	Q81916	Q81916 biomla trop	225	7	1.0	355	8	Q47484	Q47484 carabus vir
153	266	12	Q9QU80	Q9qu80 tt virus. o	226	7	1.0	355	8	Q9TDY2	Q9tdy2 carabus arx
154	268	5	Q9XY56	Q9xy56 ctenocephal	227	7	1.0	355	8	Q9GBL6	Q9gb16 carabus arx
155	271	4	Q9NPM7	Q9npm7 homo sapien	228	7	1.0	355	8	Q9TEA2	Q9tea2 carabus bla
156	272	2	Q51013	Q51013 neisseria g	229	7	1.0	355	8	Q9TEA0	Q9tea0 carabus bla
157	273	16	Q83DM2	Q83dm2 coxiella bu	230	7	1.0	355	8	Q9TE08	Q9te08 carabus sel
158	278	2	Q84C08	Q84c08 pseudomonas	231	7	1.0	355	8	Q9TDY8	Q9tdy8 carabus con
159	280	16	Q87X78	Q87x78 pseudomonas	232	7	1.0	355	8	Q37443	Q37443 carabus bla
160	281	17	Q8U4H8	Q8u4h8 pyrococcus	233	7	1.0	355	8	Q37447	Q37447 carabus bla
161	282	12	Q8UXE9	Q8uxe9 roseellinia	234	7	1.0	355	8	Q78724	Q78724 carabus bla
162	284	5	Q96089	Q96089 haemaphysal	235	7	1.0	355	8	Q9TEA7	Q9tea7 carabus bla

236	7	1.0	355	8	09GBL0	09gb10 carabus ale	309	7	1.0	355	8	09TE10	09te10 carabus oci
237	7	1.0	355	8	09B9S1	09b9s1 carabus aen	310	7	1.0	355	8	09GBK5	09gbk5 carabus con
238	7	1.0	355	8	09TDY0	09tdy0 carabus cle	311	7	1.0	355	8	09BDY9	09bdy9 carabus con
239	7	1.0	355	8	09B9S3	09b9s3 carabus lin	312	7	1.0	355	8	037445	037445 carabus bla
240	7	1.0	355	8	09GBK6	09gbk6 carabus gly	313	7	1.0	355	8	09B9R7	09b9r7 carabus bal
241	7	1.0	355	8	09GBL8	09gbl8 carabus gra	314	7	1.0	355	8	09TE89	09te89 carabus bla
242	7	1.0	355	8	09TEA6	09tea6 carabus tra	315	7	1.0	355	8	09TE13	09te13 carabus sem
243	7	1.0	355	8	09TDY1	09tdy1 carabus trl	316	7	1.0	355	8	037465	037465 carabus por
244	7	1.0	355	8	09TDY7	09tdy7 carabus tuk	317	7	1.0	355	8	099054	099054 carabus por
245	7	1.0	355	8	09TEB4	09teb4 carabus bla	318	7	1.0	355	8	09M1Z3	09m1z3 carabus geh
246	7	1.0	355	8	09TEB3	09teb3 carabus bor	319	7	1.0	355	8	09GBN1	09gbl1 carabus ema
247	7	1.0	355	8	09TEB0	09teb0 carabus bor	320	7	1.0	355	8	09GBL4	09gbl4 carabus pot
248	7	1.0	355	8	09M1L0	09m1l0 carabus bor	321	7	1.0	355	8	09TEB0	09teb0 carabus bla
249	7	1.0	355	8	09GBL2	09gbl2 carabus bor	322	7	1.0	355	8	09MR78	09mr78 carabus por
250	7	1.0	355	8	09TEB2	09teb2 carabus bor	323	7	1.0	355	8	09GBM3	09gbm3 carabus ign
251	7	1.0	355	8	037441	037441 carabus van	324	7	1.0	355	8	09GBM8	09gbm8 carabus hum
252	7	1.0	355	8	09GBL5	09gbl5 carabus ari	325	7	1.0	355	8	09GBK7	09gbk7 carabus gly
253	7	1.0	355	8	09MR77	09mr77 carabus por	326	7	1.0	355	8	09GBL9	09gbl9 carabus gra
254	7	1.0	355	8	09MR76	09mr76 carabus por	327	7	1.0	355	8	09TEB1	09teb1 carabus sel
255	7	1.0	355	8	09TDY6	09tdy6 carabus tou	328	7	1.0	355	8	09TEB7	09teb7 carabus bla
256	7	1.0	355	8	09TEB6	09teb6 carabus bla	329	7	1.0	355	8	09TE95	09te95 carabus bla
257	7	1.0	355	8	09B9M0	09b9m0 carabus hum	330	7	1.0	355	8	09M1J7	09m1j7 carabus van
258	7	1.0	355	8	09TEB2	09teb2 carabus bla	331	7	1.0	355	8	09MR81	09mr81 carabus por
259	7	1.0	355	8	079586	079586 carabus sui	332	7	1.0	355	8	09B9R8	09b9r8 carabus str
260	7	1.0	355	8	09GBM0	09gbm0 carabus sui	333	7	1.0	355	8	037448	037448 carabus bla
261	7	1.0	355	8	09TEA8	09tea8 carabus bla	334	7	1.0	355	8	09GBK9	09gbk9 carabus ale
262	7	1.0	355	8	09TEB8	09teb8 carabus bla	335	7	1.0	355	8	09B9S6	09b9s6 carabus str
263	7	1.0	355	8	09GBM5	09gbm5 carabus oia	336	7	1.0	355	8	09TEB3	09teb3 carabus bla
264	7	1.0	355	8	09GBL7	09gbl7 carabus exl	337	7	1.0	355	8	09GBM4	09gbm4 carabus mir
265	7	1.0	355	8	09B1L1	09b1l1 carabus lep	338	7	1.0	355	8	09TE12	09te12 carabus sem
266	7	1.0	355	8	09GBM2	09gbm2 carabus bra	339	7	1.0	355	8	09TE91	09te91 carabus bla
267	7	1.0	355	8	037459	037459 carabus bla	340	7	1.0	355	8	079585	079585 carabus tit
268	7	1.0	355	8	09TDY4	09tdy4 carabus lao	341	7	1.0	355	8	09TE97	09te97 carabus bla
269	7	1.0	355	8	037388	037388 carabus gen	342	7	1.0	355	8	09GBM6	09gbm6 carabus oia
270	7	1.0	355	8	047487	047487 carabus lat	343	7	1.0	355	8	09TEB3	09teb3 carabus bla
271	7	1.0	355	8	09TE15	09te15 carabus kor	344	7	1.0	355	8	09TE14	09te14 carabus bla
272	7	1.0	355	8	09GBN0	09gbn0 carabus vir	345	7	1.0	355	8	09TE14	09te14 carabus bla
273	7	1.0	355	8	09M1J6	09m1j6 carabus van	346	7	1.0	355	8	09MDJ3	09mdj3 carabus por
274	7	1.0	355	8	09TEA4	09tea4 carabus bla	347	7	1.0	355	8	09TE27	09te27 carabus bla
275	7	1.0	355	8	09TEB0	09teb0 carabus can	348	7	1.0	355	8	09M1Z6	09m1z6 carabus lee
276	7	1.0	355	8	09B9S2	09b9s2 carabus vac	349	7	1.0	355	8	09MDS6	09mds6 carabus por
277	7	1.0	355	8	09M1J5	09m1j5 carabus van	350	7	1.0	355	8	09M1Z6	09m1z6 carabus por
278	7	1.0	355	8	09B9S5	09b9s5 carabus str	351	7	1.0	355	8	09TE93	09te93 carabus bla
279	7	1.0	355	8	09TEB2	09teb2 carabus bla	352	7	1.0	355	8	09MDR3	09mdr3 carabus bla
280	7	1.0	355	8	09TEB4	09teb4 carabus bla	353	7	1.0	355	8	09TE95	09te95 carabus bla
281	7	1.0	355	8	09TE14	09te14 carabus sem	354	7	1.0	355	8	09TE92	09te92 carabus bla
282	7	1.0	355	8	037453	037453 carabus bla	355	7	1.0	355	8	09TE14	09te14 carabus bla
283	7	1.0	355	8	037518	037518 carabus mae	356	7	1.0	355	8	09TE14	09te14 carabus bla
284	7	1.0	355	8	09TEA1	09tea1 carabus bla	357	7	1.0	355	8	09MDT2	09mdt2 carabus por
285	7	1.0	355	8	09GBN3	09gbn3 carabus con	358	7	1.0	355	8	09MDR4	09mdr4 carabus bla
286	7	1.0	355	8	09TEB0	09teb0 carabus bla	359	7	1.0	355	8	09TEV2	09tev2 carabus bla
287	7	1.0	355	8	037542	037542 carabus maa	360	7	1.0	355	8	09TEV3	09tev3 carabus bla
288	7	1.0	355	8	09TEB9	09teb9 carabus mao	361	7	1.0	355	8	09TEB8	09teb8 carabus bla
289	7	1.0	355	8	09B9R6	09b9r6 carabus ruf	362	7	1.0	355	8	09TEB8	09teb8 carabus bla
290	7	1.0	355	8	09TEB7	09teb7 carabus bla	363	7	1.0	355	8	037389	037389 carabus gra
291	7	1.0	355	8	09GBK4	09gbk4 carabus con	364	7	1.0	355	8	09TEV4	09tev4 carabus bla
292	7	1.0	355	8	09B9L8	09b9l8 carabus con	365	7	1.0	355	8	09TEV5	09tev5 carabus bla
293	7	1.0	355	8	09B9L8	09b9l8 carabus con	366	7	1.0	355	8	09TEV5	09tev5 carabus bla
294	7	1.0	355	8	09B9L8	09b9l8 carabus con	367	7	1.0	355	8	037457	037457 carabus bla
295	7	1.0	355	8	037454	037454 carabus bla	368	7	1.0	355	8	09TEV5	09tev5 carabus bla
296	7	1.0	355	8	09B9L8	09b9l8 carabus bla	369	7	1.0	355	8	09TEV5	09tev5 carabus bla
297	7	1.0	355	8	037428	037428 carabus fru	370	7	1.0	355	8	09B9L8	09b9l8 carabus bla
298	7	1.0	355	8	09TEB5	09teb5 carabus fru	371	7	1.0	355	8	09B9L8	09b9l8 carabus bla
299	7	1.0	355	8	09TEB1	09teb1 carabus bla	372	7	1.0	355	8	09B9L8	09b9l8 carabus bla
300	7	1.0	355	8	047485	047485 carabus bla	373	7	1.0	355	8	09B9L8	09b9l8 carabus bla
301	7	1.0	355	8	09B9L8	09b9l8 carabus bla	374	7	1.0	355	8	09B9L8	09b9l8 carabus bla
302	7	1.0	355	8	09B9L8	09b9l8 carabus bla	375	7	1.0	355	8	09B9L8	09b9l8 carabus bla
303	7	1.0	355	8	037449	037449 carabus aen	376	7	1.0	355	8	09B9L8	09b9l8 carabus bla
304	7	1.0	355	8	09TEB8	09teb8 carabus bla	377	7	1.0	355	8	09B9L8	09b9l8 carabus bla
305	7	1.0	355	8	09TEB8	09teb8 carabus bla	378	7	1.0	355	8	09B9L8	09b9l8 carabus bla
306	7	1.0	355	8	09GBM1	09gbm1 carabus vir	379	7	1.0	355	8	09B9L8	09b9l8 carabus bla
307	7	1.0	355	8	099053	099053 carabus por	380	7	1.0	355	8	09B9L8	09b9l8 carabus bla
308	7	1.0	355	8	09TEB3	09teb3 carabus can	381	7	1.0	355	8	09B9L8	09b9l8 carabus bla

382	1.0	355	8	085G10	085G10 carabus tor	455	7	1.0	413	17	029192	029192 archaeoglob
383	1.0	355	8	085G19	085G19 carabus tor	456	7	1.0	416	16	088RT5	088RT5 pseudomonas
384	1.0	355	8	085G18	085G18 carabus tor	457	7	1.0	419	13	078T79	078T79 actinomyces
385	1.0	355	8	085G17	085G17 carabus tor	458	7	1.0	437	2	051640	051640 burkholderia
386	1.0	355	8	085G16	085G16 carabus tor	459	7	1.0	437	16	07UDY7	07UDY7 rhodospirillum
387	1.0	355	8	085G15	085G15 carabus tor	460	7	1.0	439	10	091Y67	091Y67 arabidopsis
388	1.0	355	8	085G14	085G14 carabus tor	461	7	1.0	442	13	0804X1	0804X1 fugu rubrip
389	1.0	355	8	085G13	085G13 carabus tor	462	7	1.0	447	4	08TAA5	08TAA5 homo sapien
390	1.0	355	8	085G12	085G12 carabus tor	463	7	1.0	449	11	08B1T8	08B1T8 mus musculu
391	1.0	355	8	085G11	085G11 carabus tor	464	7	1.0	453	16	08P1B8	08P1B8 xanthomonas
392	1.0	355	8	085G10	085G10 carabus tor	465	7	1.0	453	16	08P704	08P704 xanthomonas
393	1.0	355	8	085G09	085G09 carabus tor	466	7	1.0	459	10	066349	066349 brassica na
394	1.0	355	8	085G08	085G08 carabus tor	467	7	1.0	461	16	006380	006380 mycobacteri
395	1.0	355	8	085G07	085G07 carabus tor	468	7	1.0	461	16	07TWA1	07TWA1 mycobacteri
396	1.0	355	8	085G06	085G06 carabus tor	469	7	1.0	463	10	08N671	08N671 homo sapien
397	1.0	355	8	085G05	085G05 carabus tor	470	7	1.0	465	10	08GWA4	08GWA4 arabidopsis
398	1.0	355	8	085G04	085G04 carabus tor	471	7	1.0	465	10	084XL8	084XL8 xerophyta h
399	1.0	355	8	085G03	085G03 carabus tor	472	7	1.0	469	10	08LEG9	08LEG9 arabidopsis
400	1.0	355	8	085G02	085G02 carabus tor	473	7	1.0	469	16	081NT2	081NT2 bacillus an
401	1.0	355	8	085G01	085G01 carabus tor	474	7	1.0	472	5	096657	096657 caenorhabdi
402	1.0	355	8	085G00	085G00 carabus tor	475	7	1.0	476	16	081BL6	081BL6 bacillus ce
403	1.0	355	8	085G00	085G00 carabus tor	476	7	1.0	479	16	099RL5	099RL5 utaphylococ
404	1.0	355	8	085G00	085G00 carabus tor	477	7	1.0	483	16	089BC3	089BC3 bradyrhizob
405	1.0	355	8	085G00	085G00 carabus tor	478	7	1.0	487	16	08ET76	08ET76 oceanobacill
406	1.0	355	8	085G00	085G00 carabus tor	479	7	1.0	489	12	091Q01	091Q01 soybean dwa
407	1.0	355	8	085G00	085G00 carabus tor	480	7	1.0	490	16	07VH13	07VH13 helicobacte
408	1.0	355	8	085G00	085G00 carabus tor	481	7	1.0	492	5	045659	045659 caenorhabdi
409	1.0	355	8	085G00	085G00 carabus tor	482	7	1.0	492	16	088Z15	088Z15 lactobacilli
410	1.0	355	8	085G00	085G00 carabus tor	483	7	1.0	493	13	090XP7	090XP7 brachydiano
411	1.0	355	8	085G00	085G00 carabus tor	484	7	1.0	493	17	0972W0	0972W0 eulfoliolob
412	1.0	355	8	085G00	085G00 carabus tor	485	7	1.0	494	11	09ER20	09ER20 mus musculu
413	1.0	355	8	085G00	085G00 carabus tor	486	7	1.0	494	11	091X69	091X69 mus musculu
414	1.0	355	8	085G00	085G00 carabus tor	487	7	1.0	494	11	08VDV0	08VDV0 mus musculu
415	1.0	355	8	085G00	085G00 carabus tor	488	7	1.0	494	11	08BMS0	08BMS0 mus musculu
416	1.0	355	8	085G00	085G00 carabus tor	489	7	1.0	497	2	054706	054706 streptococ
417	1.0	355	8	085G00	085G00 carabus tor	490	7	1.0	497	16	054749	054749 streptococ
418	1.0	355	8	085G00	085G00 carabus tor	491	7	1.0	497	16	051503	051503 borrelia bu
419	1.0	355	8	085G00	085G00 carabus tor	492	7	1.0	497	16	09A1S4	09A1S4 streptococ
420	1.0	355	8	085G00	085G00 carabus tor	493	7	1.0	501	5	09NDP6	09NDP6 riftia pach
421	1.0	355	8	085G00	085G00 carabus tor	494	7	1.0	505	8	09SEA3	09SEA3 gymnocalyet
422	1.0	355	8	085G00	085G00 carabus tor	495	7	1.0	507	8	094P31	094P31 haagococce
423	1.0	355	8	085G00	085G00 carabus tor	496	7	1.0	507	8	095E88	095E88 erioleyce eu
424	1.0	355	8	085G00	085G00 carabus tor	497	7	1.0	507	8	095E84	095E84 brownlingia
425	1.0	355	8	085G00	085G00 carabus tor	498	7	1.0	507	8	095ED8	095ED8 poreklopori
426	1.0	355	8	085G00	085G00 carabus tor	499	7	1.0	507	8	095E96	095E96 matucana in
427	1.0	355	8	085G00	085G00 carabus tor	500	7	1.0	507	8	095E89	095E89 erioleyce is
428	1.0	355	8	085G00	085G00 carabus tor	501	7	1.0	507	8	095E80	095E80 trichoceteu
429	1.0	355	8	085G00	085G00 carabus tor	502	7	1.0	507	8	095E81	095E81 nebelmannia
430	1.0	355	8	085G00	085G00 carabus tor	503	7	1.0	507	8	095E81	095E81 strobilia c
431	1.0	355	8	085G00	085G00 carabus tor	504	7	1.0	507	8	095E82	095E82 coleocophal
432	1.0	355	8	085G00	085G00 carabus tor	505	7	1.0	507	8	095E82	095E82 rahnococceus
433	1.0	355	8	085G00	085G00 carabus tor	506	7	1.0	507	8	094PY9	094PY9 acanthoccaly
434	1.0	355	8	085G00	085G00 carabus tor	507	7	1.0	507	8	095E87	095E87 neowetderma
435	1.0	355	8	085G00	085G00 carabus tor	508	7	1.0	507	8	095E84	095E84 coplapora la
436	1.0	355	8	085G00	085G00 carabus tor	509	7	1.0	507	8	095E86	095E86 parodia ma
437	1.0	355	8	085G00	085G00 carabus tor	510	7	1.0	507	8	095E86	095E86 coplapora oo
438	1.0	355	8	085G00	085G00 carabus tor	511	7	1.0	507	8	094P94	094P94 erioleyce na
439	1.0	355	8	085G00	085G00 carabus tor	512	7	1.0	507	8	095E90	095E90 erioleyce au
440	1.0	355	8	085G00	085G00 carabus tor	513	7	1.0	507	8	095E85	095E85 coplapora br
441	1.0	355	8	085G00	085G00 carabus tor	514	7	1.0	508	2	093SM9	093SM9 elaphylococ
442	1.0	355	8	085G00	085G00 carabus tor	515	7	1.0	508	8	095E82	095E82 pfeifferia m
443	1.0	355	8	085G00	085G00 carabus tor	516	7	1.0	509	8	095ED0	095ED0 astrophytum
444	1.0	355	8	085G00	085G00 carabus tor	517	7	1.0	509	8	095E88	095E88 azetekiun ri
445	1.0	355	8	085G00	085G00 carabus tor	518	7	1.0	509	8	095EB7	095EB7 eulychinia i
446	1.0	355	8	085G00	085G00 carabus tor	519	7	1.0	509	8	095EB4	095EB4 pfeifferia i
447	1.0	355	8	085G00	085G00 carabus tor	520	7	1.0	509	8	095EC7	095EC7 calymantini
448	1.0	355	8	085G00	085G00 carabus tor	521	7	1.0	509	8	095E89	095E89 pachycereus
449	1.0	355	8	085G00	085G00 carabus tor	522	7	1.0	509	8	095E86	095E86 haitiora sal
450	1.0	355	8	085G00	085G00 carabus tor	523	7	1.0	509	8	095EC3	095EC3 acanthocete
451	1.0	355	8	085G00	085G00 carabus tor	524	7	1.0	509	8	095EB5	095EB5 corryocactu
452	1.0	355	8	085G00	085G00 carabus tor	525	7	1.0	509	8	095ED5	095ED5 bloesfeldia
453	1.0	355	8	085G00	085G00 carabus tor	526	7	1.0	509	8	095ED9	095ED9 opuntia qui
454	1.0	355	8	085G00	085G00 carabus tor	527	7	1.0	509	8	095EC0	095EC0 castellanos

528	7	1.0	509	8	Q95B91	Q95B91 parodia oct	601	7	1.0	708	2	087239	087239 laccococcus
529	7	1.0	509	8	Q95B83	Q95B83 leptemium c	602	7	1.0	735	13	057381	057381 xenopus lae
530	7	1.0	509	8	Q95B84	Q95B84 biosfeldia	603	7	1.0	746	16	Q97R74	Q97R74 streptococ
531	7	1.0	509	8	Q95B80	Q95B80 austrocylia	604	7	1.0	749	13	Q9YGB8	Q9YGB8 oncorhynch
532	7	1.0	509	8	Q95B81	Q95B81 leptocereus	605	7	1.0	754	10	Q94144	Q94144 arbidopsis
533	7	1.0	509	8	Q95B85	Q95B85 rhipallia f	606	7	1.0	765	16	08XY74	08XY74 talstonia s
534	7	1.0	509	8	Q95B81	Q95B81 echinocereu	607	7	1.0	783	13	086LL3	086LL3 giardia lam
535	7	1.0	509	8	Q95B83	Q95B83 frailea gra	608	7	1.0	783	12	Q9B126	Q9B126 cercopithe
536	7	1.0	509	8	Q95B88	Q95B88 austrocactu	609	7	1.0	787	5	Q9NFK1	Q9NFK1 drosophila
537	7	1.0	509	8	Q95B82	Q95B82 armatocereu	610	7	1.0	790	4	Q9N5Z2	Q9N5Z2 homo sapien
538	7	1.0	509	8	Q95B89	Q95B89 neoraimondi	611	7	1.0	791	10	Q94139	Q94139 arbidopsis
539	7	1.0	509	8	Q95B87	Q95B87 seilenicereu	612	7	1.0	791	10	050073	050073 arbidopsis
540	7	1.0	509	8	Q95B83	Q95B83 pfeiffera m	613	7	1.0	791	10	Q94137	Q94137 arbidopsis
541	7	1.0	509	8	Q95B82	Q95B82 pereskia st	614	7	1.0	799	16	Q9NSU9	Q9NSU9 corynebact
542	7	1.0	509	8	Q95B86	Q95B86 corryocactu	615	7	1.0	805	5	Q9SRK7	Q9SRK7 drosophila
543	7	1.0	509	8	Q95B83	Q95B83 pereskia gu	616	7	1.0	805	16	Q91WV6	Q91WV6 bacillus an
544	7	1.0	509	8	Q95B84	Q95B84 talinum pan	617	7	1.0	806	16	Q91A60	Q91A60 bacillus co
545	7	1.0	509	8	Q95B92	Q95B92 parodia mic	618	7	1.0	808	10	Q987D1	Q987D1 arbidopsis
546	7	1.0	509	8	Q95B81	Q95B81 echinocactu	619	7	1.0	826	10	Q9T041	Q9T041 arbidopsis
547	7	1.0	509	8	Q95B86	Q95B86 discocactus	620	7	1.0	826	17	Q9TQX6	Q9TQX6 methanobarc
548	7	1.0	509	8	Q95B82	Q95B82 frailea pha	621	7	1.0	826	17	Q9BUP4	Q9BUP4 methanobarc
549	7	1.0	509	8	Q95B88	Q95B88 hylocereus	622	7	1.0	842	10	Q91S88	Q91S88 arbidopsis
550	7	1.0	524	13	Q7SXH8	Q7SXH8 brachydantio	623	7	1.0	867	5	Q21186	Q21186 caenorhabdi
551	7	1.0	526	4	Q94900	Q94900 homo sapien	624	7	1.0	869	5	Q91G55	Q91G55 caenorhabdi
552	7	1.0	526	4	Q96AV5	Q96AV5 homo sapien	625	7	1.0	873	2	Q9S0Z4	Q9S0Z4 escherichia
553	7	1.0	527	16	Q9P606	Q9P606 xanthomona	626	7	1.0	917	5	Q9V4B8	Q9V4B8 drosophila
554	7	1.0	529	5	Q17403	Q17403 caenorhabdi	627	7	1.0	921	5	Q9V4Z9	Q9V4Z9 drosophila
555	7	1.0	532	17	Q9YDB4	Q9YDB4 aeropyrum p	628	7	1.0	921	6	Q9BDU0	Q9BDU0 dendrocyrax
556	7	1.0	533	5	Q9B147	Q9B147 caenorhabdi	629	7	1.0	950	10	Q9BRX0	Q9BRX0 oryza sativ
557	7	1.0	535	2	Q9JP77	Q9JP77 thermomonas	630	7	1.0	961	5	Q9SVH3	Q9SVH3 oncephalito
558	7	1.0	540	2	Q9X2V0	Q9X2V0 agrobacteri	631	7	1.0	970	10	Q9AYF2	Q9AYF2 oryza sativ
559	7	1.0	541	16	Q98RF3	Q98RF3 fusobacteri	632	7	1.0	970	10	Q7XEP3	Q7XEP3 oryza sativ
560	7	1.0	541	16	Q7WPA4	Q7WPA4 bordetella	633	7	1.0	977	13	Q919Z5	Q919Z5 xenopus lae
561	7	1.0	544	16	Q8TFN9	Q8TFN9 emericella	634	7	1.0	980	5	Q22088	Q22088 caenorhabdi
562	7	1.0	549	12	Q9DW53	Q9DW53 rat cytoleg	635	7	1.0	991	4	Q8TDH1	Q8TDH1 homo sapien
563	7	1.0	553	16	Q97810	Q97810 streptococ	636	7	1.0	1007	13	Q8U128	Q8U128 xenopus lae
564	7	1.0	553	16	Q8DOR3	Q8DOR3 streptococ	637	7	1.0	1031	16	Q985X2	Q985X2 bifidobact
565	7	1.0	556	11	Q9CVK0	Q9CVK0 mus musculi	638	7	1.0	1047	10	Q9FKW9	Q9FKW9 arbidopsis
566	7	1.0	560	10	Q49141	Q49141 arbidopsis	639	7	1.0	1048	5	Q9NAV1	Q9NAV1 caenorhabdi
567	7	1.0	560	10	Q50057	Q50057 arbidopsis	640	7	1.0	1074	16	Q811Z5	Q811Z5 antrococtu
568	7	1.0	561	16	Q9RXS1	Q9RXS1 deinococcus	641	7	1.0	1081	11	Q8BZ19	Q8BZ19 mus musculi
569	7	1.0	561	16	Q9KYS9	Q9KYS9 streptomyce	642	7	1.0	1100	4	Q96DH1	Q96DH1 homo sapien
570	7	1.0	568	16	Q88M64	Q88M64 lactobacilli	643	7	1.0	1111	9	Q855Z2	Q855Z2 mycobacteri
571	7	1.0	580	10	Q9ZOP6	Q9ZOP6 arbidopsis	644	7	1.0	1120	16	Q8FP97	Q8FP97 corynebact
572	7	1.0	581	10	Q91KX1	Q91KX1 mesembryant	645	7	1.0	1136	5	Q81UD8	Q81UD8 plasmodium
573	7	1.0	581	16	Q8D7C1	Q8D7C1 vibrio vuln	646	7	1.0	1240	5	Q8T6Z7	Q8T6Z7 drosophila
574	7	1.0	582	10	Q23492	Q23492 arbidopsis	647	7	1.0	1240	5	Q8T6Z6	Q8T6Z6 drosophila
575	7	1.0	584	10	Q9SQZ0	Q9SQZ0 arbidopsis	648	7	1.0	1240	5	Q9W084	Q9W084 drosophila
576	7	1.0	585	5	Q17491	Q17491 caenorhabdi	649	7	1.0	1243	11	Q65468	Q65468 arbidopsis
577	7	1.0	585	5	Q8SZY4	Q8SZY4 drosophila	650	7	1.0	1243	11	Q35954	Q35954 mus musculi
578	7	1.0	600	16	Q93GX8	Q93GX8 streptomyce	651	7	1.0	1300	3	Q8XOV5	Q8XOV5 neurospora
579	7	1.0	606	10	Q7XSS0	Q7XSS0 oryza sativ	652	7	1.0	1340	5	Q9GVM4	Q9GVM4 anophelo g
580	7	1.0	608	6	Q9GMB0	Q9GMB0 sus scrofa	653	7	1.0	1346	2	Q9ZG12	Q9ZG12 streptomyce
581	7	1.0	612	13	Q804W7	Q804W7 fugu rubrip	654	7	1.0	1544	3	Q86ZB3	Q86ZB3 botrytis ci
582	7	1.0	613	11	Q80V80	Q80V80 mus musculi	655	7	1.0	1569	10	Q9FHD0	Q9FHD0 arbidopsis
583	7	1.0	617	17	Q97UG5	Q97UG5 sulfolobus	656	7	1.0	1608	5	Q95VA5	Q95VA5 drosophila
584	7	1.0	618	11	P704Z3	P704Z3 mus musculi	657	7	1.0	1631	16	Q8DZ37	Q8DZ37 streptococ
585	7	1.0	620	10	Q38940	Q38940 arbidopsis	658	7	1.0	1640	3	Q86Z91	Q86Z91 gibbocolla
586	7	1.0	622	4	Q7Z7P3	Q7Z7P3 homo sapien	659	7	1.0	1660	10	Q947Z9	Q947Z9 oryza sativ
587	7	1.0	624	10	Q94CF4	Q94CF4 arbidopsis	660	7	1.0	1660	10	Q7XFK3	Q7XFK3 oryza sativ
588	7	1.0	629	16	Q87VG1	Q87VG1 pseudomonas	661	7	1.0	1666	10	Q8LP68	Q8LP68 chlamydomon
589	7	1.0	633	13	Q90Z56	Q90Z56 scopothalamu	662	7	1.0	1768	5	Q9N8K7	Q9N8K7 trypanosoma
590	7	1.0	648	5	Q9NKKD7	Q9NKKD7 drosophila	663	7	1.0	1831	4	Q86T77	Q86T77 homo sapien
591	7	1.0	658	10	Q65466	Q65466 arbidopsis	664	7	1.0	1863	4	Q81VX2	Q81VX2 homo sapien
592	7	1.0	663	17	Q8UT28	Q8UT28 pyrococcus	665	7	1.0	1865	4	Q7Z401	Q7Z401 homo sapien
593	7	1.0	674	10	Q9C5S9	Q9C5S9 arbidopsis	666	7	1.0	1877	5	Q9XW11	Q9XW11 plasmodium
594	7	1.0	678	16	Q9A4E2	Q9A4E2 caulobacter	667	7	1.0	1903	5	Q9UON7	Q9UON7 plasmodium
595	7	1.0	680	10	Q8GX18	Q8GX18 arbidopsis	668	7	1.0	1952	5	Q95SN5	Q95SN5 drosophila
596	7	1.0	682	16	Q8EMF4	Q8EMF4 mycoplasma	669	7	1.0	1966	5	Q9NHX6	Q9NHX6 drosophila
597	7	1.0	683	5	Q9VIE8	Q9VIE8 drosophila	670	7	1.0	1966	5	Q81QA6	Q81QA6 drosophila
598	7	1.0	684	10	Q80709	Q80709 arbidopsis	671	7	1.0	1968	3	Q8XOC5	Q8XOC5 neurospora
599	7	1.0	700	16	Q8ECU0	Q8ECU0 thewanelia	672	7	1.0	1985	5	Q9VSK5	Q9VSK5 drosophila
600	7	1.0	703	16	Q8R917	Q8R917 thermococcus	673	7	1.0	1985	5	Q8T9N4	Q8T9N4 drosophila

674	7	1.0	1988	5	Q86B82	Q86B82 drosophila
675	7	1.0	2393	5	Q81461	Q81461 plasmodium
676	7	1.0	2605	2	Q50858	Q50858 myxococcus
677	7	1.0	2906	11	Q9WU99	Q9WU99 ratius notv
678	7	1.0	3306	10	Q9FT44	Q9FT44 arabidopsis
679	7	1.0	3446	5	Q86AC8	Q86AC8 dicycotelel
680	7	1.0	3564	11	Q923L3	Q923L3 mus musculu
681	7	1.0	3972	16	Q9S0R8	Q9S0R8 streptomyce
682	7	1.0	4547	5	Q9W433	Q9W433 drosophila
683	7	1.0	4899	5	Q9VR91	Q9VR91 drosophila
684	6	0.8	33	12	Q8B9R9	Q8B9R9 emilliana h
685	6	0.8	33	12	Q8B9R8	Q8B9R8 emilliana h
686	6	0.8	33	12	Q8B9R7	Q8B9R7 emilliana h
687	6	0.8	33	12	Q8B9R6	Q8B9R6 emilliana h
688	6	0.8	33	12	Q8B9R5	Q8B9R5 emilliana h
689	6	0.8	33	12	Q8B9R4	Q8B9R4 emilliana h
690	6	0.8	33	12	Q8B9R3	Q8B9R3 emilliana h
691	6	0.8	33	12	Q8B9R2	Q8B9R2 emilliana h
692	6	0.8	33	16	Q8FZEO	Q8FZEO bruceella su
693	6	0.8	35	16	Q9KSL5	Q9KSL5 vibrio chol
694	6	0.8	36	3	Q96W36	Q96W36 ophiostoma
695	6	0.8	37	15	Q9DRP2	Q9DRP2 human immun
696	6	0.8	38	16	Q7W966	Q7W966 haemophilus
697	6	0.8	39	6	Q29360	Q29360 sus scrofa
698	6	0.8	40	2	Q9R4D0	Q9R4D0 thermus aqu
699	6	0.8	40	15	Q8UM87	Q8UM87 human immun
700	6	0.8	40	15	Q8USM4	Q8USM4 human immun

ALIGNMENTS

RESULT 1
Q96CW2 PRELIMINARY; PRT; 737 AA.

AC Q96JW2; 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein FLJ1935.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Isegal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,
 RA Magatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ichida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Maehuo Y.,
 RA Nishimura K., Iwayanagi T.,
 RT "MEDO human cDNA sequencing project."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; AK027841; BAB55404.1; -
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR009003; Cys_ser_trypsin.
 DR InterPro; IPR007442; EGF_2.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00084; sushi; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 KW Hypothetical protein; EGF-like domain; Hydroxylase; Protease;
 KW Serine protease.
 SQ SEQUENCE 737 AA; 81952 MW; 4F51689C5EB32B44 CRC64;

Query Match 61.9%; Score 446; DB 4; Length 737;
 Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 275 LERRNCSDPGPVNGYKQITGPGGLINGRAKIGTVVSPFCNNSTVLSGNERKTCQNGE 334
 292 LERRNCSDPGPVNGYKQITGPGGLINGRAKIGTVVSPFCNNSTVLSGNERKTCQNGE 351
 335 WSGKOPICIKACREPKISDLYRRVLPVQVSGRETPHQLYSAAFSKQKLGAPTKKPL 394
 352 WSGKOPICIKACREPKISDLYRRVLPVQVSGRETPHQLYSAAFSKQKLGAPTKKPL 411
 395 PGGLDPMGVHHTLOQLQYICISPPFRRLGSSRRCTLRGKMGSRAPSCIPIGKLENTA 454
 412 PGGLDPMGVHHTLOQLQYICISPPFRRLGSSRRCTLRGKMGSRAPSCIPIGKLENTA 471
 455 PRTQGLRMPMOAIVRRTSGVDSGLHKGAPFLVCSGALNERTVVAACHVTDLGKVTM 514
 472 PRTQGLRMPMOAIVRRTSGVDSGLHKGAPFLVCSGALNERTVVAACHVTDLGKVTM 531
 515 IKTADLKVLGKFRYRDDDEKTIQSLQISAILHPNVDPILLDDIALILKLDKARIST 574
 532 IKTADLKVLGKFRYRDDDEKTIQSLQISAILHPNVDPILLDDIALILKLDKARIST 591
 575 RVQPTCLASRLDLSFQSHITVAGMVLADVRSRPFNDLRSVSVVDSLCEEQH 634
 592 RVQPTCLASRLDLSFQSHITVAGMVLADVRSRPFNDLRSVSVVDSLCEEQH 651
 635 EDHGIPVSTVDNMFCSWEPPTAPSDICTAETGIAVSPFGRAAPPRHMLGLVMSYD 694
 652 EDHGIPVSTVDNMFCSWEPPTAPSDICTAETGIAVSPFGRAAPPRHMLGLVMSYD 711
 695 KTCSHRLSTAFKVLPEKWMIRNMK 720
 712 KTCSHRLSTAFKVLPEKWMIRNMK 737

RESULT 2

Q9Y432 PRELIMINARY; PRT; 181 AA.
 AC Q9Y432; 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN DKFZP586H2123.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RA Ansoorge W., Winkner U., Mewes H.W., Gassenhuber J., Wiemann S.,
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050214; CAB43317.1; -
 DR PIR; T08805; T08805.
 DR HSP; P00742; IHCG.

DR MEROPS; S01.998; .
 DR GO; GO:0008223; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys_ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR Pfam; PF00089; trypsin; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 KM Hypothetical protein; Hydrolase; Protease; Serine protease.
 FT NON_TER
 SQ SEQUENCE 181 AA; 1962 MW; ABC793BBE682D439 CRC64;
 Query Match 24.7%; Score 178; DB 4; Length 181;
 Best Local Similarity 100.0%; Pred. No. 4.2e-179; Indels 0; Gaps 0;
 Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 543 ISAILHPNYDILLADADIAIKLLDKARISTRVOPICLAASRDISTSFQESHITVAGWN 602
 DB 4 ISAILHPNYDILLADADIAIKLLDKARISTRVOPICLAASRDISTSFQESHITVAGWN 63
 QY 603 VLADVRSGFKNDITRSGVSVVSDLLCEQEHEDHGIPVSYDNMFCSMEPTASDICT 662
 DB 64 VLADVRSGFKNDITRSGVSVVSDLLCEQEHEDHGIPVSYDNMFCSMEPTASDICT 123
 QY 663 AETGIAVSPFGRASPEPRWHLMGLVSWSYDTCGSHRLSTAFKVLFPKDIERNMK 720
 DB 124 AETGIAVSPFGRASPEPRWHLMGLVSWSYDTCGSHRLSTAFKVLFPKDIERNMK 181
 RESULT 3
 Q8BU25 PRELIMINARY; PRT; 720 AA.
 ID Q8BU25
 AC Q8BU25
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Hypothetical EGF-like domain.
 GN E43002GOSRIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOJ; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK088017; BAC40098.1; .
 DR MGI; MGI:2445082; E430002G05RIK.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR009003; Cys_ser_trypsin.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR00436; Sush1_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sush1; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00033; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 720 AA; 80300 MW; C098E076D903A5A0 CRC64;
 Query Match 8.5%; Score 61; DB 11; Length 720;
 Best Local Similarity 100.0%; Pred. No. 6.7e-55; Indels 0; Gaps 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 74 NECDSCLHPGCTIFENCKSCRNAGSWGGLDDFYVKGFGYCAECRAGWYGDGMRGQVLR 133
 DB 74 NECDSCLHPGCTIFENCKSCRNAGSWGGLDDFYVKGFGYCAECRAGWYGDGMRGQVLR 133
 QY 134 A 134
 DB 134 A 134
 RESULT 4
 Q8K2B8 PRELIMINARY; PRT; 720 AA.
 ID Q8K2B8
 AC Q8K2B8
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to DKFZP56H2123 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strubeberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; BC031841; AAH31841.1; .
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR009003; Cys_ser_trypsin.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR00436; Sush1_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sush1; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 KM EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 720 AA; 80377 MW; 7172B7F15690FD08 CRC64;
 Query Match 5.7%; Score 41; DB 11; Length 720;
 Best Local Similarity 100.0%; Pred. No. 9.1e-34; Indels 0; Gaps 0;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR SMART; SM00181; EGF; 2.
 DR SMART; SM00179; EGF_Ca; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 KM Hypothetical protein.
 SQ SEQUENCE 720 AA; 80300 MW; C098E076D903A5A0 CRC64;
 Query Match 8.5%; Score 61; DB 11; Length 720;
 Best Local Similarity 100.0%; Pred. No. 6.7e-55; Indels 0; Gaps 0;
 Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 74 NECDSCLHPGCTIFENCKSCRNAGSWGGLDDFYVKGFGYCAECRAGWYGDGMRGQVLR 133
 DB 74 NECDSCLHPGCTIFENCKSCRNAGSWGGLDDFYVKGFGYCAECRAGWYGDGMRGQVLR 133
 QY 134 A 134
 DB 134 A 134
 RESULT 4
 Q8K2B8 PRELIMINARY; PRT; 720 AA.
 ID Q8K2B8
 AC Q8K2B8
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to DKFZP56H2123 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strubeberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL; BC031841; AAH31841.1; .
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR009003; Cys_ser_trypsin.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR00436; Sush1_SCR_CCP.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00084; Sush1; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 KM EGF-like domain; Hydrolase; Protease; Serine protease.
 SQ SEQUENCE 720 AA; 80377 MW; 7172B7F15690FD08 CRC64;
 Query Match 5.7%; Score 41; DB 11; Length 720;
 Best Local Similarity 100.0%; Pred. No. 9.1e-34; Indels 0; Gaps 0;
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 FL0LLISLSPREXTVINEACPGAEANINMGCECEYDQIEC 53
 ||||||||||||||||||||||||||||||||||||||||
 DB 13 FL0LLISLSPREXTVINEACPGAEANINMGCECEYDQIEC 53

RESULT 5

ID 091WZ0 PRELIMINARY; PRT; 222 AA.
 AC 091WZ0.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Bone morphogenetic protein 1 (Fragment).
 GN BMP-1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Metar; TISSUE=Embryo;
 RA Kataoka H., Enomoto K.,
 RT "Partial CDNA sequence isolated by RT-PCR."
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 DR EMBL; AB073100; BAB69961.1; -
 DR GO; GO:0008533; F:astacin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000859; COB.
 DR InterPro; IPR001506; Peptidase_M12A.
 DR Pfam; PF01431; CUB; 2.
 DR Pfam; PF00431; CUB; 2.
 DR SMART; SM00042; CUB; 2.
 DR PROSITE; PS01180; CUB; 2.
 DR NON_TER 1
 FT NON_TER 1
 FT SEQUENCE 222 AA; 25426 MW; FA9052DA98B57A CRC64;

Query Match 1.2%; Score 9; DB 11; Length 222;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDG 187
 ||||||||
 DB 80 YDYVEVRDG 88

RESULT 6

ID 086553 PRELIMINARY; PRT; 276 AA.
 AC 086553.
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Putative dehydrogenase.
 GN SC0619 OR SCIF2.16C.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
 OC Streptomyces; Streptomycetaceae; Streptomyces.
 OC NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Seeger K.J., Harris D.,
 RT Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Parthill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);

RX MEDLINE=97000351; PubMed=843436;
 RA Redenbach M., Kleiser H.M., Denaplatte D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabbittowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parthill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)."
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
 (SDR) FAMILY.
 DR EMBL; AL939128; CAA20507.1; -
 DR PIR; T29125; T29125.
 DR HSP; O64105; IOAA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF01106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 KM Oxidoreductase; Complete proteome.
 SQ SEQUENCE 276 AA; 29010 MW; 30F038B70D63C7C CRC64;

Query Match 1.2%; Score 9; DB 16; Length 276;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 670 AVSFGGRAS 678
 ||||||||
 DB 225 AVSFGGRAS 233

RESULT 7

ID 057658 PRELIMINARY; PRT; 691 AA.
 AC 057658.
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Bone morphogenetic protein 1 (Fragment).
 GN BMP1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20267865; PubMed=10806368;
 RA Reynolds S.D., Zhang D., Puzas J.E., O'Keefe R.J., Rosier R.N.,
 RA Reynolds P.R.;
 RT "Cloning of the chick BMP1/Tolloid cDNA and expression in skeletal
 tissues."
 RL Gene 248:233-243(2000).
 CC -1- SIMILARITY: CONTAINS 3 CUB DOMAINS.
 DR EMBL; U75331; AAC02259.1; -
 DR HSP; P00736; IAPQ.
 DR MEROPS; M12.005; -
 DR GO; GO:0008533; F:astacin activity; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR00152; Asx_hydroxyl_1.S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR001506; Peptidase M12A.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01400; Ascatin; 1.
 DR Pfam; PF00431; CUB; 3.
 DR Pfam; PF00008; EGF; 1.
 DR PRINTS; PRO0480; ASTACIN.
 DR SMART; SM00042; CUB; 3.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00235; ZmC; 1.
 DR PROSITE; PS0010; ASX_HYDROXYL; 1.
 DR PROSITE; PS01180; CUB; 3.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR EGF_Like domain.
 KW EGF_Like domain.
 FT NON TER 1
 SQ SEQUENCE 691 AA; 77843 MW; 01245982B8DC8F28 CRC64;

Query Match 1.2%; Score 9; DB 13; Length 691;
 Best Local Similarity 100.0%; Pred. No. 5.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDQ 187
 |||||
 DB 338 YDYVEVRDQ 346

RESULT 8
 Q8QFX6 PRELIMINARY; PRT; 923 AA.
 AC Q8QFX6;
 DT 01-JUN-2002 (TRENBLREL. 21, Created)
 DT 01-JUN-2002 (TRENBLREL. 21, Last sequence update)
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
 DE Neuroplilin-1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
 RT "Neuroplilin-1 is required for normal vascular development and is a
 mediator of VEGF-dependent angiogenesis in zebrafish."
 RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 CUB DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 MAM DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FS/8 TYPE C DOMAIN.
 DR EMBL; AY064213; AAL40862.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000421; FA58_C.
 DR InterPro; IPR008979; Gal_Bind_Like.
 DR InterPro; IPR000998; MAM_domain.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00754; FS_F8_type_C; 2.
 DR Pfam; PF00629; MAM; 1.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00231; MAM; 1.
 DR SMART; SM00137; MAM; 1.

DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01285; FA58C_1; 1.
 DR PROSITE; PS01286; FA58C_2; 2.
 DR PROSITE; PS50022; FA58C_3; 2.
 DR PROSITE; PS00740; MAM_1; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 KW Glycoprotein; Receptor; Transmembrane.
 SQ SEQUENCE 923 AA; 102541 MW; 2ED84B129AA92B2D CRC64;

Query Match 1.2%; Score 9; DB 13; Length 923;
 Best Local Similarity 100.0%; Pred. No. 7.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 179 YDYVEVRDQ 187
 |||||
 DB 82 YDYVEVRDQ 90

RESULT 9
 Q8AXP1 PRELIMINARY; PRT; 923 AA.
 ID Q8AXP1;
 AC Q8AXP1;
 DT 01-MAR-2003 (TRENBLREL. 23, Created)
 DT 01-MAR-2003 (TRENBLREL. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLREL. 25, Last annotation update)
 DE Neuroplilin-1.
 GN NP-1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shoji W., Tawarayama H.;
 RT "The cloning and expression of neuroplilin-1."
 RL Submitted (JUL-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AB088776; BAC53657.1; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000421; FA58_C.
 DR InterPro; IPR008979; Gal_Bind_Like.
 DR InterPro; IPR000998; MAM_domain.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00754; FS_F8_type_C; 2.
 DR Pfam; PF00629; MAM; 1.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00231; FA58C; 2.
 DR SMART; SM00137; MAM; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01285; FA58C_1; 1.
 DR PROSITE; PS01286; FA58C_2; 2.
 DR PROSITE; PS50022; FA58C_3; 2.
 DR PROSITE; PS00740; MAM_1; 1.
 DR PROSITE; PS50060; MAM_2; 1.
 SQ SEQUENCE 923 AA; 102541 MW; 0E6CE33ED28A21F7 CRC64;

OY 179 YDYVEVRDQ 187
 |||||
 DB 82 YDYVEVRDQ 90

Query Match 1.2%; Score 9; DB 13; Length 923;
 Best Local Similarity 100.0%; Pred. No. 7.5; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 Q9UQ00 PRELIMINARY; PRT; 926 AA.
 ID Q9UQ00;
 AC Q9UQ00;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)

DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein KIAA0932 (fragment).
 GN KIAA0932.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99246063; PubMed=1021032; Kikuno R., Hikosawa M.,
 RA Nagaoka T., Ishikawa K., Suyama M., Kottani H., Nomura N., Ohara O.,
 RA Miyajima N., Tanaka A., Kottani H., Nomura N., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. XIII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 6:63-70(1999).
 CC -1- SIMILARITY: CONTAINS 5 CUB DOMAINS.
 DR EMBL; AB023149; BAA76776.1; -.
 DR HSSP; P00736; IAPQ.
 DR MEROPS; M12.018; -.
 DR GO; GO:0008533; F:actinin activity; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0008237; F:metalloproteinase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR001506; Peptidase_M12A.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01400; Astacin; 1.
 DR Pfam; PF00431; CUB; 5.
 DR Pfam; PF00008; EGF; 2.
 DR PRINTS; PRO0480; ASTACIN.
 DR SMART; SM00042; CUB; 5.
 DR SMART; SM00179; EGF_CA; 2.
 DR SMART; SM00235; Zmnc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 2.
 DR PROSITE; PS01180; CUB; 5.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KM Hypothetical protein; EGF-like domain.
 FT NON_TER
 SQ SEQUENCE 926 AA; 103873 MW; 58FA35CDDDE10970B CRC64;
 Query Match 1.2%; Score 9; DB 4; Length 926;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 179 YDYVEVRDG 187
 DB 317 YDYVEVRDG 325
 RESULT 11
 QY6L7 PRELIMINARY; PRT; 1015 AA.
 AC QY6L7;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Tolloid-like 2 protein.
 GN TLL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;
 RX MEDLINE=99447609; PubMed=10516436;
 RA Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Eddy R.L.,
 RA Shows T.B., Greenspan D.S.;
 RT "Assignment of TLL1 and TLL2, which encode human BMP-1/Tolloid-
 RT related metalloproteinases, to chromosomes 4q32-q33 and 10q23-q24 and
 RT assignment of murine Tll2 to chromosome 19."
 RL Cytogenet. Cell Genet. 86:64-65(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=99410337; PubMed=10479448;
 RA Scott I.C., Biltz I.L., Pappano W.N., Clark T.G., Steigltz B.M.,
 RA Thomas C.L., Maas S.A., Takahara K., Cho K.W.Y., Greenspan D.S.;
 RT "Mammalian BMP-1/Tolloid-related metalloproteinases, including novel
 RT family member mammalian tollid-like 2, have differential enzymatic
 RT activities and distributions of expression relevant to patterning and
 RT skeletogenesis."
 RL Dev. Biol. 213:283-300(1999).
 CC -1- SIMILARITY: CONTAINS 5 CUB DOMAINS.
 DR EMBL; AF059516; AAD42979.1; -.
 DR HSSP; P00736; IAPQ.
 DR MEROPS; M12.018; -.
 DR GO; GO:0008533; F:actinin activity; IEA.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0008237; F:metalloproteinase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR001506; Peptidase_M12A.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01400; Astacin; 1.
 DR Pfam; PF00431; CUB; 5.
 DR Pfam; PF00008; EGF; 2.
 DR PRINTS; PRO0480; ASTACIN.
 DR SMART; SM00042; CUB; 5.
 DR SMART; SM00179; EGF_CA; 2.
 DR SMART; SM00235; Zmnc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 2.
 DR PROSITE; PS01180; CUB; 5.
 DR PROSITE; PS01186; EGF_2; 2.
 DR PROSITE; PS01187; EGF_CA; 2.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KM EGF-like domain.
 SQ SEQUENCE 1015 AA; 113556 MW; 25F5B23065861593 CRC64;
 Query Match 1.2%; Score 9; DB 4; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 8.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 179 YDYVEVRDG 187
 DB 406 YDYVEVRDG 414
 RESULT 12
 Q23995 PRELIMINARY; PRT; 1464 AA.
 AC Q23995;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE TOLLID related 1.
 GN TOK OR TLLR-1 OR CG6863.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.

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OX NCBI_TaxID=7227;
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON S;
RA MEDLINE=95113176; PubMed=7813777;
RA Nguyen T., Jamal J., Shmell M.J., Arora K., O'Connor M.B.;
RT "Characterization of tolloid-related-1: a BMP-1-like product that is
RL required during larval and pupal stages of Drosophila development.";
CC -1 SIMILARITY: CONTAINS 5 CUB DOMAINS.
DR EMBL: U12634; AAA70057.1; -.
DR HSSP: P00736; IAPQ.
DR MEROPS: M12.011; -.
DR FlyBase: FBgn0004885; tok.
DR GO: GO:0008533; F:actinin activity; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0008237; F:metallopeptidase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR006026; Peptidase_M.
DR InterPro: IPR001506; Peptidase_M12A.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR Pfam: PF01400; Actactin; 1.
DR Pfam: PF00431; CUB; 5.
DR Pfam: PF00008; EGF; 2.
DR PRINTS: PR00480; ASTACTIN.
DR SMART: SM00042; CUB; 5.
DR SMART: SM00179; EGF_CA; 2.
DR SMART: SM00235; ZmC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 2.
DR PROSITE: PS01180; CUB; 5.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
KW EGF-like domain.
SQ SEQUENCE 1464 AA; 165053 MW; 94373260D3862E6 CRC64;
Query Match 1.2%; Score 9; DB 5; Length 1464;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 179 YDYVEVRDG 187
DB 897 YDYVEVRDG 905
RESULT 13
ID Q9VC47 PRELIMINARY; FRT; 1464 AA.
AC Q9VC47;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE TOK protein (GH23184P).
GN TOK OR CG6863.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Empidoidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blake J.R.G., Champé M., Pfeiffer B.D.,

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RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Aspayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baltes R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintoy S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brockett P.,
RA Butts K.C., Buzam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Dove A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flesler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Mishina N.V., Mobarry C., Moritz J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhu Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster";
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Aspayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Friese E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Murgall C.J.,
RA Nuno J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.,
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC -1 SIMILARITY: CONTAINS 5 CUB DOMAINS.
DR EMBL: AE003749; AAF56328.1; -.
DR HSSP: AY051585; AAK93009.1; -.
DR HSSP: P00736; IAPQ.
DR MEROPS: M12.011; -.
DR FlyBase: FBgn0004885; tok.
DR GO: GO:0008533; F:actinin activity; IEA.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0008237; F:metallopeptidase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR000152; Asx_hydroxyl_S.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR006026; Peptidase_M.
DR InterPro: IPR001506; Peptidase_M12A.
DR InterPro: IPR006025; Pept_M_Zn_BS.
DR Pfam: PF01400; Actactin; 1.
DR Pfam: PF00431; CUB; 5.
DR Pfam: PF00008; EGF; 2.
DR PRINTS: PR00480; ASTACTIN.
DR SMART: SM00042; CUB; 5.
DR SMART: SM00179; EGF_CA; 2.
DR SMART: SM00235; ZmC; 1.
DR PROSITE: PS00010; ASX_HYDROXYL; 2.
DR PROSITE: PS01180; CUB; 5.
DR PROSITE: PS01186; EGF_2; 2.
DR PROSITE: PS01187; EGF_CA; 2.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
KW EGF-like domain; Hydrolyase; Metal-binding; Metalloprotease; Protease;

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KW Zinc.
SQ SEQUENCE 1464 AA; 165218 MW; 029BE1560DBE9056 CRC64;
Query Match 1.2%; Score 9; DB 5; Length 1464;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 179 YDYVEVRDG 187
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DB 897 YDYVEVRDG 905

RESULT 14
Q24132 PRELIMINARY; PRT; 1464 AA.
AC Q24132;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE TOLKIN.
GN TOK OR TOLKIN OR CG6863.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96042912; PubMed=8536976;
RA Finelli A.L., Xie T., Bosse C.A., Blackman R.K., Padgett R.W.;
RT "The tolkin gene is a tollid/BMP-1 homologue that is essential for
RT Drosophila development."
RC Genotics 141:271-281(1995).
CC -I- SIMILARITY: CONTAINS 5 CUB DOMAINS.
DR EMBL; U34777; AAC47015.1; -
DR PIR; S58984; S58984.
DR HSSP; P00736; 1APQ.
DR MEROPS; M12.011; -
DR FlyBase; Fgn0004885; tok.
DR GO; GO:0008533; F:astacin activity; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0008237; F:metalloproteinase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; ASX_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001506; Peptidase_M12A.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR Pfam; PF01400; Astacin; 1.
DR Pfam; PF00431; CUB; 5.
DR Pfam; PF00008; EGF; 2.
DR PRINTS; P000480; ASTACIN.
DR SMART; SM00042; CUB; 5.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00235; ZNMG; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.
DR PROSITE; PS01180; CUB; 5.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW EGF-like domain.
SQ SEQUENCE 1464 AA; 165106 MW; 5955B6DEA9E37170 CRC64;

Query Match 1.2%; Score 9; DB 5; Length 1464;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 179 YDYVEVRDG 187
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DB 897 YDYVEVRDG 905

RESULT 15
O16004 PRELIMINARY; PRT; 2531 AA.
AC O16004;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Notch homolog.
OS Lytechinus variegatus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae;
OC Lytechinus.
OX NCBI_TaxID=7654;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97454256; PubMed=9310331;
RA Sherwood D.R., McClay D.R.;
RT "Identification and localization of a sea urchin Notch homologue:
RT insights into vegetal plate regionalization and Notch receptor
RT regulation."
RL Development 124:3363-3374(1997).
DR EMBL; AF000634; AAB82088.1; -
DR HSSP; P01132; IEGF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR008297; Notch.
DR InterPro; IPR008000; Notch_dom.
DR Pfam; PF00023; ank; 6.
DR Pfam; PF00008; EGF; 34.
DR Pfam; PF00066; notch; 3.
DR PRINTS; P00010; EGFLOOD.
DR PRINTS; P01452; NOTCH.
DR SMART; SM00248; ANK; 5.
DR SMART; SM00179; EGF_CA; 23.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS50088; ANK_REPEAT; 5.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 21.
DR PROSITE; PS00022; EGF_1; 33.
DR PROSITE; PS01186; EGF_2; 25.
DR PROSITE; PS01187; EGF_CA; 20.
DR PIRSF; PIRSF002279; Notch; 1.
KW ANK repeat; EGF-like domain; Repeat.
SQ SEQUENCE 2531 AA; 273982 MW; 5BF42BEC627CA303 CRC64;

Query Match 1.2%; Score 9; DB 5; Length 2531;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 260 CACLAGYTG 268
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DB 537 CACLAGYTG 545

Search completed: August 18, 2004, 16:33:39
Job time : 59 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:25:04 ; Search time 50 Seconds
(without alignments)
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Title: US-10-063-546-38

Perfect score: 720

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Gapop 60.0 , Gapext 60.0

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- 10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	720	100.0	720	9	US-09-989-279-231
4	720	100.0	720	9	US-09-989-727-231
5	720	100.0	720	9	US-09-989-731-231
6	720	100.0	720	9	US-09-989-732-231
7	720	100.0	720	9	US-09-991-073-231
8	720	100.0	720	9	US-09-990-442-231
9	720	100.0	720	9	US-09-991-163-231
10	720	100.0	720	9	US-09-993-604-231
11	720	100.0	720	9	US-09-990-456-231
12	720	100.0	720	9	US-09-989-721-231
13	720	100.0	720	9	US-09-992-598-231
14	720	100.0	720	9	US-09-989-293A-231
15	720	100.0	720	9	US-09-989-735-231

16	720	100.0	720	9	US-09-990-444-231	Sequence 231, App
17	720	100.0	720	9	US-09-991-181-231	Sequence 231, App
18	720	100.0	720	9	US-09-989-730-231	Sequence 231, App
19	720	100.0	720	9	US-09-990-436-231	Sequence 231, App
20	720	100.0	720	9	US-09-993-687-231	Sequence 231, App
21	720	100.0	720	10	US-09-989-734-231	Sequence 231, App
22	720	100.0	720	10	US-09-997-653-231	Sequence 231, App
23	720	100.0	720	10	US-09-993-667-231	Sequence 231, App
24	720	100.0	720	10	US-09-997-428-231	Sequence 231, App
25	720	100.0	720	10	US-09-997-666-231	Sequence 231, App
26	720	100.0	720	10	US-09-990-438-231	Sequence 231, App
27	720	100.0	720	10	US-09-990-562-231	Sequence 231, App
28	720	100.0	720	10	US-09-990-711-231	Sequence 231, App
29	720	100.0	720	10	US-09-989-726-231	Sequence 231, App
30	720	100.0	720	10	US-09-998-156-231	Sequence 231, App
31	720	100.0	720	10	US-09-990-437-231	Sequence 231, App
32	720	100.0	720	10	US-09-991-157-231	Sequence 231, App
33	720	100.0	720	10	US-09-997-514-231	Sequence 231, App
34	720	100.0	720	10	US-09-997-573-231	Sequence 231, App
35	720	100.0	720	10	US-09-991-172-231	Sequence 231, App
36	720	100.0	720	10	US-09-990-726-231	Sequence 231, App
37	720	100.0	720	10	US-09-997-559-231	Sequence 231, App
38	720	100.0	720	10	US-09-997-601-231	Sequence 231, App
39	720	100.0	720	10	US-09-990-443-231	Sequence 231, App
40	720	100.0	720	10	US-09-991-854-231	Sequence 231, App
41	720	100.0	720	10	US-09-997-628-231	Sequence 231, App
42	720	100.0	720	10	US-09-997-683-231	Sequence 231, App
43	720	100.0	720	10	US-09-989-729A-231	Sequence 231, App
44	720	100.0	720	10	US-09-997-349-231	Sequence 231, App
45	720	100.0	720	10	US-09-990-440-231	Sequence 231, App
46	720	100.0	720	10	US-09-993-463-231	Sequence 231, App
47	720	100.0	720	10	US-09-997-542-231	Sequence 231, App
48	720	100.0	720	10	US-09-993-748-231	Sequence 231, App
49	720	100.0	720	10	US-09-990-439-231	Sequence 231, App
50	720	100.0	720	10	US-09-990-427-231	Sequence 231, App
51	720	100.0	720	10	US-09-989-328-231	Sequence 231, App
52	720	100.0	720	10	US-09-993-583-231	Sequence 231, App
53	720	100.0	720	10	US-09-991-992-231	Sequence 231, App
54	720	100.0	720	10	US-09-992-521-231	Sequence 231, App
55	720	100.0	720	10	US-09-997-333-231	Sequence 231, App
56	720	100.0	720	10	US-09-997-384-231	Sequence 231, App
57	720	100.0	720	10	US-09-998-041-231	Sequence 231, App
58	720	100.0	720	10	US-09-997-585-231	Sequence 231, App
59	720	100.0	720	10	US-09-997-614-231	Sequence 231, App
60	720	100.0	720	10	US-09-989-863-231	Sequence 231, App
61	720	100.0	720	10	US-09-997-529-231	Sequence 231, App
62	720	100.0	720	10	US-09-989-725-231	Sequence 231, App
63	720	100.0	720	10	US-09-989-733-231	Sequence 231, App
64	720	100.0	720	11	US-09-992-643-231	Sequence 231, App
65	720	100.0	720	12	US-10-206-915-170	Sequence 170, App
66	720	100.0	720	12	US-10-199-670-170	Sequence 170, App
67	720	100.0	720	12	US-10-201-858-170	Sequence 170, App
68	720	100.0	720	12	US-10-205-890-170	Sequence 170, App
69	720	100.0	720	12	US-10-208-024-170	Sequence 170, App
70	720	100.0	720	12	US-10-201-853-170	Sequence 170, App
71	720	100.0	720	12	US-10-063-745-38	Sequence 38, App1
72	720	100.0	720	12	US-09-989-724-231	Sequence 231, App
73	720	100.0	720	12	US-09-989-728-231	Sequence 231, App
74	720	100.0	720	12	US-09-990-441-231	Sequence 38, App1
75	720	100.0	720	12	US-10-063-513-38	Sequence 38, App1
76	720	100.0	720	12	US-10-063-513-38	Sequence 38, App1
77	720	100.0	720	12	US-10-063-515-38	Sequence 38, App1
78	720	100.0	720	12	US-10-063-549-38	Sequence 38, App1
79	720	100.0	720	12	US-10-063-551-38	Sequence 38, App1
80	720	100.0	720	12	US-10-063-569-38	Sequence 38, App1
81	720	100.0	720	12	US-10-174-581-170	Sequence 170, App
82	720	100.0	720	12	US-10-176-483-170	Sequence 170, App
83	720	100.0	720	12	US-10-176-483-170	Sequence 170, App
84	720	100.0	720	12	US-10-176-914-170	Sequence 170, App
85	720	100.0	720	12	US-10-176-915-170	Sequence 170, App
86	720	100.0	720	12	US-09-997-857-231	Sequence 231, App
87	720	100.0	720	12	US-10-063-555-38	Sequence 38, App1
88	720	100.0	720	12	US-10-063-555-38	Sequence 38, App1

89	720	100.0	720	12	US-10-063-563-38	Sequence 38, App1	162	720	100.0	720	14	US-10-184-658-170	Sequence 170, App
90	720	100.0	720	12	US-10-063-594-38	Sequence 38, App1	163	720	100.0	720	14	US-10-176-991-170	Sequence 170, App
91	720	100.0	720	12	US-10-063-553-38	Sequence 38, App1	164	720	100.0	720	14	US-10-173-695-170	Sequence 170, App
92	720	100.0	720	12	US-10-063-554-38	Sequence 38, App1	165	720	100.0	720	14	US-10-173-697-170	Sequence 170, App
93	720	100.0	720	12	US-10-176-484-170	Sequence 170, App	166	720	100.0	720	14	US-10-173-705-170	Sequence 170, App
94	720	100.0	720	12	US-10-180-550-170	Sequence 170, App	167	720	100.0	720	14	US-10-174-576-170	Sequence 170, App
95	720	100.0	720	12	US-10-183-014-170	Sequence 170, App	168	720	100.0	720	14	US-10-174-585-170	Sequence 170, App
96	720	100.0	720	12	US-10-187-738-170	Sequence 170, App	169	720	100.0	720	14	US-10-174-585-170	Sequence 170, App
97	720	100.0	720	12	US-10-187-740-170	Sequence 170, App	170	720	100.0	720	14	US-10-175-741-170	Sequence 170, App
98	720	100.0	720	12	US-10-187-883-170	Sequence 170, App	171	720	100.0	720	14	US-10-176-481-170	Sequence 170, App
99	720	100.0	720	12	US-10-194-363-170	Sequence 170, App	172	720	100.0	720	14	US-10-176-485-170	Sequence 170, App
100	720	100.0	720	12	US-10-194-460-170	Sequence 170, App	173	720	100.0	720	14	US-10-176-487-170	Sequence 170, App
101	720	100.0	720	12	US-10-194-463-170	Sequence 170, App	174	720	100.0	720	14	US-10-176-493-170	Sequence 170, App
102	720	100.0	720	12	US-10-194-484-170	Sequence 170, App	175	720	100.0	720	14	US-10-176-756-170	Sequence 170, App
103	720	100.0	720	12	US-10-195-884-170	Sequence 170, App	176	720	100.0	720	14	US-10-176-911-170	Sequence 170, App
104	720	100.0	720	12	US-10-195-896-170	Sequence 170, App	177	720	100.0	720	14	US-10-176-913-170	Sequence 170, App
105	720	100.0	720	12	US-10-196-744-170	Sequence 170, App	178	720	100.0	720	14	US-10-176-925-170	Sequence 170, App
106	720	100.0	720	12	US-10-196-755-170	Sequence 170, App	179	720	100.0	720	14	US-10-176-978-170	Sequence 170, App
107	720	100.0	720	12	US-10-196-757-170	Sequence 170, App	180	720	100.0	720	14	US-10-179-510-170	Sequence 170, App
108	720	100.0	720	12	US-10-197-704-170	Sequence 170, App	181	720	100.0	720	14	US-10-180-543-170	Sequence 170, App
109	720	100.0	720	12	US-10-197-710-170	Sequence 170, App	182	720	100.0	720	14	US-10-180-544-170	Sequence 170, App
110	720	100.0	720	12	US-10-198-758-170	Sequence 170, App	183	720	100.0	720	14	US-10-180-546-170	Sequence 170, App
111	720	100.0	720	12	US-10-198-766-170	Sequence 170, App	184	720	100.0	720	14	US-10-180-547-170	Sequence 170, App
112	720	100.0	720	12	US-10-199-304-170	Sequence 170, App	185	720	100.0	720	14	US-10-180-549-170	Sequence 170, App
113	720	100.0	720	12	US-10-199-309-170	Sequence 170, App	186	720	100.0	720	14	US-10-180-555-170	Sequence 170, App
114	720	100.0	720	12	US-10-199-313-170	Sequence 170, App	187	720	100.0	720	14	US-10-180-559-170	Sequence 170, App
115	720	100.0	720	12	US-10-199-456-170	Sequence 170, App	188	720	100.0	720	14	US-10-181-000-170	Sequence 170, App
116	720	100.0	720	12	US-10-201-329-170	Sequence 170, App	189	720	100.0	720	14	US-10-181-010-170	Sequence 170, App
117	720	100.0	720	12	US-10-202-412-170	Sequence 170, App	190	720	100.0	720	14	US-10-183-012-170	Sequence 170, App
118	720	100.0	720	12	US-10-206-919-170	Sequence 170, App	191	720	100.0	720	14	US-10-184-614-170	Sequence 170, App
119	720	100.0	720	12	US-10-206-922-170	Sequence 170, App	192	720	100.0	720	14	US-10-184-623-170	Sequence 170, App
120	720	100.0	720	12	US-10-206-928-170	Sequence 170, App	193	720	100.0	720	14	US-10-184-635-170	Sequence 170, App
121	720	100.0	720	12	US-10-206-928-170	Sequence 170, App	194	720	100.0	720	14	US-10-184-637-170	Sequence 170, App
122	720	100.0	720	12	US-10-207-914-170	Sequence 170, App	195	720	100.0	720	14	US-10-184-646-170	Sequence 170, App
123	720	100.0	720	12	US-10-207-921-170	Sequence 170, App	196	720	100.0	720	14	US-10-184-647-170	Sequence 170, App
124	720	100.0	720	12	US-10-207-922-170	Sequence 170, App	197	720	100.0	720	14	US-10-184-652-170	Sequence 170, App
125	720	100.0	720	12	US-10-208-027-170	Sequence 170, App	198	720	100.0	720	14	US-10-187-594-170	Sequence 170, App
126	720	100.0	720	12	US-09-997-641-231	Sequence 231, App	199	720	100.0	720	14	US-10-187-596-170	Sequence 170, App
127	720	100.0	720	12	US-09-991-150-231	Sequence 231, App	200	720	100.0	720	14	US-10-187-745-170	Sequence 170, App
128	720	100.0	720	12	US-10-174-570-170	Sequence 170, App	201	720	100.0	720	14	US-10-187-788-170	Sequence 170, App
129	720	100.0	720	12	US-10-183-005-170	Sequence 170, App	202	720	100.0	720	14	US-10-187-886-170	Sequence 170, App
130	720	100.0	720	12	US-10-006-867-38	Sequence 38, App1	203	720	100.0	720	14	US-10-199-464-170	Sequence 170, App
131	720	100.0	720	13	US-10-052-886-170	Sequence 170, App	204	720	100.0	720	14	US-10-196-756-170	Sequence 170, App
132	720	100.0	720	13	US-10-063-547-38	Sequence 38, App1	205	720	100.0	720	14	US-10-176-751-170	Sequence 170, App
133	720	100.0	720	14	US-10-174-590-170	Sequence 170, App	206	720	100.0	720	14	US-10-176-760-170	Sequence 170, App
134	720	100.0	720	14	US-10-176-758-170	Sequence 170, App	207	720	100.0	720	14	US-10-176-990-170	Sequence 170, App
135	720	100.0	720	14	US-10-175-737-170	Sequence 170, App	208	720	100.0	720	14	US-10-180-541-170	Sequence 170, App
136	720	100.0	720	14	US-10-063-616-38	Sequence 38, App1	209	720	100.0	720	14	US-10-180-542-170	Sequence 170, App
137	720	100.0	720	14	US-10-173-706-170	Sequence 170, App	210	720	100.0	720	14	US-10-180-548-170	Sequence 170, App
138	720	100.0	720	14	US-10-175-738-170	Sequence 170, App	211	720	100.0	720	14	US-10-180-551-170	Sequence 170, App
139	720	100.0	720	14	US-10-175-752-170	Sequence 170, App	212	720	100.0	720	14	US-10-180-998-170	Sequence 170, App
140	720	100.0	720	14	US-10-176-482-170	Sequence 170, App	213	720	100.0	720	14	US-10-180-999-170	Sequence 170, App
141	720	100.0	720	14	US-10-176-757-170	Sequence 170, App	214	720	100.0	720	14	US-10-183-013-170	Sequence 170, App
142	720	100.0	720	14	US-10-176-913-170	Sequence 170, App	215	720	100.0	720	14	US-10-184-612-170	Sequence 170, App
143	720	100.0	720	14	US-10-180-552-170	Sequence 170, App	216	720	100.0	720	14	US-10-184-616-170	Sequence 170, App
144	720	100.0	720	14	US-10-180-557-170	Sequence 170, App	217	720	100.0	720	14	US-10-184-617-170	Sequence 170, App
145	720	100.0	720	14	US-10-063-502-38	Sequence 38, App1	218	720	100.0	720	14	US-10-184-622-170	Sequence 170, App
146	720	100.0	720	14	US-10-173-700-170	Sequence 170, App	219	720	100.0	720	14	US-10-184-628-170	Sequence 170, App
147	720	100.0	720	14	US-10-174-572-170	Sequence 170, App	220	720	100.0	720	14	US-10-184-629-170	Sequence 170, App
148	720	100.0	720	14	US-10-174-579-170	Sequence 170, App	221	720	100.0	720	14	US-10-184-630-170	Sequence 170, App
149	720	100.0	720	14	US-10-174-582-170	Sequence 170, App	222	720	100.0	720	14	US-10-184-631-170	Sequence 170, App
150	720	100.0	720	14	US-10-174-588-170	Sequence 170, App	223	720	100.0	720	14	US-10-184-632-170	Sequence 170, App
151	720	100.0	720	14	US-10-175-740-170	Sequence 170, App	224	720	100.0	720	14	US-10-184-636-170	Sequence 170, App
152	720	100.0	720	14	US-10-175-749-170	Sequence 170, App	225	720	100.0	720	14	US-10-184-640-170	Sequence 170, App
153	720	100.0	720	14	US-10-175-743-170	Sequence 170, App	226	720	100.0	720	14	US-10-184-650-170	Sequence 170, App
154	720	100.0	720	14	US-10-176-488-170	Sequence 170, App	227	720	100.0	720	14	US-10-184-651-170	Sequence 170, App
155	720	100.0	720	14	US-10-176-492-170	Sequence 170, App	228	720	100.0	720	14	US-10-187-588-170	Sequence 170, App
156	720	100.0	720	14	US-10-176-747-170	Sequence 170, App	229	720	100.0	720	14	US-10-187-597-170	Sequence 170, App
157	720	100.0	720	14	US-10-176-750-170	Sequence 170, App	230	720	100.0	720	14	US-10-187-598-170	Sequence 170, App
158	720	100.0	720	14	US-10-176-985-170	Sequence 170, App	231	720	100.0	720	14	US-10-187-600-170	Sequence 170, App
159	720	100.0	720	14	US-10-176-987-170	Sequence 170, App	232	720	100.0	720	14	US-10-187-601-170	Sequence 170, App
160	720	100.0	720	14	US-10-176-992-170	Sequence 170, App	233	720	100.0	720	14	US-10-187-602-170	Sequence 170, App
161	720	100.0	720	14	US-10-176-993-170	Sequence 170, App	234	720	100.0	720	14	US-10-187-603-170	Sequence 170, App

235	720	100.0	720	14	US-10-187-741-170	Sequence 170, App	308	720	100.0	720	14	US-10-194-425-170	Sequence 170, App
236	720	100.0	720	14	US-10-187-743-170	Sequence 170, App	309	720	100.0	720	14	US-10-194-485-170	Sequence 170, App
237	720	100.0	720	14	US-10-187-746-170	Sequence 170, App	310	720	100.0	720	14	US-10-195-885-170	Sequence 170, App
238	720	100.0	720	14	US-10-187-747-170	Sequence 170, App	311	720	100.0	720	14	US-10-195-898-170	Sequence 170, App
239	720	100.0	720	14	US-10-187-751-170	Sequence 170, App	312	720	100.0	720	14	US-10-196-748-170	Sequence 170, App
240	720	100.0	720	14	US-10-187-753-170	Sequence 170, App	313	720	100.0	720	14	US-10-196-750-170	Sequence 170, App
241	720	100.0	720	14	US-10-187-754-170	Sequence 170, App	314	720	100.0	720	14	US-10-197-693-170	Sequence 170, App
242	720	100.0	720	14	US-10-187-757-170	Sequence 170, App	315	720	100.0	720	14	US-10-197-700-170	Sequence 170, App
243	720	100.0	720	14	US-10-187-884-170	Sequence 170, App	316	720	100.0	720	14	US-10-197-705-170	Sequence 170, App
244	720	100.0	720	14	US-10-188-767-170	Sequence 170, App	317	720	100.0	720	14	US-10-197-708-170	Sequence 170, App
245	720	100.0	720	14	US-10-188-769-170	Sequence 170, App	318	720	100.0	720	14	US-10-198-764-170	Sequence 170, App
246	720	100.0	720	14	US-10-188-770-170	Sequence 170, App	319	720	100.0	720	14	US-10-198-765-170	Sequence 170, App
247	720	100.0	720	14	US-10-188-773-170	Sequence 170, App	320	720	100.0	720	14	US-10-198-768-170	Sequence 170, App
248	720	100.0	720	14	US-10-188-781-170	Sequence 170, App	321	720	100.0	720	14	US-10-198-769-170	Sequence 170, App
249	720	100.0	720	14	US-10-194-361-170	Sequence 170, App	322	720	100.0	720	14	US-10-199-305-170	Sequence 170, App
250	720	100.0	720	14	US-10-194-423-170	Sequence 170, App	323	720	100.0	720	14	US-10-199-306-170	Sequence 170, App
251	720	100.0	720	14	US-10-195-897-170	Sequence 170, App	324	720	100.0	720	14	US-10-199-310-170	Sequence 170, App
252	720	100.0	720	14	US-10-195-901-170	Sequence 170, App	325	720	100.0	720	14	US-10-199-311-170	Sequence 170, App
253	720	100.0	720	14	US-10-195-902-170	Sequence 170, App	326	720	100.0	720	14	US-10-199-314-170	Sequence 170, App
254	720	100.0	720	14	US-10-196-743-170	Sequence 170, App	327	720	100.0	720	14	US-10-199-317-170	Sequence 170, App
255	720	100.0	720	14	US-10-196-760-170	Sequence 170, App	328	720	100.0	720	14	US-10-199-665-170	Sequence 170, App
256	720	100.0	720	14	US-10-173-708-170	Sequence 170, App	329	720	100.0	720	14	US-10-199-666-170	Sequence 170, App
257	720	100.0	720	14	US-10-176-479-170	Sequence 170, App	330	720	100.0	720	14	US-10-199-669-170	Sequence 170, App
258	720	100.0	720	14	US-10-176-748-170	Sequence 170, App	331	720	100.0	720	14	US-10-201-534-170	Sequence 170, App
259	720	100.0	720	14	US-10-176-916-170	Sequence 170, App	332	720	100.0	720	14	US-10-201-770-170	Sequence 170, App
260	720	100.0	720	14	US-10-179-507-170	Sequence 170, App	333	720	100.0	720	14	US-10-201-855-170	Sequence 170, App
261	720	100.0	720	14	US-10-179-516-170	Sequence 170, App	334	720	100.0	720	14	US-10-201-856-170	Sequence

381	720	100.0	720	14	US-10-194-456-170	Sequence 170, App	Sequence 170, App	454	720	100.0	720	14	US-10-205-892-170	Sequence 170, App
382	720	100.0	720	14	US-10-196-758-170	Sequence 170, App	Sequence 170, App	455	720	100.0	720	14	US-10-205-894-170	Sequence 170, App
383	720	100.0	720	14	US-10-198-770-170	Sequence 170, App	Sequence 170, App	456	720	100.0	720	14	US-10-205-896-170	Sequence 170, App
384	720	100.0	720	14	US-10-199-308-170	Sequence 170, App	Sequence 170, App	457	720	100.0	720	14	US-10-205-898-170	Sequence 170, App
385	720	100.0	720	14	US-10-200-617-170	Sequence 170, App	Sequence 170, App	458	720	100.0	720	14	US-10-205-901-170	Sequence 170, App
386	720	100.0	720	14	US-10-205-893-170	Sequence 170, App	Sequence 170, App	459	720	100.0	720	14	US-10-205-903-170	Sequence 170, App
387	720	100.0	720	14	US-10-205-897-170	Sequence 170, App	Sequence 170, App	460	720	100.0	720	14	US-10-206-909-170	Sequence 170, App
388	720	100.0	720	14	US-10-196-754-170	Sequence 170, App	Sequence 170, App	461	720	100.0	720	14	US-10-206-910-170	Sequence 170, App
389	720	100.0	720	14	US-10-174-571-170	Sequence 170, App	Sequence 170, App	462	720	100.0	720	14	US-10-206-911-170	Sequence 170, App
390	720	100.0	720	14	US-10-176-746-170	Sequence 170, App	Sequence 170, App	463	720	100.0	720	14	US-10-206-912-170	Sequence 170, App
391	720	100.0	720	14	US-10-176-923-170	Sequence 170, App	Sequence 170, App	464	720	100.0	720	14	US-10-206-914-170	Sequence 170, App
392	720	100.0	720	14	US-10-183-011-170	Sequence 170, App	Sequence 170, App	465	720	100.0	720	14	US-10-206-914-170	Sequence 170, App
393	720	100.0	720	14	US-10-184-633-170	Sequence 170, App	Sequence 170, App	466	720	100.0	720	14	US-10-206-920-170	Sequence 170, App
394	720	100.0	720	14	US-10-184-639-170	Sequence 170, App	Sequence 170, App	467	720	100.0	720	14	US-10-206-921-170	Sequence 170, App
395	720	100.0	720	14	US-10-187-742-170	Sequence 170, App	Sequence 170, App	468	720	100.0	720	14	US-10-206-923-170	Sequence 170, App
396	720	100.0	720	14	US-10-187-748-170	Sequence 170, App	Sequence 170, App	469	720	100.0	720	14	US-10-206-925-170	Sequence 170, App
397	720	100.0	720	14	US-10-188-766-170	Sequence 170, App	Sequence 170, App	470	720	100.0	720	14	US-10-206-926-170	Sequence 170, App
398	720	100.0	720	14	US-10-188-771-170	Sequence 170, App	Sequence 170, App	471	720	100.0	720	14	US-10-206-927-170	Sequence 170, App
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401	720	100.0	720	14	US-10-192-009-170	Sequence 170, App	Sequence 170, App	474	720	100.0	720	14	US-10-207-918-170	Sequence 170, App
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404	720	100.0	720	14	US-10-192-016-170	Sequence 170, App	Sequence 170, App	477	720	100.0	720	14	US-10-207-925-170	Sequence 170, App
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528	720	100.0	720	14	US-10-179-526-170	Sequence 170, App	601	720	100.0	720	14	US-10-176-981-170	Sequence 170, App
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530	720	100.0	720	14	US-10-179-511-170	Sequence 170, App	603	720	100.0	720	14	US-10-176-988-170	Sequence 170, App
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ALIGNMENTS

RESULT 1

US-09-989-722-231

Sequence 231, Application US/09989722

Patent No. US20020072067A1

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APPLICANT: Godowski, Paul J.

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APPLICANT: Gurney, Austin L.

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APPLICANT: Paoni, Nicholas P.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C63

CURRENT APPLICATION NUMBER: US/09/989,722

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

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PRIOR FILING DATE: 1997-11-12

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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09
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 Best Local Similarity 100.0%; Pred. No. 0;
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Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gorrissen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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 PRIOR FILING DATE: 1998-07-02
 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 720; DB 9; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;
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 DB 61 VVGTYIPICRNEENECDSCLHPGCTIFENCKSCRNKSGWGTLDFFYVKGFYCAECRAGW 120
 QY 121 YGDCMRCQVLRAPKQIILLESYPLNAHCEWTHAKPGFVIQLRPFVMSLEFDYMCQYD 180
 DB 121 YGDCMRCQVLRAPKQIILLESYPLNAHCEWTHAKPGFVIQLRPFVMSLEFDYMCQYD 180
 QY 181 YVEVDGNRQGIITKRVCGNERPAPIQISGSLHLVLFHSDGSKNFDGFHAIYEITACS 240
 DB 181 YVEVDGNRQGIITKRVCGNERPAPIQISGSLHLVLFHSDGSKNFDGFHAIYEITACS 240

QY 241 SSPCFHDGTCLVDKAGSYKACLAGYTGQRCENLLERNCSDFGGPVNGYQKITGGPGLI 300
 DB 241 SSPCFHDGTCLVDKAGSYKACLAGYTGQRCENLLERNCSDFGGPVNGYQKITGGPGLI 300
 QY 301 NGRHAKIGTVVSFFCNNSVVLGSGNEKRTCOQNGESGKQPICIKACREPKISDLVRRVRL 360
 DB 301 NGRHAKIGTVVSFFCNNSVVLGSGNEKRTCOQNGESGKQPICIKACREPKISDLVRRVRL 360
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 DB 361 PMQVQSRETPHLQLYSAAFSKQKLSQAPTKKPPALPGDLPNGYQHLLHTQLQYECISPFYR 420
 QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL 480
 DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL 480
 QY 481 HKGAWFLVCGALVNERVTVAHAHCVTDLGKVTMIKTADLVKLVGKFYRDDDEKTIQS 540
 DB 481 HKGAWFLVCGALVNERVTVAHAHCVTDLGKVTMIKTADLVKLVGKFYRDDDEKTIQS 540
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 DB 541 LQISAILHPNYDPILLADIAILKLLDKARISTRVQPICLAASRDLSFQESHITVAG 600
 QY 601 WNVLADVRSPGFKNDTLRSGVSVVDSLLCEOEHDHGIPVSVTDNMFCASWEPTAPSDI 660
 DB 601 WNVLADVRSPGFKNDTLRSGVSVVDSLLCEOEHDHGIPVSVTDNMFCASWEPTAPSDI 660
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 DB 661 CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSDYDKTCSHRLSTAFKTLVLPFKDWIERNMK 720

RESULT 3

US-09-989-279-231
 ; Sequence 231, Application US/09989279
 ; Patent No. US20020072496A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
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 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C56
 ; CURRENT APPLICATION NUMBER: US/09/989,279
 ; CURRENT FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186

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;; PRIOR FILING DATE: 1998-07-01.
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;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

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Db 661 CTAETGGTAAVSPGRASPEPRHLMGLVSVSYDKTCSHRLSTFTKVLPPKDWIERNMK 720

RESULT 4
US-09-989-727-231

;; Sequence 231, Application US/09989727
;; Patent No. US20020072497A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C65
;; CURRENT APPLICATION NUMBER: US/09/989,727
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1997-10-17
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73 PRIOR FILING DATE: 1998-06-23

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49 PRIOR APPLICATION NUMBER: 60/091978
50 PRIOR FILING DATE: 1998-07-07
51 PRIOR APPLICATION NUMBER: 60/091982
52 PRIOR FILING DATE: 1998-07-07
53 PRIOR APPLICATION NUMBER: 60/092182
54 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 720; DB 9; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 VVGYTIPCCRNENECDSLHPGCTIFENCKSCRNCSWGGLDDFYVKGFYCAECRAGW 120
Qy 121 YGDCMRCQVLRAPKQILLLESYPLNAHCEWTHAKPGFVQLFRVMSLEFDYWCQYD 180
Db 121 YGDCMRCQVLRAPKQILLLESYPLNAHCEWTHAKPGFVQLFRVMSLEFDYWCQYD 180
Qy 181 YVEVRDGNRDGQIIKRVCGNERPAPIOSIGSSLVHLFHSKGNFDFGHATYEEITACS 240

DB 181 YVEVRDGDNRDQGIKRVCGNERPAPIQSIGSSHLVLFHSDGSKDPGPHAYEIBITACS 240
QY 241 SSPCFHDGTCVLDKAGSYKACIAGYTGORCENLLEERCNSDPGGPVNGYQKITGPGIJI 300
DB 241 SSPCFHDGTCVLDKAGSYKACIAGYTGORCENLLEERCNSDPGGPVNGYQKITGPGIJI 300
QY 301 NGRHAKIGTVVSPFCNNSVYLSGNEKRTCCQNGWSGKQPCICACREPKISDLVRRVYL 360
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DB 361 PMQVQSRETPHLQVLSAAFSKOKLQSAPTKKPALPFGDLPNGVQHLLHTOLOVECISSPFYR 420
QY 421 RLGSRRTRCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYVRTSGVHDGSL 480
DB 421 RLGSRRTRCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYVRTSGVHDGSL 480
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DB 481 HKGAWFLVCSGALVNRRTVVAAHCVTDLGKVTMIKTADLKVVLGKPYRDDDRDEKTIQS 540
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DB 661 CTAETGGIAAVSPGRASPEPRHMLGLVSWSDYKTCSHRLSTAFTKVLPFKDWIERNMK 720

RESULT 5
US-09-989-731-231
Sequence 231, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Garber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
CURRENT FILING DATE: 2001-11-20
CURRENT APPLICATION NUMBER: US/09/989,731
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1997-11-24
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Query Match 100.0%; Score 720; DB 9; Length 720;
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DB 661 CTAETGGIAAVSFFGRASPEPRWHLMLGVNSYDKTCSHRLSTAFKVLFPKDWIERNMK 720

RESULT 6

US-09-989-732-231
Sequenco 231, Application US/09989732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Goritsen, Mary E.
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APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavín, Ivar J.
APPLICANT: Nepier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 720; DB 9; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 VVGYYTIPCCRNNEECDSCLHPGCTIFENCKSCRNCSGGTLDLDFYVKGFYCAECRAGW 120
QY 121 YGDCMRCGQVLRAPKQOILLESYPLNACEWTHAKPGFVIQLRFWMLSLDFYMCQYD 180
DB 121 YGDCMRCGQVLRAPKQOILLESYPLNACEWTHAKPGFVIQLRFWMLSLDFYMCQYD 180
QY 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNFDGFHAIYEETACS 240

DB 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNFDGFHAIYEETACS 240
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DB 241 SSPCFHDGTCVLDKAGSYKACACLAGYTGORCENLEERNCSDDPGPVNGYOKITGGPGLI 300
QY 301 NGRHAKIGTVVSVFFCNNSYVLSGNEKRTCCQNGSWSGKQPICIKACRBPKIIDLVRRLV 360
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DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480
QY 481 HKGAWFLVCSGALVNERTVVAACHCVDLKGKVTMIKTADLKVLGKGYRDDDRDKTIQS 540
DB 481 HKGAWFLVCSGALVNERTVVAACHCVDLKGKVTMIKTADLKVLGKGYRDDDRDKTIQS 540
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RESULT 7

US-09-991-073-331

; Sequence 231, Application US/09991073

; Patent No. US2002012756A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C15

; CURRENT APPLICATION NUMBER: US/09/991,073

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

[illegible]

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/ PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 720; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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54 PRIOR FILING DATE: 1998-07-07
55 PRIOR APPLICATION NUMBER: 60/092182
56 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 720; DB 9; Length 720;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIQSSHLVLFHSDGSKNFDGPHAIYEEITACS 240
Db 181 YVEVRDGNRDGQIIKRVCGNERPAPIQSIQSSHLVLFHSDGSKNFDGPHAIYEEITACS 240
QY 241 SSPCFHDGTCVLDKAGSYKACACLAGYTGQRCENLLBERNCSDPGGPNVGKQITGGPGLI 300
Db 241 SSPCFHDGTCVLDKAGSYKACACLAGYTGQRCENLLBERNCSDPGGPNVGKQITGGPGLI 300
QY 301 NGRHAKITGVVSPFCNNSYVLGNEKRTCOQNGWSKQPCICACREPKISDLVRRVRL 360
Db 301 NGRHAKITGVVSPFCNNSYVLGNEKRTCOQNGWSKQPCICACREPKISDLVRRVRL 360
QY 361 PMQVQSBRETLHQLYSAPSKQLOSAATKPPALPGDLPMGYOHLHTQLQYECISPEYR 420
Db 361 PMQVQSBRETLHQLYSAPSKQLOSAATKPPALPGDLPMGYOHLHTQLQYECISPEYR 420
QY 421 RLSSRRTRCLRTGWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYVRTSGVHDGSL 480
Db 421 RLSSRRTRCLRTGWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYVRTSGVHDGSL 480
QY 481 HKGAFLVCSGALVWERTVVAACHVTDLQKVTMIKTADLKVVLGKPYRDDREKTIQS 540
Db 481 HKGAFLVCSGALVWERTVVAACHVTDLQKVTMIKTADLKVVLGKPYRDDREKTIQS 540
QY 541 LQISAITLHNPYPIILLDADIAILKLLDKARISTRVQPICLAASRDISTFQESHITVAG 600
Db 541 LQISAITLHNPYPIILLDADIAILKLLDKARISTRVQPICLAASRDISTFQESHITVAG 600
QY 601 WNVLDVRSFGKNDTLRSVSVSDLLCEEQEDHGIPVSVTDNMFCASWEPTAPSDI 660
Db 601 WNVLDVRSFGKNDTLRSVSVSDLLCEEQEDHGIPVSVTDNMFCASWEPTAPSDI 660
QY 661 CTABTGIAAVSPGRASPSPRHMLGLVNSVDKTCSHRLSTAFKVLPPFKDWIERNMK 720
Db 661 CTABTGIAAVSPGRASPSPRHMLGLVNSVDKTCSHRLSTAFKVLPPFKDWIERNMK 720

RESULT 9
US-09-991-163-231
; Sequence 231, Application US/09991163
; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C17
; CURRENT APPLICATION NUMBER: US/09/991,163
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
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; PRIOR APPLICATION NUMBER: 60/089105
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; PRIOR APPLICATION NUMBER: 60/089440

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3	PRIOR FILING DATE: 1998-06-16
4	PRIOR APPLICATION NUMBER: 60/089514
5	PRIOR FILING DATE: 1998-06-16
6	PRIOR APPLICATION NUMBER: 60/089532
7	PRIOR FILING DATE: 1998-06-17
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9	PRIOR FILING DATE: 1998-06-17
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16	PRIOR APPLICATION NUMBER: 60/089653
17	PRIOR FILING DATE: 1998-06-17
18	PRIOR APPLICATION NUMBER: 60/089801
19	PRIOR FILING DATE: 1998-06-18
20	PRIOR APPLICATION NUMBER: 60/089907
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43	PRIOR FILING DATE: 1998-06-24
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54	PRIOR APPLICATION NUMBER: 60/090676
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57	PRIOR FILING DATE: 1998-06-25
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59	PRIOR FILING DATE: 1998-06-25
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62	PRIOR APPLICATION NUMBER: 60/090695
63	PRIOR FILING DATE: 1998-06-25
64	PRIOR APPLICATION NUMBER: 60/090696
65	PRIOR FILING DATE: 1998-06-25
66	PRIOR APPLICATION NUMBER: 60/090862
67	PRIOR FILING DATE: 1998-06-26

1	PRIOR APPLICATION NUMBER: 60/0910863
2	PRIOR FILING DATE: 1998-06-26
3	PRIOR APPLICATION NUMBER: 60/0913650
4	PRIOR FILING DATE: 1998-07-01
5	PRIOR APPLICATION NUMBER: 60/0914787
6	PRIOR FILING DATE: 1998-07-02
7	PRIOR APPLICATION NUMBER: 60/0915444
8	PRIOR FILING DATE: 1998-07-01
9	PRIOR APPLICATION NUMBER: 60/0915159
10	PRIOR FILING DATE: 1998-07-02
11	PRIOR APPLICATION NUMBER: 60/0916562
12	PRIOR FILING DATE: 1998-07-02
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14	PRIOR FILING DATE: 1998-07-02
15	PRIOR APPLICATION NUMBER: 60/0919787
16	PRIOR FILING DATE: 1998-07-07
17	PRIOR APPLICATION NUMBER: 60/0919822
18	PRIOR FILING DATE: 1998-07-07
19	PRIOR APPLICATION NUMBER: 60/0921823
20	PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 720; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;

[illegible]

RESULT 10
US-09-993-604-231
Sequence 231, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2710P1C25
CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 720; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MELGCWTQLGLTFLQLLLISSLPREYTVINACPGAENWIMCRCEBYDQIECVCPGKRE 60
Db 1 MELGCWTQLGLTFLQLLLISSLPREYTVINACPGAENWIMCRCEBYDQIECVCPGKRE 60
Qy 61 VVGVTIPCCRNENECSDLIHPGCTTIPENCKSRNGSWGGLDDFFVYKGYCAECRAGW 120
Db 61 VVGVTIPCCRNENECSDLIHPGCTTIPENCKSRNGSWGGLDDFFVYKGYCAECRAGW 120
Qy 121 YGGDMRCGOVLAPKPGQILLESPLNNAHCEWTHAKPGFVIQLRFVWLSLEFDYMCQYD 180
Db 121 YGGDMRCGOVLAPKPGQILLESPLNNAHCEWTHAKPGFVIQLRFVWLSLEFDYMCQYD 180

Qy 181 YVEVRDGDNRDQIIRKVCGERPAPIQSIGSSHLVPHSDGSKNFDGPHAIYEETACS 240
Db 181 YVEVRDGDNRDQIIRKVCGERPAPIQSIGSSHLVPHSDGSKNFDGPHAIYEETACS 240
Qy 241 SSPCFHDGTCLVDKAGSYKACACLAGYTGQRCENLLEERCNSDPGGVNGYQKITGGPGILI 300
Db 241 SSPCFHDGTCLVDKAGSYKACACLAGYTGQRCENLLEERCNSDPGGVNGYQKITGGPGILI 300
Qy 301 NGRHAKIGTVVFFCNCNSYVLSGNEKRTCOQNGESGKQPICIKACREPKISDLVERRVL 360
Db 301 NGRHAKIGTVVFFCNCNSYVLSGNEKRTCOQNGESGKQPICIKACREPKISDLVERRVL 360
Qy 361 PMQVQSRETPHLQLYSAAFKOKLASAPTKKPPALPGDLPNGYQHHLHTOLQYECISPPFYR 420
Db 361 PMQVQSRETPHLQLYSAAFKOKLASAPTKKPPALPGDLPNGYQHHLHTOLQYECISPPFYR 420
Qy 421 RLGSSERTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480
Db 421 RLGSSERTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480
Qy 481 HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKIFYRDDDEXTIOS 540
Db 481 HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKIFYRDDDEXTIOS 540
Qy 541 LQISAILHPNYDPILLDDADIAILKLLDKARISTRVQPICLAASRDLSSTFOESHITVAG 600
Db 541 LQISAILHPNYDPILLDDADIAILKLLDKARISTRVQPICLAASRDLSSTFOESHITVAG 600
Qy 601 WNVLDVRSFGKNDTLRSQVSVVDSLLCEQHEHDHGIPIVSTDMNMFCAEWPTAPSDI 660
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Db 661 CTAETGGIAAVSPGRASPEPRWHLNGLVSWSDYKTCSHRLSTAFKVLFPFKDWIERNMK 720

RESULT 11
US-09-990-456-231
Sequence 231, Application US/09990456
Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787

[illegible]

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		Best Local Similarity		100.08; Pred. No. 0;
		Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	1	MELGCTWGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEDYDQIECVCPGKRE	60	
Qy	61	VGVYTPICRNEENECDSCLHPGCTIPENCKSRNGSWGTLDDFYVKGYPYCAECRAGW	120	
Db	61	VGVYTPICRNEENECDSCLHPGCTIPENCKSRNGSWGTLDDFYVKGYPYCAECRAGW	120	
Qy	121	YGGDMRCQGVLRAPKGQILLESPLNACHSWTHAKPGFVIOIRFVNLSEFFDMCOYD	180	
Db	121	YGGDMRCQGVLRAPKGQILLESPLNACHSWTHAKPGFVIOIRFVNLSEFFDMCOYD	180	
Qy	181	YVEVRDGNDRGQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEITACS	240	
Db	181	YVEVRDGNDRGQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEITACS	240	
Qy	241	SSPCFHDGTCVLDKAGSKYKACLAGYTQRCENLLEERNCSDDPGPVNGYQKITGGPGLI	300	
Db	241	SSPCFHDGTCVLDKAGSKYKACLAGYTQRCENLLEERNCSDDPGPVNGYQKITGGPGLI	300	
Qy	301	NGRHAKIGTVVSFFCNSVYLSGNEKRTCCQNGEWSGKQPCIKACREPKISDLVRRVL	360	
Db	301	NGRHAKIGTVVSFFCNSVYLSGNEKRTCCQNGEWSGKQPCIKACREPKISDLVRRVL	360	
Qy	361	PMQVQSRRTPLHQLYSAAFSKQKQSAPTCKPALPFGDLPNGYQHLHTQLQYECISPFYR	420	
Db	361	PMQVQSRRTPLHQLYSAAFSKQKQSAPTCKPALPFGDLPNGYQHLHTQLQYECISPFYR	420	
Qy	421	RLGSSRRRTCLRTGKWSGRAPSCIPCIGKIENITAPKTQGLRWPQAAIYRRTSGVHDSGL	480	
Db	421	RLGSSRRRTCLRTGKWSGRAPSCIPCIGKIENITAPKTQGLRWPQAAIYRRTSGVHDSGL	480	
Qy	481	HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLVKLGKFKYRDDDRDEKTIQS	540	
Db	481	HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLVKLGKFKYRDDDRDEKTIQS	540	
Qy	541	LQISAILHPNYDPIILLDADIAILKLDKARISTRVQPCICLAASRDLSSTFQESHITVAG	600	
Db	541	LQISAILHPNYDPIILLDADIAILKLDKARISTRVQPCICLAASRDLSSTFQESHITVAG	600	
Qy	601	WNVLDVRSFPGKNDTLRSQVSVVDSLLCEQHEHGHIPSVTDNMFCASWEPTAPSDI	660	
Db	601	WNVLDVRSFPGKNDTLRSQVSVVDSLLCEQHEHGHIPSVTDNMFCASWEPTAPSDI	660	
Qy	661	CTAETGGIAAASFPGRASPEPRHLMGLVSVSYDKTCSHRLSTAFTKVLPFKDWTERNKK	720	
Db	661	CTAETGGIAAASFPGRASPEPRHLMGLVSVSYDKTCSHRLSTAFTKVLPFKDWTERNKK	720	

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; Sequence 231, Application US/09989721
; Patent No. US20020142961A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Grittisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C55
; CURRENT FILING DATE: 2001-11-19
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/049787
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 , PRIOR APPLICATION NUMBER: 60/091978
 , PRIOR FILING DATE: 1998-07-07
 , PRIOR APPLICATION NUMBER: 60/091982
 , PRIOR FILING DATE: 1998-07-07
 , PRIOR APPLICATION NUMBER: 60/092182
 , PRIOR FILING DATE: 1998-07-09

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 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRCEYDQISCVPCKKE 60
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 DB 61 VVGYYTIPCCRNEECDSCLHPGGCTIFENCKSCRNGSGGTLDDFYVKGFFYCAECRAGW 120
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121	YGDCWRCQGVLRAPKGQILLESYPLNAHCWTHAKPGFVQIURFVMLISLEDFYMCQD	180
181	YVEVRDGNRDQIIIKRYCGNERPAPIQSIGSSLHVLFHSDGSKNFDGPHAIYEETACS	240
181	YVEVRDGNRDQIIIKRYCGNERPAPIQSIGSSLHVLFHSDGSKNFDGPHAIYEETACS	240
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241	SPFCFHDGTCVLDKAGSYKCACLAGYTGORCENILLEERNCSDDGGPVNGYKITGGPGLI	300
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361	PMQVQSRETPHLQLYSAAFSKQLQSAPTKKPALPFGDLPMWGQHLLHTQLQYECISPPFYR	420
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RESULT 13

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; Sequence 231, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14

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/ PRIOR FILING DATE: 1998-06-12
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 / PRIOR APPLICATION NUMBER: 60/091978
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 / PRIOR APPLICATION NUMBER: 60/091982
 / PRIOR FILING DATE: 1998-07-07
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 / PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 720; DB 9; Length 720;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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/ Sequence 231, Application US/09989293A

/ Patent No. US20020177164A1

/ GENERAL INFORMATION:

/ APPLICANT: Ashkenazi, Avi J.

/ APPLICANT: Baker, Kevin P.

/ APPLICANT: Botstein, David

/ APPLICANT: Deenoyers, Luc

/ APPLICANT: Eaton, Dan L.

/ APPLICANT: Ferrara, Napoleone

/ APPLICANT: Fong, Sherman

/ APPLICANT: Gerber, Hanspeter

/ APPLICANT: Gerritsen, Mary E.

/ APPLICANT: Goddard, Audrey

/ APPLICANT: Godowski, Paul J.

/ APPLICANT: Grimaldi, J. Christopher

/ APPLICANT: Gurney, Austin L.

/ APPLICANT: Kljavin, Ivar J.

/ APPLICANT: Napier, Mary A.

/ APPLICANT: Pan, James

/ APPLICANT: Paoni, Nicholas F.

/ APPLICANT: Roy, Margaret Ann

/ APPLICANT: Stewart, Timothy A.

/ APPLICANT: Tumas, Daniel

/ APPLICANT: Watanabe, Colin K.

/ APPLICANT: Williams, P. Mickey

/ APPLICANT: Wood, William I.

/ APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

/ TITLE OF INVENTION: Acids Encoding the Same

/ FILE REFERENCE: P2730P1C66

/ CURRENT APPLICATION NUMBER: US/09/989,293A

/ CURRENT FILING DATE: 2001-11-20

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/ PRIOR FILING DATE: 1997-10-17

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/ PRIOR FILING DATE: 1998-06-04

/ PRIOR APPLICATION NUMBER: 60/088026

/ PRIOR FILING DATE: 1998-06-04

/ PRIOR APPLICATION NUMBER: 60/088028

/ PRIOR FILING DATE: 1998-06-04

/ PRIOR APPLICATION NUMBER: 60/088029

/ PRIOR FILING DATE: 1998-06-04

/ PRIOR APPLICATION NUMBER: 60/088030

/ PRIOR FILING DATE: 1998-06-04

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PRIOR FILING DATE: 1998-07-02			
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Db	241	SSPCFHDGTCLDKAGSYKACACLAGYTGORCENLLEERNCSDDPGFVNGYQKITGGPGLI	300
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Qy	481	HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLVKLVKGYRDDDRDEKTIOS	540
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RESULT 15

US-09-989-735-231
; Sequence 231, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735

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/ PRIOR FILING DATE: 1998-07-02
/ PRIOR APPLICATION NUMBER: 60/091978
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/091982
/ PRIOR FILING DATE: 1998-07-07
/ PRIOR APPLICATION NUMBER: 60/092182
/ PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 0;
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QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLEERNCSDPGGPVNGYQKITGGPGLI 300
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Db 661 CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK 720

Search completed: August 18, 2004, 16:30:55
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:22:34 ; Search time 19 Seconds
(without alignments)
1956.353 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 720

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Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 700 summaries

Databao : Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	9	1.2	101	3	US-09-374-135-4
2	9	1.2	110	4	US-09-341-461-28
3	9	1.2	730	3	US-08-872-757-2
4	9	1.2	730	4	US-08-850-048A-2
5	9	1.2	788	1	US-08-572-225-1
6	9	1.2	986	4	US-09-285-385C-19
7	9	1.2	1015	4	US-09-285-385C-2
8	8	1.1	51	3	US-09-188-930-342
9	8	1.1	51	4	US-09-312-283C-342
10	8	1.1	96	4	US-09-472-087-99
11	8	1.1	152	3	US-09-188-930-187
12	8	1.1	152	4	US-09-312-283C-187
13	8	1.1	155	4	US-09-472-087-20
14	8	1.1	155	4	US-09-472-087-112
15	8	1.1	1019	1	US-08-296-014A-4
16	8	1.1	1019	2	US-08-596-405-4
17	8	1.1	1019	2	US-08-877-620-4
18	8	1.1	1019	4	US-08-287-368-4
19	8	1.1	1083	1	US-08-286-014A-2
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22	8	1.1	1083	4	US-09-287-368-2
23	8	1.1	3571	4	US-09-911-842A-2
24	7	1.0	42	1	US-08-293-778-11
25	7	1.0	80	4	US-09-621-976-4542
26	7	1.0	83	4	US-09-543-681A-5389
27	7	1.0	105	4	US-09-187-859-18

28	7	1.0	105	4	US-09-839-542B-18	Sequence 18, Appl
29	7	1.0	105	4	US-09-535-852-18	Sequence 18, Appl
30	7	1.0	111	4	US-09-252-991A-23343	Sequence 23343, A
31	7	1.0	121	4	US-09-252-991A-22436	Sequence 22436, A
32	7	1.0	121	4	US-09-621-976-5058	Sequence 5058, Ap
33	7	1.0	142	4	US-09-489-039A-10461	Sequence 10461, A
34	7	1.0	144	3	US-08-906-769-153	Sequence 153, App
35	7	1.0	144	3	US-08-906-616-153	Sequence 153, App
36	7	1.0	144	3	US-08-639-075A-153	Sequence 153, App
37	7	1.0	144	3	US-09-004-731-81	Sequence 81, Appl
38	7	1.0	144	3	US-09-012-431-153	Sequence 153, App
39	7	1.0	144	3	US-08-749-699-81	Sequence 81, Appl
40	7	1.0	144	3	US-09-012-692-153	Sequence 153, App
41	7	1.0	144	3	US-08-906-613-153	Sequence 153, App
42	7	1.0	144	3	US-09-004-729-81	Sequence 81, Appl
43	7	1.0	172	4	US-09-198-452A-368	Sequence 368, App
44	7	1.0	187	4	US-09-107-532A-6736	Sequence 6736, Ap
45	7	1.0	210	4	US-09-198-452A-869	Sequence 869, App
46	7	1.0	214	4	US-09-543-681A-4600	Sequence 4600, Ap
47	7	1.0	226	4	US-09-489-039A-7662	Sequence 7662, Ap
48	7	1.0	233	3	US-09-004-731-27	Sequence 27, Appl
49	7	1.0	233	3	US-08-749-699-27	Sequence 27, Appl
50	7	1.0	233	4	US-09-004-729-27	Sequence 27, Appl
51	7	1.0	245	4	US-09-252-991A-26491	Sequence 26491, A
52	7	1.0	255	4	US-09-540-236-2829	Sequence 2829, Ap
53	7	1.0	257	4	US-09-328-352-7049	Sequence 7049, Ap
54	7	1.0	259	3	US-08-944-483-52	Sequence 52, Appl
55	7	1.0	265	4	US-09-050-739-16	Sequence 16, Appl
56	7	1.0	266	3	US-09-004-731-24	Sequence 24, Appl
57	7	1.0	266	3	US-08-749-699-24	Sequence 24, Appl
58	7	1.0	266	4	US-09-004-729-24	Sequence 24, Appl
59	7	1.0	288	3	US-09-032-215-42	Sequence 42, Appl
60	7	1.0	295	3	US-08-338-368-2	Sequence 2, Appl
61	7	1.0	310	4	US-09-107-532A-4185	Sequence 4185, Ap
62	7	1.0	314	4	US-09-636-382A-2	Sequence 2, Appl
63	7	1.0	376	2	US-08-558-269-10	Sequence 10, Appl
64	7	1.0	376	3	US-09-410-882-10	Sequence 10, Appl
65	7	1.0	399	4	US-09-252-991A-28974	Sequence 28974, A
66	7	1.0	422	4	US-09-489-039A-12443	Sequence 12443, A
67	7	1.0	437	4	US-09-489-039A-7612	Sequence 7612, Ap
68	7	1.0	448	4	US-09-328-352-5694	Sequence 5694, Ap
69	7	1.0	503	4	US-09-071-035-360	Sequence 360, App
70	7	1.0	525	4	US-09-252-991A-23870	Sequence 23870, A
71	7	1.0	556	4	US-09-795-691-2	Sequence 2, Appl
72	7	1.0	579	1	US-08-295-411-4	Sequence 4, Appl
73	7	1.0	579	2	US-08-955-471-4	Sequence 4, Appl
74	7	1.0	579	3	US-09-117-708-14	Sequence 14, Appl
75	7	1.0	579	5	PCT-US92-10242-4	Sequence 4, Appl
76	7	1.0	615	1	US-07-998-972A-3	Sequence 3, Appl
77	7	1.0	615	1	US-08-463-953-3	Sequence 3, Appl
78	7	1.0	615	1	US-08-462-261-3	Sequence 3, Appl
79	7	1.0	615	5	PCT-US92-11357-3	Sequence 3, Appl
80	7	1.0	622	4	US-08-952-967-8	Sequence 8, Appl
81	7	1.0	805	4	US-09-252-991A-17822	Sequence 2, Appl
82	7	1.0	808	4	US-09-565-909-2	Sequence 2, Appl
83	7	1.0	986	3	US-08-872-757-4	Sequence 4, Appl
84	7	1.0	986	4	US-09-850-048A-4	Sequence 4, Appl
85	7	1.0	1074	4	US-09-071-035-358	Sequence 358, App
86	7	1.0	1074	4	US-09-071-035-394	Sequence 394, App
87	7	1.0	1096	4	US-09-134-000C-5764	Sequence 5764, Ap
88	7	1.0	1346	3	US-09-320-878-4	Sequence 4, Appl
89	7	1.0	1346	3	US-09-105-537-37	Sequence 37, Appl
90	7	1.0	1346	4	US-09-141-908-5	Sequence 5, Appl
91	7	1.0	1346	4	US-09-657-440-4	Sequence 4, Appl
92	7	1.0	11877	3	US-09-105-537-6	Sequence 6, Appl
93	6	0.8	11	3	US-08-464-961-2	Sequence 2, Appl
94	6	0.8	11	3	US-08-957-130-17	Sequence 17, Appl
95	6	0.8	11	3	US-08-969-315-2	Sequence 2, Appl
96	6	0.8	11	5	PCT-US96-08233-2	Sequence 2, Appl
97	6	0.8	12	4	US-09-205-258-304	Sequence 304, App
98	6	0.8	13	1	US-08-179-481-87	Sequence 87, Appl
99	6	0.8	17	1	US-08-205-938A-14	Sequence 14, Appl
100	6	0.8	17	5	PCT-US95-02626-14	Sequence 14, Appl

101	6	0.8	20	1	US-08-205-938A-13	Sequence 13, Appl	174	6	0.8	94	4	US-08-328-500-10	Sequence 10, Appl
102	6	0.8	20	5	PCT-US95-02626-13	Sequence 13, Appl	175	6	0.8	96	3	US-09-230-637-44	Sequence 44, Appl
103	6	0.8	25	4	US-09-660-587-28	Sequence 28, Appl	176	6	0.8	101	4	US-09-390-134B-42	Sequence 42, Appl
104	6	0.8	25	4	US-09-361-358A-28	Sequence 28, Appl	177	6	0.8	103	4	US-09-199-637A-271	Sequence 271, Appl
105	6	0.8	25	4	US-09-201-458-20	Sequence 20, Appl	178	6	0.8	103	4	US-09-252-991A-32642	Sequence 32642, A
106	6	0.8	25	4	US-09-811-007A-28	Sequence 28, Appl	179	6	0.8	103	4	US-09-543-681A-8232	Sequence 8232, Ap
107	6	0.8	35	1	US-08-145-708A-15	Sequence 15, Appl	180	6	0.8	103	4	US-09-621-976-4109	Sequence 4109, Ap
108	6	0.8	35	2	US-08-331-454-15	Sequence 15, Appl	181	6	0.8	106	4	US-09-087-031E-13	Sequence 13, Appl
109	6	0.8	37	2	US-09-066-074-14	Sequence 14, Appl	182	6	0.8	107	4	US-09-732-210-230	Sequence 230, App
110	6	0.8	37	2	US-08-555-912A-14	Sequence 14, Appl	183	6	0.8	107	4	US-09-489-039A-9954	Sequence 9954, Ap
111	6	0.8	37	3	US-08-348-518C-24	Sequence 24, Appl	184	6	0.8	108	4	US-09-489-039A-9392	Sequence 9392, Ap
112	6	0.8	37	3	US-08-476-509B-24	Sequence 24, Appl	185	6	0.8	108	4	US-09-489-039A-11679	Sequence 11679, A
113	6	0.8	37	3	US-09-252-404A-39	Sequence 39, Appl	186	6	0.8	109	4	US-09-134-000C-6718	Sequence 6718, Ap
114	6	0.8	37	4	US-09-275-900-14	Sequence 14, Appl	187	6	0.8	110	4	US-09-376-330-24	Sequence 24, Appl
115	6	0.8	37	4	US-09-821-861-16	Sequence 16, Appl	188	6	0.8	111	4	US-09-252-991A-17096	Sequence 17096, A
116	6	0.8	38	1	US-08-145-708A-14	Sequence 14, Appl	189	6	0.8	112	4	US-09-107-532A-7068	Sequence 7068, Ap
117	6	0.8	38	2	US-08-331-454-14	Sequence 14, Appl	190	6	0.8	121	1	US-08-307-498-7	Sequence 7, Appli
118	6	0.8	40	3	US-08-706-344C-19	Sequence 19, Appl	191	6	0.8	121	3	US-09-299-268-7	Sequence 7, Appli
119	6	0.8	40	4	US-08-469-260A-467	Sequence 467, App	192	6	0.8	122	4	US-09-732-210-598	Sequence 598, App
120	6	0.8	40	4	US-08-488-446-467	Sequence 467, App	193	6	0.8	122	4	US-09-732-210-600	Sequence 600, App
121	6	0.8	40	4	US-08-467-344A-467	Sequence 467, App	194	6	0.8	123	3	US-09-124-900-10	Sequence 10, Appl
122	6	0.8	41	1	US-08-168-091A-41	Sequence 41, Appl	195	6	0.8	123	3	US-09-134-001C-3283	Sequence 3283, Ap
123	6	0.8	42	4	US-09-066-330-3	Sequence 3, Appli	196	6	0.8	124	4	US-08-311-731A-202	Sequence 202, App
124	6	0.8	43	1	US-07-398-003A-73	Sequence 73, Appl	197	6	0.8	125	4	US-09-543-681A-1717	Sequence 1717, Ap
125	6	0.8	43	1	US-08-453-274B-73	Sequence 73, Appl	198	6	0.8	127	4	US-09-134-001C-2936	Sequence 2936, Ap
126	6	0.8	43	1	US-08-453-695A-73	Sequence 73, Appl	199	6	0.8	127	4	US-09-134-001C-2937	Sequence 2937, Ap
127	6	0.8	43	1	US-08-368-161A-73	Sequence 73, Appl	200	6	0.8	127	4	US-09-809-739-10	Sequence 10, Appl
128	6	0.8	43	2	US-08-453-702A-73	Sequence 73, Appl	201	6	0.8	128	4	US-09-134-001C-2881	Sequence 2881, Ap
129	6	0.8	43	2	US-08-751-305-4	Sequence 4, Appli	202	6	0.8	128	4	US-09-134-000C-3953	Sequence 3953, Ap
130	6	0.8	43	3	US-09-099-639-73	Sequence 73, Appl	203	6	0.8	132	4	US-09-252-991A-29618	Sequence 29618, A
131	6	0.8	43	5	PCT-US93-12588-73	Sequence 73, Appl	204	6	0.8	133	4	US-09-252-991A-32343	Sequence 32343, A
132	6	0.8	43	5	PCT-US95-08071-73	Sequence 73, Appl	205	6	0.8	134	4	US-09-134-001C-3817	Sequence 3817, Ap
133	6	0.8	44	3	US-09-220-528-85	Sequence 85, Appl	206	6	0.8	134	4	US-09-252-991A-24835	Sequence 24835, A
134	6	0.8	45	3	US-08-899-437-13	Sequence 13, Appl	207	6	0.8	136	4	US-09-252-991A-24892	Sequence 24892, A
135	6	0.8	45	3	US-09-126-121-13	Sequence 13, Appl	208	6	0.8	138	3	US-08-630-172-1	Sequence 1, Appli
136	6	0.8	46	3	US-08-753-007A-16	Sequence 16, Appl	209	6	0.8	138	3	US-09-375-419-1	Sequence 1, Appli
137	6	0.8	46	3	US-09-398-496-16	Sequence 16, Appl	210	6	0.8	139	3	US-08-444-818-174	Sequence 174, App
138	6	0.8	46	4	US-09-003-541-4	Sequence 4, Appli	211	6	0.8	140	4	US-09-252-991A-31623	Sequence 31623, A
139	6	0.8	50	3	US-09-004-406C-10	Sequence 10, Appl	212	6	0.8	141	3	US-08-906-769-135	Sequence 135, App
140	6	0.8	50	3	US-09-004-406C-11	Sequence 11, Appl	213	6	0.8	141	3	US-08-906-616-135	Sequence 135, App
141	6	0.8	52	1	US-08-294-189-17	Sequence 17, Appl	214	6	0.8	141	3	US-08-639-075A-135	Sequence 135, App
142	6	0.8	56	4	US-09-055-075C-48	Sequence 48, Appl	215	6	0.8	141	3	US-09-012-431-135	Sequence 135, App
143	6	0.8	56	4	US-09-319-124-48	Sequence 48, Appl	216	6	0.8	141	3	US-09-012-692-135	Sequence 135, App
144	6	0.8	56	4	US-09-765-815-9	Sequence 9, Appli	217	6	0.8	141	3	US-08-906-613-135	Sequence 135, App
145	6	0.8	59	4	US-09-800-729-163	Sequence 163, App	218	6	0.8	144	4	US-09-199-637A-17	Sequence 17, Appl
146	6	0.8	62	4	US-09-107-532A-5665	Sequence 5665, Ap	219	6	0.8	144	4	US-09-134-001C-4218	Sequence 4218, Ap
147	6	0.8	62	4	US-09-497-491-27	Sequence 27, Appl	220	6	0.8	146	4	US-09-252-991A-21532	Sequence 21532, A
148	6	0.8	64	4	US-09-482-273-117	Sequence 117, App	221	6	0.8	146	4	US-09-252-991A-18563	Sequence 18563, A
149	6	0.8	64	4	US-09-252-991A-17573	Sequence 17573, A	222	6	0.8	149	2	US-08-038-364-18	Sequence 18, Appl
150	6	0.8	70	4	US-09-732-210-883	Sequence 883, App	223	6	0.8	149	3	US-09-158-710-18	Sequence 18, Appl
151	6	0.8	72	4	US-09-540-236-2199	Sequence 2199, App	224	6	0.8	150	4	US-09-252-991A-17720	Sequence 17720, A
152	6	0.8	74	4	US-09-543-681A-8341	Sequence 8341, Ap	225	6	0.8	151	4	US-08-679-493A-74	Sequence 74, Appl
153	6	0.8	74	4	US-09-134-000C-6316	Sequence 6316, Ap	226	6	0.8	151	4	US-09-288-143-123	Sequence 123, App
154	6	0.8	76	4	US-09-328-352-4331	Sequence 4331, Ap	227	6	0.8	153	4	US-09-252-991A-23634	Sequence 23634, A
155	6	0.8	77	3	US-08-718-904-6	Sequence 6, Appli	228	6	0.8	153	4	US-09-134-000C-5186	Sequence 5186, Ap
156	6	0.8	77	4	US-09-449-249-6	Sequence 6, Appli	229	6	0.8	154	4	US-09-387-418A-8	Sequence 8, Appli
157	6	0.8	85	4	US-09-732-210-1467	Sequence 1467, Ap	230	6	0.8	156	1	US-08-469-667-20	Sequence 20, Appl
158	6	0.8	86	1	US-07-847-743B-19	Sequence 19, Appl	231	6	0.8	156	4	US-09-224-110-20	Sequence 20, Appl
159	6	0.8	86	1	US-08-456-201-19	Sequence 19, Appl	232	6	0.8	156	4	US-09-252-991A-24413	Sequence 24413, A
160	6	0.8	86	2	US-08-330-161-17	Sequence 17, Appl	233	6	0.8	157	2	PCT-US95-07289-20	Sequence 20, Appl
161	6	0.8	86	2	US-08-456-241-19	Sequence 19, Appl	234	6	0.8	157	2	US-08-811-949-41	Sequence 41, Appl
162	6	0.8	86	2	US-08-440-401-17	Sequence 17, Appl	235	6	0.8	157	3	US-08-872-855-6	Sequence 6, Appli
163	6	0.8	86	2	US-08-419-878B-17	Sequence 17, Appl	236	6	0.8	157	3	US-08-981-392-68	Sequence 68, Appl
164	6	0.8	86	4	US-09-134-001C-3359	Sequence 3359, Ap	237	6	0.8	157	3	US-09-071-035-446	Sequence 446, App
165	6	0.8	86	4	US-09-173-480-17	Sequence 17, Appl	238	6	0.8	159	3	US-08-796-792-2	Sequence 2, Appli
166	6	0.8	86	5	PCT-US92-04295A-19	Sequence 19, Appl	239	6	0.8	159	4	US-09-491-795-2	Sequence 2, Appli
167	6	0.8	87	4	US-09-352-991A-28740	Sequence 28740, A	240	6	0.8	162	1	US-08-266-451B-29	Sequence 29, Appl
168	6	0.8	90	4	US-09-352-991A-24074	Sequence 24074, A	241	6	0.8	162	2	US-08-748-725-29	Sequence 29, Appl
169	6	0.8	93	4	US-09-252-991A-17535	Sequence 17535, A	242	6	0.8	164	4	US-09-540-236-2636	Sequence 2636, Ap
170	6	0.8	94	3	US-08-946-329A-79	Sequence 79, Appl	243	6	0.8	164	4	US-09-489-039A-11750	Sequence 11750, A
171	6	0.8	94	3	US-08-466-368-5	Sequence 5, Appli	244	6	0.8	170	4	US-09-252-991A-22362	Sequence 22362, A
172	6	0.8	94	4	US-08-470-998-2	Sequence 2, Appli	245	6	0.8	172	4	US-09-252-991A-29480	Sequence 29480, A
173	6	0.8	94	4			246	6	0.8	172	4	US-09-328-352-5691	Sequence 5691, Ap

247	6	0.8	176	4	US-09-252-991A-24281	Sequence 24281, A	320	6	0.8	208	4	US-09-518-950-2	Sequence 2, Appli
248	6	0.8	176	4	US-09-252-991A-24805	Sequence 24805, A	321	6	0.8	208	4	US-09-449-249-5	Sequence 5, Appli
249	6	0.8	176	4	US-09-489-039A-12706	Sequence 12706, A	322	6	0.8	208	4	US-09-449-249-7	Sequence 7, Appli
250	6	0.8	177	2	US-08-770-544-20	Sequence 20, Appl	323	6	0.8	208	4	US-09-252-991A-23641	Sequence 22641, A
251	6	0.8	177	4	US-09-579-259-20	Sequence 20, Appl	324	6	0.8	208	4	US-10-138-158-18	Sequence 18, Appl
252	6	0.8	177	4	US-09-543-681A-5159	Sequence 5159, Ap	325	6	0.8	209	3	US-08-375-762-71	Sequence 71, Appl
253	6	0.8	177	4	US-09-650-324A-20	Sequence 20, Appl	326	6	0.8	209	3	US-09-295-028-71	Sequence 71, Appl
254	6	0.8	179	3	US-09-612-126-11	Sequence 11, Appl	327	6	0.8	209	4	US-09-106-582-71	Sequence 71, Appl
255	6	0.8	180	4	US-09-543-681A-7669	Sequence 7669, Ap	328	6	0.8	209	4	US-09-311-311C-20	Sequence 20, Appl
256	6	0.8	181	4	US-09-252-991A-17818	Sequence 17818, A	329	6	0.8	209	4	US-09-252-991A-23571	Sequence 23571, A
257	6	0.8	181	4	US-09-134-000C-4633	Sequence 4633, Ap	330	6	0.8	209	4	US-09-159-469-71	Sequence 71, Appl
258	6	0.8	183	3	US-09-621-976-4025	Sequence 4025, Ap	331	6	0.8	209	4	US-09-693-542-71	Sequence 71, Appl
259	6	0.8	184	3	US-08-907-800A-2	Sequence 2, Appli	332	6	0.8	210	3	US-09-162-184-33	Sequence 33, Appl
260	6	0.8	184	3	US-08-969-317-2	Sequence 2, Appli	333	6	0.8	210	3	US-09-489-777A-33	Sequence 33, Appl
261	6	0.8	185	3	US-08-975-762-11	Sequence 11, Appl	334	6	0.8	210	4	US-09-252-991A-27171	Sequence 27171, A
262	6	0.8	185	3	US-08-821-324-11	Sequence 11, Appl	335	6	0.8	211	3	US-09-252-991A-28553	Sequence 28553, A
263	6	0.8	185	3	US-09-295-028-11	Sequence 11, Appl	336	6	0.8	212	3	US-08-861-774E-22	Sequence 22, Appl
264	6	0.8	185	4	US-09-166-582-11	Sequence 11, Appl	337	6	0.8	212	3	US-08-861-774E-34	Sequence 34, Appl
265	6	0.8	185	4	US-09-159-469-11	Sequence 11, Appl	338	6	0.8	213	3	US-08-861-774E-60	Sequence 60, Appl
266	6	0.8	185	4	US-09-693-542-11	Sequence 11, Appl	339	6	0.8	213	3	US-08-861-774E-72	Sequence 72, Appl
267	6	0.8	186	3	US-09-612-126-8	Sequence 8, Appli	340	6	0.8	213	3	US-08-861-774E-30	Sequence 30, Appl
268	6	0.8	187	4	US-08-635-886C-207	Sequence 207, App	341	6	0.8	214	3	US-08-861-774E-32	Sequence 32, Appl
269	6	0.8	187	4	US-08-635-886C-208	Sequence 208, App	342	6	0.8	214	3	US-08-861-774E-44	Sequence 44, Appl
270	6	0.8	187	4	US-08-635-886C-209	Sequence 209, App	343	6	0.8	214	3	US-08-861-774E-48	Sequence 48, Appl
271	6	0.8	187	4	US-08-974-690C-207	Sequence 207, App	344	6	0.8	214	3	US-08-861-774E-54	Sequence 54, Appl
272	6	0.8	187	4	US-08-974-690C-208	Sequence 208, App	345	6	0.8	214	3	US-08-861-774E-66	Sequence 66, Appl
273	6	0.8	187	4	US-08-974-690C-209	Sequence 209, App	346	6	0.8	214	3	US-08-861-774E-76	Sequence 76, Appl
274	6	0.8	191	2	US-08-290-665A-187	Sequence 187, App	347	6	0.8	214	3	US-08-861-774E-78	Sequence 78, Appl
275	6	0.8	191	2	US-08-290-665A-189	Sequence 189, App	348	6	0.8	214	5	PCT-US96-08950-2	Sequence 2, Appli
276	6	0.8	191	2	US-08-230-865A-190	Sequence 190, App	349	6	0.8	214	5	PCT-US96-09127-2	Sequence 2, Appli
277	6	0.8	191	5	PCT-US95-10398-187	Sequence 187, App	350	6	0.8	215	1	US-08-266-451B-27	Sequence 27, Appl
278	6	0.8	191	5	PCT-US95-10398-189	Sequence 189, App	351	6	0.8	215	1	US-08-748-725-27	Sequence 27, Appl
279	6	0.8	191	5	PCT-US95-10398-190	Sequence 190, App	352	6	0.8	215	3	US-08-861-774E-40	Sequence 40, Appl
280	6	0.8	192	4	US-09-138-452A-276	Sequence 276, App	353	6	0.8	215	3	US-08-861-774E-58	Sequence 58, Appl
281	6	0.8	193	1	US-08-248-466B-14	Sequence 14, Appl	354	6	0.8	216	3	US-08-861-774E-62	Sequence 62, Appl
282	6	0.8	193	3	US-09-041-889-5	Sequence 5, Appli	355	6	0.8	216	3	US-08-861-774E-46	Sequence 46, Appl
283	6	0.8	193	3	US-08-837-058-5	Sequence 5, Appli	356	6	0.8	218	3	US-08-861-774E-50	Sequence 50, Appl
284	6	0.8	193	4	US-09-417-264-5	Sequence 5, Appli	357	6	0.8	218	3	US-09-134-000C-3898	Sequence 3898, Ap
285	6	0.8	193	4	US-08-635-886C-210	Sequence 210, App	358	6	0.8	218	4	US-09-828-303-23	Sequence 23, Appl
286	6	0.8	194	4	US-08-974-690C-210	Sequence 210, App	359	6	0.8	219	3	US-08-861-774E-70	Sequence 70, Appl
287	6	0.8	194	4	US-09-516-914-9	Sequence 9, Appli	360	6	0.8	219	4	US-09-252-991A-28228	Sequence 28228, A
288	6	0.8	194	4	US-09-489-039A-8286	Sequence 8286, Ap	361	6	0.8	219	4	US-09-198-452A-634	Sequence 634, App
289	6	0.8	196	3	US-08-981-392-35	Sequence 35, Appl	362	6	0.8	221	4	US-09-874-926-2	Sequence 2, Appli
290	6	0.8	198	4	US-09-252-991A-22691	Sequence 22691, A	363	6	0.8	221	4	US-09-252-991A-24147	Sequence 24147, A
291	6	0.8	199	4	US-09-252-991A-31135	Sequence 31135, A	364	6	0.8	222	4	US-09-252-991A-19065	Sequence 19065, A
292	6	0.8	200	4	US-09-101-272G-73	Sequence 73, Appl	365	6	0.8	223	4	US-09-198-452A-623	Sequence 623, App
293	6	0.8	200	4	US-09-252-991A-28054	Sequence 28054, A	366	6	0.8	224	4	US-08-630-915A-221	Sequence 221, App
294	6	0.8	200	4	US-09-489-039A-7536	Sequence 7526, Ap	367	6	0.8	229	4	US-09-516-143A-6	Sequence 6, Appli
295	6	0.8	201	4	US-08-679-493A-190	Sequence 190, App	368	6	0.8	230	4	US-09-543-681A-6357	Sequence 6357, Ap
296	6	0.8	202	4	US-09-252-991A-26505	Sequence 26505, A	369	6	0.8	231	4	US-09-069-023-36	Sequence 36, Appl
297	6	0.8	202	4	US-08-284-391B-31	Sequence 31, Appl	370	6	0.8	233	4	US-08-861-774E-52	Sequence 52, Appl
298	6	0.8	203	3	US-09-218-950-31	Sequence 31, Appl	371	6	0.8	234	3	US-08-287-959-8	Sequence 8, Appli
299	6	0.8	203	3	US-09-543-681A-4329	Sequence 4329, Ap	372	6	0.8	235	1	US-09-107-532A-6979	Sequence 6979, Ap
300	6	0.8	203	4	US-09-252-991A-29225	Sequence 29225, A	373	6	0.8	235	4	US-09-134-000C-4896	Sequence 4896, Ap
301	6	0.8	204	4	US-09-543-681A-8020	Sequence 8020, Ap	374	6	0.8	236	4	US-09-252-991A-23406	Sequence 23406, A
302	6	0.8	204	4	US-09-134-001C-4766	Sequence 4766, Ap	375	6	0.8	237	3	US-09-004-731-44	Sequence 44, Appl
303	6	0.8	205	4	US-09-252-991A-29334	Sequence 29334, A	376	6	0.8	238	3	US-08-679-493A-76	Sequence 76, Appl
304	6	0.8	205	4	US-09-134-000C-3913	Sequence 3913, Ap	377	6	0.8	239	3	US-09-004-729-44	Sequence 44, Appl
305	6	0.8	205	4	US-08-679-493A-75	Sequence 75, Appl	378	6	0.8	239	4	US-09-328-352-7328	Sequence 7328, Ap
306	6	0.8	206	4	US-09-543-681A-4763	Sequence 4763, Ap	379	6	0.8	239	4	US-09-328-352-7253	Sequence 7253, Ap
307	6	0.8	207	4	US-09-198-452A-1020	Sequence 1020, Ap	380	6	0.8	239	4	US-09-004-731-41	Sequence 41, Appl
308	6	0.8	208	1	US-07-935-309-2	Sequence 2, Appli	381	6	0.8	240	3	US-09-032-215-47	Sequence 47, Appl
309	6	0.8	208	1	US-08-894-682-1	Sequence 1, Appli	382	6	0.8	240	3	US-08-749-699-41	Sequence 41, Appl
310	6	0.8	208	2	US-09-039-364-2	Sequence 2, Appli	383	6	0.8	242	3	US-09-004-729-41	Sequence 41, Appl
311	6	0.8	208	2	US-08-766-551-9	Sequence 9, Appli	384	6	0.8	242	3	US-09-004-729-41	Sequence 41, Appl
312	6	0.8	208	2	US-08-086-082-1	Sequence 1, Appli	385	6	0.8	242	4	US-09-252-991A-19021	Sequence 19021, A
313	6	0.8	208	2	US-08-718-904-5	Sequence 5, Appli	386	6	0.8	242	4	US-09-107-532A-6244	Sequence 6244, Ap
314	6	0.8	208	3	US-08-612-973-30	Sequence 30, Appl	387	6	0.8	242	4	US-09-461-325-463	Sequence 463, App
315	6	0.8	208	3	US-09-181-974-2	Sequence 2, Appli	388	6	0.8	243	4	US-09-252-991A-29762	Sequence 29762, A
316	6	0.8	208	3	US-09-158-710-2	Sequence 30, Appl	389	6	0.8	244	4	US-10-012-542-463	Sequence 463, App
317	6	0.8	208	3			390	6	0.8	244	4		
318	6	0.8	208	3			391	6	0.8	244	4		
319	6	0.8	208	3			392	6	0.8	244	4		

393	6	0.8	245	4	US-08-956-171B-5222	Sequence 5222, Ap	466	6	0.8	306	2	US-08-560-098A-45	Sequence 45, Appl
394	6	0.8	248	1	US-08-366-451B-2	Sequence 2, Appli	467	6	0.8	306	4	US-09-252-991A-27054	Sequence 27054, A
395	6	0.8	248	2	US-08-748-725-2	Sequence 2, Appli	468	6	0.8	306	4	US-09-328-351A-5398	Sequence 5398, Ap
396	6	0.8	248	3	US-08-944-483-71	Sequence 71, Appl	469	6	0.8	307	4	US-09-193-634-53	Sequence 53, Appl
397	6	0.8	248	4	US-09-252-991A-17358	Sequence 17358, A	470	6	0.8	308	4	US-09-107-532A-6023	Sequence 6023, Ap
398	6	0.8	249	3	US-09-010-809-21	Sequence 21, Appl	471	6	0.8	309	2	US-08-849-480A-6	Sequence 6, Appli
399	6	0.8	250	3	US-09-010-809-3	Sequence 3, Appli	472	6	0.8	310	3	US-08-477-460B-6	Sequence 6, Appli
400	6	0.8	251	4	US-08-630-915A-8	Sequence 8, Appli	473	6	0.8	310	3	US-08-379-516-6	Sequence 6, Appli
401	6	0.8	252	3	US-08-944-483-72	Sequence 72, Appl	474	6	0.8	310	3	US-09-329-916-6	Sequence 6, Appli
402	6	0.8	253	2	US-09-027-337-8	Sequence 8, Appli	475	6	0.8	310	3	US-08-485-372A-6	Sequence 6, Appli
403	6	0.8	253	3	US-08-975-762-52	Sequence 52, Appl	476	6	0.8	310	4	US-09-409-006A-6	Sequence 6, Appli
404	6	0.8	253	3	US-08-944-483-73	Sequence 73, Appl	477	6	0.8	310	4	US-08-484-681-6	Sequence 6, Appli
405	6	0.8	253	3	US-09-295-028-52	Sequence 52, Appl	478	6	0.8	310	5	PCT-US93-07422-6	Sequence 6, Appli
406	6	0.8	253	4	US-09-106-582-52	Sequence 52, Appl	479	6	0.8	311	4	US-09-543-681A-5602	Sequence 5602, Ap
407	6	0.8	253	4	US-09-644-600-8	Sequence 8, Appli	480	6	0.8	311	4	US-09-489-039A-13013	Sequence 13013, A
408	6	0.8	253	4	US-09-159-469-52	Sequence 52, Appl	481	6	0.8	312	4	US-09-071-035-70	Sequence 70, Appl
409	6	0.8	253	4	US-09-489-039A-13739	Sequence 13739, A	482	6	0.8	312	4	US-09-351-150A-11	Sequence 11, Appl
410	6	0.8	253	4	US-09-554-600A-8	Sequence 8, Appli	483	6	0.8	312	4	US-09-599-360B-96	Sequence 96, Appl
411	6	0.8	254	2	US-08-563-542-52	Sequence 52, Appl	484	6	0.8	313	4	US-09-148-545-233	Sequence 233, Ap
412	6	0.8	254	2	US-08-560-098A-49	Sequence 49, Appl	485	6	0.8	313	4	US-09-252-991A-25243	Sequence 25243, A
413	6	0.8	255	3	US-09-612-126-1	Sequence 1, Appli	486	6	0.8	318	6	5223394-11	Patent No. 5223394
414	6	0.8	256	3	US-09-230-637-29	Sequence 29, Appl	487	6	0.8	320	4	US-09-134-001C-3522	Sequence 3522, Ap
415	6	0.8	256	4	US-09-489-039A-8774	Sequence 8774, Ap	488	6	0.8	320	4	US-09-134-001C-3823	Sequence 3823, Ap
416	6	0.8	257	2	US-08-467-265-16	Sequence 16, Appl	489	6	0.8	320	4	US-09-489-039A-10349	Sequence 10349, A
417	6	0.8	257	3	US-08-467-265-16	Sequence 16, Appl	490	6	0.8	320	4	US-09-489-039A-13881	Sequence 13881, A
418	6	0.8	257	3	US-09-407-891-16	Sequence 16, Appl	491	6	0.8	320	4	US-09-134-000C-5021	Sequence 5021, Ap
419	6	0.8	257	4	US-09-375-907-5	Sequence 5, Appli	492	6	0.8	322	4	US-09-252-991A-29347	Sequence 29347, A
420	6	0.8	258	4	US-09-327-357-198	Sequence 198, App	493	6	0.8	325	3	US-08-311-731A-249	Sequence 249, App
421	6	0.8	258	4	US-09-252-991A-32929	Sequence 32929, A	494	6	0.8	326	4	US-09-066-046-29	Sequence 29, Appl
422	6	0.8	261	4	US-09-252-991A-29007	Sequence 29007, A	495	6	0.8	326	4	US-09-066-047-15	Sequence 15, Appl
423	6	0.8	264	2	US-08-484-505-120	Sequence 120, App	496	6	0.8	326	4	US-09-411-977-3	Sequence 3, Appli
424	6	0.8	264	3	US-08-481-985B-120	Sequence 120, App	497	6	0.8	326	4	US-09-543-681A-7709	Sequence 7709, Ap
425	6	0.8	264	3	US-08-370-476-120	Sequence 120, App	498	6	0.8	327	4	US-09-252-991A-33067	Sequence 33067, A
426	6	0.8	272	4	US-09-252-991A-27911	Sequence 27911, A	499	6	0.8	331	2	US-08-560-098A-46	Sequence 46, Appl
427	6	0.8	276	3	US-08-953-326-18	Sequence 18, Appl	500	6	0.8	332	4	US-09-134-001C-4323	Sequence 4323, Ap
428	6	0.8	276	4	US-09-553-662-18	Sequence 18, Appl	501	6	0.8	333	4	US-09-328-352-7516	Sequence 7516, Ap
429	6	0.8	276	4	US-10-062-994-18	Sequence 18, Appl	502	6	0.8	334	4	US-09-218-363-11	Sequence 11, Appl
430	6	0.8	277	4	US-09-252-991A-17567	Sequence 17567, A	503	6	0.8	336	1	US-07-904-073-2	Sequence 2, Appli
431	6	0.8	278	4	US-09-252-991A-28712	Sequence 28712, A	504	6	0.8	336	1	US-07-904-071-2	Sequence 2, Appli
432	6	0.8	278	4	US-09-328-352-5824	Sequence 5824, Ap	505	6	0.8	336	1	US-08-442-043A-16	Sequence 16, Appl
433	6	0.8	280	4	US-09-107-532A-6088	Sequence 6088, Ap	506	6	0.8	336	4	US-08-441-893A-16	Sequence 16, Appl
434	6	0.8	281	4	US-09-660-587-9	Sequence 9, Appli	507	6	0.8	337	4	US-09-252-991A-26757	Sequence 26757, A
435	6	0.8	281	4	US-09-261-358A-9	Sequence 9, Appli	508	6	0.8	337	4	US-09-252-991A-30261	Sequence 30261, A
436	6	0.8	281	4	US-09-201-458-5	Sequence 5, Appli	509	6	0.8	338	4	US-09-107-532A-5819	Sequence 5819, Ap
437	6	0.8	281	4	US-09-314-701-2	Sequence 2, Appli	510	6	0.8	340	4	US-09-543-681A-7850	Sequence 7850, Ap
438	6	0.8	281	4	US-09-811-007A-9	Sequence 9, Appli	511	6	0.8	341	4	US-09-543-681A-4713	Sequence 4713, Ap
439	6	0.8	282	4	US-09-252-991A-25948	Sequence 25948, A	512	6	0.8	342	4	US-09-252-991A-30257	Sequence 30257, A
440	6	0.8	284	4	US-08-976-063B-2	Sequence 2, Appli	513	6	0.8	343	4	US-09-252-991A-22307	Sequence 22307, A
441	6	0.8	285	3	US-09-027-137-3	Sequence 3, Appli	514	6	0.8	345	3	US-09-027-900-11	Sequence 11, Appl
442	6	0.8	285	4	US-09-344-441-3	Sequence 3, Appli	515	6	0.8	345	4	US-09-489-039A-10740	Sequence 10740, A
443	6	0.8	287	3	US-08-549-515-10	Sequence 10, Appl	516	6	0.8	346	4	US-09-252-991A-21487	Sequence 21487, A
444	6	0.8	288	4	US-09-489-039A-8919	Sequence 8919, Ap	517	6	0.8	347	2	US-08-811-949-1	Sequence 1, Appli
445	6	0.8	289	4	US-09-071-035-72	Sequence 72, Appl	518	6	0.8	347	4	US-09-636-215-590	Sequence 590, App
446	6	0.8	289	4	US-09-252-991A-22483	Sequence 22483, A	519	6	0.8	347	4	US-09-685-166A-590	Sequence 590, App
447	6	0.8	292	3	US-09-027-137-1	Sequence 1, Appli	520	6	0.8	348	4	US-09-360-376-13	Sequence 13, Appl
448	6	0.8	292	4	US-09-344-441-1	Sequence 1, Appli	521	6	0.8	349	4	US-09-489-039A-7582	Sequence 7582, Ap
449	6	0.8	292	4	US-09-328-352-6642	Sequence 6642, Ap	522	6	0.8	351	1	US-08-324-483-2	Sequence 2, Appli
450	6	0.8	292	4	US-09-543-681A-7918	Sequence 7918, Ap	523	6	0.8	354	2	US-08-811-949-61	Sequence 61, Appl
451	6	0.8	295	4	US-09-134-000C-3737	Sequence 3737, Ap	524	6	0.8	355	1	US-08-137-116-1	Sequence 1, Appli
452	6	0.8	295	6	5223394-9	Patent No. 5223394	525	6	0.8	355	1	US-08-217-618-1	Sequence 1, Appli
453	6	0.8	296	4	US-09-252-991A-17385	Sequence 17385, A	526	6	0.8	355	1	US-08-427-640-2	Sequence 2, Appli
454	6	0.8	297	4	US-09-543-681A-7800	Sequence 7800, Ap	527	6	0.8	355	1	US-08-427-640-6	Sequence 6, Appli
455	6	0.8	298	4	US-09-252-991A-25360	Sequence 25360, A	528	6	0.8	355	1	US-08-217-617A-1	Sequence 1, Appli
456	6	0.8	300	1	US-08-148-910-1	Sequence 1, Appli	529	6	0.8	355	2	US-08-217-616-1	Sequence 1, Appli
457	6	0.8	300	1	US-08-448-937A-1	Sequence 1, Appli	530	6	0.8	355	2	US-08-811-949-45	Sequence 45, Appl
458	6	0.8	300	4	US-09-252-991A-20115	Sequence 20115, A	531	6	0.8	355	2	US-08-811-949-47	Sequence 47, Appl
459	6	0.8	301	4	US-09-252-991A-25396	Sequence 25396, A	532	6	0.8	355	2	US-08-811-949-53	Sequence 53, Appl
460	6	0.8	301	4	US-09-134-000C-6014	Sequence 6014, Ap	533	6	0.8	355	2	US-08-811-949-59	Sequence 59, Appl
461	6	0.8	302	4	US-09-252-991A-21231	Sequence 21231, A	534	6	0.8	355	3	US-08-794-528-1	Sequence 1, Appli
462	6	0.8	302	4	US-09-338-352-4508	Sequence 4508, Ap	535	6	0.8	355	4	US-09-252-991A-22326	Sequence 22326, A
463	6	0.8	303	4	US-09-540-236-2119	Sequence 2119, Ap	536	6	0.8	355	4	US-09-198-452A-871	Sequence 871, App
464	6	0.8	303	4	US-09-107-532A-5585	Sequence 5585, Ap	537	6	0.8	355	6	5223256-1	Patent No. 5223256
465	6	0.8	304	4	US-09-489-039A-9424	Sequence 9424, Ap	538	6	0.8	356	1	US-08-427-640-4	Sequence 4, Appli

539	6	0.8	356	1	US-08-427-640-8	Sequence 8, Appli	612	6	0.8	401	4	US-09-252-991A-17090	Sequence 17090, A
540	6	0.8	356	4	US-09-252-991A-30030	Sequence 30030, A	613	6	0.8	402	1	US-08-236-311-1	Sequence 1, Appli
541	6	0.8	362	4	US-09-252-991A-18494	Sequence 18494, A	614	6	0.8	402	3	US-08-457-918-1	Sequence 1, Appli
542	6	0.8	364	1	US-09-252-991A-19037	Sequence 19037, A	615	6	0.8	403	4	US-09-802-213-5	Sequence 5, Appli
543	6	0.8	365	1	US-08-093-741-83	Sequence 83, Appli	616	6	0.8	405	4	US-09-144-914-5	Sequence 5, Appli
544	6	0.8	365	1	US-08-720-012-83	Sequence 83, Appli	617	6	0.8	405	4	US-09-252-991A-23838	Sequence 23838, A
545	6	0.8	365	3	US-09-231-529-3	Sequence 3, Appli	618	6	0.8	405	4	US-09-134-000C-5465	Sequence 5465, Ap
546	6	0.8	365	3	US-08-977-816-3	Sequence 3, Appli	619	6	0.8	408	4	US-09-252-991A-21303	Sequence 21303, A
547	6	0.8	366	4	US-09-252-991A-24466	Sequence 24466, A	620	6	0.8	408	4	US-09-198-452A-141	Sequence 141, App
548	6	0.8	367	3	US-08-895-707-6	Sequence 6, Appli	621	6	0.8	410	1	US-08-792-283A-9	Sequence 9, Appli
549	6	0.8	367	4	US-09-252-991A-17240	Sequence 17240, A	622	6	0.8	410	2	US-09-105-908-9	Sequence 9, Appli
550	6	0.8	367	4	US-09-328-352-7662	Sequence 7662, Ap	623	6	0.8	410	3	US-08-630-172-17	Sequence 17, Appli
551	6	0.8	372	4	US-09-252-991A-28586	Sequence 28586, A	624	6	0.8	410	3	US-09-271-713-9	Sequence 9, Appli
552	6	0.8	372	4	US-09-973-963-4	Sequence 4, Appli	625	6	0.8	410	3	US-09-375-419-17	Sequence 17, Appli
553	6	0.8	373	4	US-09-404-296B-4	Sequence 4, Appli	626	6	0.8	410	4	US-09-252-991A-25812	Sequence 25812, A
554	6	0.8	374	2	US-08-820-170A-25	Sequence 25, Appli	627	6	0.8	410	4	US-09-252-991A-31937	Sequence 31937, A
555	6	0.8	374	3	US-09-055-699-25	Sequence 25, Appli	628	6	0.8	410	4	US-09-489-039A-10283	Sequence 10283, A
556	6	0.8	374	3	US-09-273-555-25	Sequence 25, Appli	629	6	0.8	411	1	US-08-087-163-1	Sequence 1, Appli
557	6	0.8	374	4	US-09-565-538-25	Sequence 25, Appli	630	6	0.8	411	1	US-08-286-748B-18	Sequence 18, Appli
558	6	0.8	374	4	US-09-661-468-25	Sequence 25, Appli	631	6	0.8	411	1	US-08-153-799-18	Sequence 18, Appli
559	6	0.8	374	4	US-09-976-165-25	Sequence 25, Appli	632	6	0.8	411	2	US-08-560-098A-48	Sequence 48, Appli
560	6	0.8	374	4	US-09-227-853A-2	Sequence 2, Appli	633	6	0.8	411	3	US-09-376-689-2	Sequence 2, Appli
561	6	0.8	374	4	US-09-540-236-2230	Sequence 2330, Ap	634	6	0.8	411	3	US-09-181-816-1	Sequence 1, Appli
562	6	0.8	374	5	PCT-US95-06385-2	Sequence 2, Appli	635	6	0.8	411	4	US-09-403-736-2	Sequence 2, Appli
563	6	0.8	375	3	US-08-872-979-3	Sequence 3, Appli	636	6	0.8	414	4	US-09-252-991A-27828	Sequence 27828, A
564	6	0.8	375	4	US-09-328-352-6191	Sequence 6191, Ap	637	6	0.8	415	1	US-08-110-286A-6	Sequence 6, Appli
565	6	0.8	375	4	US-09-489-039A-11560	Sequence 11560, A	638	6	0.8	415	3	US-08-981-189B-10	Sequence 10, Appli
566	6	0.8	377	4	US-09-679-279-3	Sequence 3, Appli	639	6	0.8	415	4	US-08-482-746-6	Sequence 6, Appli
567	6	0.8	377	4	US-09-489-039A-12546	Sequence 12546, A	640	6	0.8	415	4	US-08-180-109A-9	Sequence 9, Appli
568	6	0.8	378	4	US-09-553-498-10	Sequence 10, Appli	641	6	0.8	415	4	US-09-180-109A-12	Sequence 12, Appli
569	6	0.8	378	4	US-09-618-869-10	Sequence 10, Appli	642	6	0.8	415	4	US-09-580-734-6	Sequence 6, Appli
570	6	0.8	378	4	US-09-673-395A-618	Sequence 618, App	643	6	0.8	415	4	US-08-374-009-6	Sequence 6, Appli
571	6	0.8	379	4	US-09-252-991A-17472	Sequence 17472, A	644	6	0.8	415	4	US-09-191-724-6	Sequence 6, Appli
572	6	0.8	381	4	US-09-673-395A-441	Sequence 441, App	645	6	0.8	415	4	US-09-799-978-16	Sequence 16, Appli
573	6	0.8	383	1	US-08-486-037B-2	Sequence 2, Appli	646	6	0.8	420	4	US-09-252-991A-17500	Sequence 17500, A
574	6	0.8	383	2	US-08-558-269-6	Sequence 6, Appli	647	6	0.8	422	4	US-09-489-847-357	Sequence 357, App
575	6	0.8	383	3	US-09-410-882-6	Sequence 6, Appli	648	6	0.8	424	4	US-09-134-001C-5009	Sequence 5009, Ap
576	6	0.8	385	3	US-09-071-224-19	Sequence 19, Appli	649	6	0.8	424	4	US-09-173-300-45	Sequence 45, Appli
577	6	0.8	386	3	US-08-895-707-7	Sequence 7, Appli	650	6	0.8	424	4	US-09-107-532A-5459	Sequence 5459, Ap
578	6	0.8	386	3	US-09-045-284A-2	Sequence 2, Appli	651	6	0.8	425	3	US-09-071-224-6	Sequence 6, Appli
579	6	0.8	386	4	US-09-190-911-1	Sequence 1, Appli	652	6	0.8	425	4	US-09-134-001C-5619	Sequence 5619, Ap
580	6	0.8	386	4	US-09-785-240-11	Sequence 11, Appli	653	6	0.8	425	4	US-09-540-236-3466	Sequence 3466, Ap
581	6	0.8	386	4	US-09-489-039A-7410	Sequence 7410, Ap	654	6	0.8	426	4	US-09-252-991A-25192	Sequence 25192, A
582	6	0.8	389	2	US-08-811-949-67	Sequence 67, Appli	655	6	0.8	427	4	US-09-198-452A-31	Sequence 31, Appli
583	6	0.8	389	3	US-09-071-224-27	Sequence 27, Appli	656	6	0.8	427	4	US-09-328-352-5205	Sequence 5205, Ap
584	6	0.8	389	4	US-09-107-532A-6185	Sequence 6185, Ap	657	6	0.8	428	1	US-08-570-157-5	Sequence 5, Appli
585	6	0.8	390	4	US-09-252-991A-26543	Sequence 26543, A	658	6	0.8	428	3	US-08-029-170-31	Sequence 31, Appli
586	6	0.8	391	4	US-09-543-681A-7029	Sequence 7029, Ap	659	6	0.8	428	4	US-08-403-797-2	Sequence 2, Appli
587	6	0.8	392	1	US-08-706-539-9	Sequence 9, Appli	660	6	0.8	428	4	US-09-076-510-5	Sequence 5, Appli
588	6	0.8	392	3	US-09-027-007-9	Sequence 9, Appli	661	6	0.8	428	4	US-09-004-349-5	Sequence 5, Appli
589	6	0.8	393	2	US-08-560-098A-44	Sequence 44, Appli	662	6	0.8	429	4	US-09-252-991A-28788	Sequence 28788, A
590	6	0.8	393	3	US-08-967-024C-24	Sequence 24, Appli	663	6	0.8	430	6	US-07-942-157A-3	Sequence 3, Appli
591	6	0.8	393	3	US-08-967-024C-25	Sequence 25, Appli	664	6	0.8	430	6	5219569-2	Patent No. 5219569
592	6	0.8	394	3	US-08-466-368-2	Sequence 2, Appli	665	6	0.8	431	3	US-09-376-689-4	Sequence 4, Appli
593	6	0.8	394	4	US-09-144-914-4	Sequence 4, Appli	666	6	0.8	431	3	US-09-101-272G-1	Sequence 1, Appli
594	6	0.8	394	4	US-09-252-991A-18502	Sequence 18502, A	667	6	0.8	431	4	US-09-540-236-5536	Sequence 3536, Ap
595	6	0.8	394	4	US-08-328-500-2	Sequence 2, Appli	668	6	0.8	431	4	5188829-1	Patent No. 5188829
596	6	0.8	394	6	5233418-2	Patent No. 5233418	669	6	0.8	432	2	US-08-560-098A-47	Sequence 47, Appli
597	6	0.8	395	1	US-08-485-859-2	Sequence 2, Appli	670	6	0.8	432	3	US-08-477-460B-2	Sequence 2, Appli
598	6	0.8	395	1	US-08-706-539-11	Sequence 11, Appli	671	6	0.8	432	3	US-08-379-516-2	Sequence 2, Appli
599	6	0.8	395	1	US-08-522-166-2	Sequence 2, Appli	672	6	0.8	432	3	US-09-329-916-2	Sequence 2, Appli
600	6	0.8	395	1	US-08-488-382A-2	Sequence 2, Appli	673	6	0.8	432	3	US-08-485-372A-2	Sequence 2, Appli
601	6	0.8	395	2	US-08-480-912-2	Sequence 2, Appli	674	6	0.8	432	4	US-09-409-006A-2	Sequence 2, Appli
602	6	0.8	395	3	US-09-027-007-11	Sequence 11, Appli	675	6	0.8	432	4	US-08-484-681-2	Sequence 2, Appli
603	6	0.8	396	4	US-09-252-991A-18619	Sequence 18619, A	676	6	0.8	432	5	PCT-US93-07422-2	Sequence 2, Appli
604	6	0.8	397	1	US-08-647-928-8	Sequence 8, Appli	677	6	0.8	433	2	US-08-867-149-1	Sequence 1, Appli
605	6	0.8	397	4	US-09-489-039A-13498	Sequence 13498, A	678	6	0.8	433	2	US-08-808-374-1	Sequence 1, Appli
606	6	0.8	398	2	US-08-284-331B-29	Sequence 29, Appli	679	6	0.8	433	3	US-09-100-409A-1	Sequence 1, Appli
607	6	0.8	398	3	US-09-218-950-29	Sequence 29, Appli	680	6	0.8	433	4	US-09-364-230-14	Sequence 14, Appli
608	6	0.8	399	4	US-09-489-039A-8859	Sequence 8859, Ap	681	6	0.8	433	6	5171838-13	Patent No. 5171838
609	6	0.8	400	4	US-09-134-001C-4785	Sequence 4785, Ap	682	6	0.8	434	1	US-08-236-311-4	Sequence 4, Appli
610	6	0.8	400	4	US-09-252-991A-31296	Sequence 31296, A	683	6	0.8	434	3	US-08-457-918-4	Sequence 4, Appli
611	6	0.8	401	4	US-09-489-847-202	Sequence 202, App	684	6	0.8	434	4	US-09-252-991A-23131	Sequence 23131, A

685 6 0.8 434 4 US-09-543-681A-7154 Sequence 7154, Ap
686 6 0.8 437 2 US-08-811-949-49 Sequence 49, Appl
687 6 0.8 437 2 US-08-811-949-51 Sequence 51, Appl
688 6 0.8 437 2 US-08-811-949-55 Sequence 55, Appl
689 6 0.8 437 2 US-08-811-949-57 Sequence 57, Appl
690 6 0.8 438 4 US-09-252-931A-28398 Sequence 28398, A
691 6 0.8 438 4 US-09-489-039A-8464 Sequence 8464, Ap
692 6 0.8 439 2 US-08-959-638-9 Sequence 9, Appl
693 6 0.8 439 4 US-09-543-681A-7293 Sequence 7293, Ap
694 6 0.8 440 4 US-09-489-039A-10782 Sequence 10782, A
695 6 0.8 441 3 US-09-457-046B-54 Sequence 54, Appl
696 6 0.8 441 4 US-09-297-937C-11 Sequence 11, Appl
697 6 0.8 443 1 US-08-570-157-6 Sequence 6, Appl
698 6 0.8 443 4 US-09-076-510-6 Sequence 6, Appl
699 6 0.8 443 4 US-09-004-349-6 Sequence 6, Appl
700 6 0.8 444 1 US-07-937-609-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-374-135-4
; Sequence 4, Application US/09374135
; Patent No. 6277972
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel E.
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: BPC-1: A SECRETED BRAIN-SPECIFIC PROTEIN EXPRESSED AND
; FILE REFERENCE: 1703-017.US1
; CURRENT APPLICATION NUMBER: US/09/374.135
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/095.982
; PRIOR FILING DATE: 1998-08-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Mouse
US-09-374-135-4

Query Match 1.2%; Score 9; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
Db 47 YDYVEVRDG 55

RESULT 2

US-09-341-461-28
; Sequence 28, Application US/09341461
; Patent No. 6586389
; GENERAL INFORMATION:
; APPLICANT: Hammond, Timothy G.
; APPLICANT: Verroust, Pierre J.
; TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
; FILE REFERENCE: D6148
; CURRENT APPLICATION NUMBER: US/09/341.461
; CURRENT FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: PCT/US99/01259
; PRIOR FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 40
; SEQ ID NO 28
; LENGTH: 110

Query Match 1.2%; Score 9; DB 3; Length 730;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
Db 377 YDYVEVRDG 385

RESULT 4

US-09-850-048A-2

; TYPE: PRT
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: amino acid sequence of Bmp-1 CUB1 domain
US-09-341-461-28

Query Match 1.2%; Score 9; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
Db 56 YDYVEVRDG 64

RESULT 3

US-08-872-757-2
; Sequence 2, Application US/08872757
; Patent No. 6258584
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hgima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Aleksander
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
; TITLE OF INVENTION: PROCESSES; METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/872,757
; FILING DATE: 10-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,187
; FILING DATE: 01-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-028-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-872-757-2

Query Match 1.2%; Score 9; DB 3; Length 730;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
Db 377 YDYVEVRDG 385

```

; Sequence 2, Application US/09850048A
; Patent No. 6562613
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
;              Hojima, Yoshio
;              Li, Shi-Wu
;              Sieron, Aleksander
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND
;                   PROCESSES; METHODS AND USES THEREOF
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/850,048A
; FILING DATE: 07-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,187
; FILING DATE: 1996-03-01
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-028-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-850-048A-2

Query Match 1.2%; Score 9; DB 4; Length 730;
Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 179 YDYVEVRDG 187
Db 377 YDYVEVRDG 385

RESULT 5
US-08-572-225-1
; Sequence 1, Application US/08572225
; Patent No. 5807981
; GENERAL INFORMATION:
; APPLICANT: Prockop, Darwin J.
; APPLICANT: Hojima, Yoshio
; APPLICANT: Li, Shi-Wu
; APPLICANT: Sieron, Aleksander
; APPLICANT: Brenner, Mitch
; TITLE OF INVENTION: RECOMBINANT C-PROTEINASE AND ITS USE FOR
; TITLE OF INVENTION: DRUG DEVELOPMENT FOR THE TREATMENT OF DISEASE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

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; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/572,225
; FILING DATE: 13-DEC-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8389-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-572-225-1

Query Match 1.2%; Score 9; DB 1; Length 788;
Best Local Similarity 100.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 179 YDYVEVRDG 187
Db 179 YDYVEVRDG 187

RESULT 6
US-09-285-385C-19
; Sequence 19, Application US/09285385C
; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296.96111
; CURRENT APPLICATION NUMBER: US/09/285,385C
; CURRENT FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 986
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-285-385C-19

Query Match 1.2%; Score 9; DB 4; Length 986;
Best Local Similarity 100.0%; Pred. No. 3.3; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 179 YDYVEVRDG 187
Db 377 YDYVEVRDG 385

RESULT 7
US-09-285-385C-2
; Sequence 2, Application US/09285385C

```

; Patent No. 6579702
; GENERAL INFORMATION:
; APPLICANT: Groenepan, Daniel S.
; APPLICANT: Scott, Ian C.
; APPLICANT: Thomas, Christina L.
; TITLE OF INVENTION: MAMMALIAN TOLLOID-LIKE GENE AND PROTEIN
; FILE REFERENCE: 960296.96111
; CURRENT APPLICATION NUMBER: US/09/285,385C
; CURRENT FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/111873
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 60/080550
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1015
; TYPE: PRT
; ORGANISM: human
US-09-285-385C-2

Query Match 1.2%; Score 9; DB 4; Length 1015;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDYVEVRDG 187
Db 406 YDYVEVRDG 414

RESULT 8
US-09-188-930-342
; Sequence 342, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 342
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-342

Query Match 1.1%; Score 8; DB 3; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 GYTQORCE 272
Db 36 GYTQORCE 43

RESULT 9
US-09-312-283C-342
; Sequence 342, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.

; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-342

Query Match 1.1%; Score 8; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 GYTQORCE 272
Db 36 GYTQORCE 43

RESULT 10
US-09-472-087-99
; Sequence 99, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-99

Query Match 1.1%; Score 8; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 QSIGSSLH 215
Db 27 QSIGSSLH 34

RESULT 11
US-09-188-930-187
; Sequence 187, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 187
 LENGTH: 152
 TYPE: PRT
 ORGANISM: mouse
 US-09-188-930-187

Query Match 1.1%; Score 8; DB 3; Length 152;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 GYTGORCE 272
 Db 88 GYTGORCE 95
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RESULT 12

US-09-312-283C-187
 Sequence 187, Application US/09312283C
 Patent No. 6573095

GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Onrust, Rene
 APPLICANT: Murison, James G.
 APPLICANT: Kumble, Krishanand D.
 TITLE OF INVENTION: Compositions Isolated from Skin Cells
 TITLE OF INVENTION: and Methods for Their Use
 FILE REFERENCE: 11000.1011C2
 CURRENT APPLICATION NUMBER: US/09/312,283C
 CURRENT FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 425
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 187
 LENGTH: 152
 TYPE: PRT
 ORGANISM: Mouse
 US-09-312-283C-187

Query Match 1.1%; Score 8; DB 4; Length 152;
 Best Local Similarity 100.0%; Pred. No. 6.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 265 GYTGORCE 272
 Db 88 GYTGORCE 95
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RESULT 13

US-09-472-087-20
 Sequence 20, Application US/09472087
 Patent No. 6682736

GENERAL INFORMATION:
 APPLICANT: HANSON, DOUGLAS C.
 APPLICANT: NEVEU, MARK J.
 APPLICANT: MUELLER, EILLEN E.
 APPLICANT: HANKE, JEFFREY H.
 APPLICANT: GILMAN, STEVEN C.
 APPLICANT: DAVIS, C. GEOFFREY
 APPLICANT: CORVALAN, JOSE R.
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
 FILE REFERENCE: ABX-PF1
 CURRENT APPLICATION NUMBER: US/09/472,087
 CURRENT FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 60/113,647
 PRIOR FILING DATE: 1998-12-23
 NUMBER OF SEQ ID NOS: 147
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 20
 LENGTH: 155
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-472-087-20

Query Match 1.1%; Score 8; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 QSIGSSSLH 215
 Db 21 QSIGSSSLH 28
 |||||

RESULT 14

US-09-472-087-112
 Sequence 112, Application US/09472087
 Patent No. 6682736

GENERAL INFORMATION:
 APPLICANT: HANSON, DOUGLAS C.
 APPLICANT: NEVEU, MARK J.
 APPLICANT: MUELLER, EILLEN E.
 APPLICANT: HANKE, JEFFREY H.
 APPLICANT: GILMAN, STEVEN C.
 APPLICANT: DAVIS, C. GEOFFREY
 APPLICANT: CORVALAN, JOSE R.
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
 FILE REFERENCE: ABX-PF1
 CURRENT APPLICATION NUMBER: US/09/472,087
 CURRENT FILING DATE: 1999-12-23
 PRIOR APPLICATION NUMBER: 60/113,647
 PRIOR FILING DATE: 1998-12-23
 NUMBER OF SEQ ID NOS: 147
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 112
 LENGTH: 155
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-472-087-112

Query Match 1.1%; Score 8; DB 4; Length 155;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 QSIGSSSLH 215
 Db 21 QSIGSSSLH 28
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RESULT 15

US-08-296-014A-4

Sequence 4, Application US/08296014A
 Patent No. 5716834

GENERAL INFORMATION:
 APPLICANT: Ding, Jeak Ling
 APPLICANT: Ho, Bow
 TITLE OF INVENTION: The Cloned Factor C cDNA of the
 TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
 TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Birch, Stewart, Kolasch & Birch
 STREET: 8110 Gatehouse Road, Suite 500 East
 CITY: Falls Church
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22042
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/296,014A
 FILING DATE:
 CLASSIFICATION: 435

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-296-014A-4

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Query Match      1.1%; Score 8; DB 1; Length 1019;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      574 TRVQPICL 581
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Db      879 TRVQPICL 886

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Search completed: August 18, 2004, 16:25:58
Job time : 21 secs

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2	9	1.2	639	1	BMPH_STRPU	P98069 strongyloce
3	9	1.2	986	1	BMP1_HUMAN	P13497 homo sapien
4	9	1.2	991	1	BMP1_MOUSE	P98063 mus musculu
5	8	1.1	158	1	Y260_AQUAE	O66619 aquifex ae
6	8	1.1	360	1	MTSB_LACILC	P34878 lactococcu
7	8	1.1	395	1	VIBC_VIBCH	O07898 vibrio chol
8	8	1.1	407	1	FAY_BOVIN	P14567 bos taurus
9	8	1.1	486	1	YD8H_SCHPO	Q10367 schizosacch
10	8	1.1	740	1	CATB_STREX	O87864 streptomyc
11	8	1.1	1019	1	LFC_CARRO	Q26422 carcinosc
12	8	1.1	1019	1	LFC_TACTR	P28175 tachyleus
13	7	1.0	167	1	YPA2_ASCIM	P22375 ascobolus i
14	7	1.0	193	1	Y377_MYCGE	P47617 mycoplasma
15	7	1.0	196	1	CRBD_CHICK	P49152 gallus gall
16	7	1.0	201	1	ABP1_WAIZE	P13689 zea mays (m
17	7	1.0	209	1	NODS_BRAJA	P26026 bradyrhizob
18	7	1.0	212	1	OMPW_ECOLI	P21364 escherichia
19	7	1.0	212	1	OMPW_SALTI	Q827e2 salmonella
20	7	1.0	212	1	OMPW_SALTU	Q82p50 salmonella
21	7	1.0	255	1	V29K_PBEV	P14850 pea early b
22	7	1.0	260	1	COLT_RANRI	P22923 rana ridibu
23	7	1.0	263	1	COLL_RANCA	P11885 rana catsesb
24	7	1.0	291	1	PCAR_PSEPU	Q52154 pseudomonas
25	7	1.0	295	1	PEPM_MYTED	P56839 mytilus edu
26	7	1.0	303	1	LPXC_XANAX	Q8ppa3 xanthomonas
27	7	1.0	305	1	LPXC_RALSO	Q9khl6 ralstonia s
28	7	1.0	308	1	T2RC_MOUSE	P59532 mus musculu
29	7	1.0	315	1	Y001_CAUCR	O9ac59 caulobacter
30	7	1.0	348	1	KTCG_YFEAS	Q8xet4 pyrobaculum
31	7	1.0	351	1	MSS2_PEARF	P40990 saccharomyc
32	7	1.0	359	1	MANR_PSEPU	P11444 pseudomonas
33	7	1.0	360	1	AROB_BUCAP	Q8x939 buchnera ap

107	1	YAL3	ARCFCU	029249	archaeoglob	180	1	HBGF	CERAE	009118	cercopithec
108	1	POLG	HCVEO	P27953	hepatitis c	181	1	HBGF	HUMAN	Q99075	homo sapien
109	1	YENG	YEAST	P40031	saccharomyc	182	1	HBGF	PIG	Q01580	eus scrofa
110	1	CRAA	ORYLA	O73919	oryzias lat	183	1	NEF	HVIRH	P05858	human immun
111	1	YB80	METJA	Q58580	methanococc	184	1	RS3	METJA	P54034	methanococc
112	1	HB82	ANAMI	P83273	anarhichas	185	1	LFTR	DEIRA	Q9784	deinococcus
113	1	Y328	METJA	Q57774	methanococc	186	1	TER7	VIBAN	P51560	vibrio angu
114	1	IAA	HORVU	P16969	hordeum vul	187	1	MOTA	BPT4	P22915	bacterioph
115	1	Y490	UREPA	Q99000	ureaplasma	188	1	NEF	HVIOY	P20886	human immun
116	1	RBFA	STRAW	Q82k55	streptomyc	189	1	YBS1	YEAST	P38243	saccharomyc
117	1	MP63	MYCTU	P97175	mycobacteri	190	1	NEF	HVIZ6	P04602	human immun
118	1	SSRP	SALTY	P43658	salmonella	191	1	PCV	YEAST	P35718	saccharomyc
119	1	SSRP	YERPE	Q82n14	yersinia pe	192	1	OSF1	HUMAN	Q92882	homo sapien
120	1	FMAS	ECOLI	Q57254	escherichia	193	1	GT12	DROME	Q9V998	drosophila
121	1	RBPA	STRCO	Q94527	streptomyc	194	1	GT14	DROME	Q9V996	drosophila
122	1	SSRP	PHOLL	Q7n1u1	photorhabd	195	1	OSF1	MOUSE	Q62422	mus musculus
123	1	REG4	PVRAB	Q9v029	pyrococcus	196	1	THIE	YERPE	Q82a21	yersinia pe
124	1	REG4	PVRHO	O58741	pyrococcus	197	1	FUCA	HAIN	P44777	haemophilus
125	1	ATFX	CHNE	Q4608	ochrosphaer	198	1	GT15	DROME	Q9V995	drosophila
126	1	LEUD	CLOAB	Q97ee1	clostridium	199	1	OMPW	VIBCH	P27866	vibrio chol
127	1	T2DA	XENLA	Q91858	xenopus lae	200	1	YBGJ	ECOLI	P75744	escherichia
128	1	SPAT	SALTY	P40703	salmonella	201	1	1433	SPIOL	P29308	spinacia ol
129	1	DPS	ECOLI	P27430	escherichia	202	1	PURQ	CAMJE	Q9phz7	campylobact
130	1	NUSM	BRALA	O79423	branchiost	203	1	TRKA	STRCO	O53949	streptomyc
131	1	NABP	ALCEU	P39186	alcaligenes	204	1	RLK1	SPIOL	P31144	spinacia ol
132	1	Y52L	SYNY3	Q55911	synechocyst	205	1	RL4	CHLPN	Q9z798	chlamydia p
133	1	SYT8	HUMAN	Q8nbv8	homo sapien	206	1	DTXR	CORDI	P33120	corynebacte
134	1	Y856	PVRHO	O58586	pyrococcus	207	1	COX2	BURDE	P30671	basterina dep
135	1	RL9	BORBU	O51139	borrelia bu	208	1	COX2	ASTPE	Q37411	asteterina pe
136	1	GRPE	METHH	O27350	methanobact	209	1	COX2	PISOC	P25002	piasaater oc
137	1	SP	LYERS	O82088	lycopersico	210	1	KCY	MYCTU	Q32211	mycobacteri
138	1	NUDH	SALTY	Q8XG03	salmonella	211	1	VNS1	IADA2	P03501	influenza a
139	1	YBN2	YEAST	P38218	saccharomyc	212	1	VNS1	IAMA6	P13137	influenza a
140	1	BDH	BOVIN	Q02337	bos taurus	213	1	VNS1	IAP11	P13141	influenza a
141	1	ATPD	STAAH	Q99af2	staphylococ	214	1	VNS1	IAP13	P13143	influenza a
142	1	NEF	HVIMN	P05856	human immun	215	1	VNS1	IATKB	P30910	influenza a
143	1	REC6	SCHPO	P40385	schizosacch	216	1	VNS1	IATKC	P30911	influenza a
144	1	YEG2	ARCFCU	O28810	archaeoglob	217	1	VNS1	IATRT	P30912	influenza a
145	1	UPK2	HUMAN	O00526	homo sapien	218	1	GPHP	ALCEU	P40853	alcaligenes
146	1	UPK2	MOUSE	P38575	mus musculus	219	1	YKNW	BACSU	O31709	bacillus su
147	1	FLAV	AQUAE	Q67866	aquifex aeo	220	1	BCLA	HUMAN	O95999	b cell ly
148	1	RL25	CHLMU	O9plc2	chlamydia m	221	1	H1	NEUCR	Q810u2	neurospora
149	1	RL25	CHLTR	O84805	chlamydia t	222	1	NOQO	AGRT5	P35118	agrobacteri
150	1	RRF	BUCAP	Q8K988	buchnera ap	223	1	OPE2	NFVOP	P89029	oryza pseu
151	1	UPK2	BOVIN	Q08537	bos taurus	224	1	APH1	DROME	Q9V992	drosophila
152	1	NOS1	SHEEP	Q29498	ovis aries	225	1	NEF	HVISC	P05857	human immun
153	1	RL18	YEAST	P07279	saccharomyc	226	1	M4A7	HUMAN	Q9GzW8	homo sapien
154	1	Y552	VIBVU	Q8dCg8	vibrio vuln	227	1	YB46	PASMU	P57911	pasteurella
155	1	Y418	VIBCH	Q9kuu7	vibrio chol	228	1	LEC1	ULREU	P22972	ulex europe
156	1	YH16	PTRAB	Q9uxz1	pyrococcus	229	1	CYSQ	ECOS7	Q8XG96	escherichia
157	1	PAAD	RICPR	Q9ud09	rickettsia	230	1	CYSQ	ECOL6	Q8XG95	escherichia
158	1	UBIX	ECOLI	P09550	escherichia	231	1	CYSQ	ECOLI	Q8XG95	escherichia
159	1	UBIX	SALTY	P40787	salmonella	232	1	CYSQ	SALTY	Q82153	salmonella
160	1	YQ88	VIBPA	Q871c4	vibrio para	233	1	CYSQ	SALTY	P26264	salmonella
161	1	PAAD	CHLPN	Q92884	chlamydia p	234	1	CYSQ	SHIFL	P59735	shigella fl
162	1	ASC2	HUMAN	Q99929	homo sapien	235	1	HBM4	CHLVI	Q93335	chleobium
163	1	DCD	BUCBP	P59464	buchnera ap	236	1	NP2	SULSO	Q97vx5	sulfolobus
164	1	H10	HUMAN	P07305	homo sapien	237	1	PGY2	MASLA	P29732	mastigoclad
165	1	GSFH	VIBCH	P45774	vibrio chol	238	1	1436	ARATH	P48349	arabidopsis
166	1	PAAD	THAAR	P57767	thauera aro	239	1	H12	DROVI	Q94555	drosophila
167	1	LRP1	MYCTU	O10785	mycobacteri	240	1	MTR3	YEAST	P48240	saccharomyc
168	1	RG9	ARATH	P25864	arabidopsis	241	1	DISA	DICDI	P02886	dictyosteli
169	1	GT13	DROME	Q9V997	drosophila	242	1	DISC	DICDI	P02887	dictyosteli
170	1	PAAD	BACPF	P94300	bacillus ps	243	1	YD10	HAIN	P44158	haemophilus
171	1	SOOE	ONCVO	Q07449	onchocerca	244	1	1432	LYCES	P32028	lycopersico
172	1	QOX3	BACSU	P34958	bacillus su	245	1	1434	SOLUT	Q43643	solanum tub
173	1	YNGF	ECOLI	P73131	escherichia	246	1	1435	LYCES	P32110	lycopersico
174	1	NEF	HVLS3	P19545	human immun	247	1	143A	TOBAC	P93342	nicotiana t
175	1	TENT	BACSU	P25053	bacillus su	248	1	143B	TOBAC	Q93995	nicotiana t
176	1	HPI	DROME	P05205	drosophila	249	1	TRYA	MANSE	P35045	manduca sex
177	1	NEF	HV112	P04324	human immun	250	1	TRYB	MANSE	P35046	manduca sex
178	1	NEF	HV1BR	P03406	human immun	251	1	YL99	YERPE	Q8zeh4	yersinia pe
179	1	NEF	HV1PV	P03405	human immun	252	1	AP1B	HUMAN	Q8ww43	homo sapien

253	6	0.8	257	1	PDX3_MOUSE	P20108	mus musculus	326	6	0.8	304	1	HTPX_BACHD	Q9k9e6	bacillus ha
254	6	0.8	258	1	1435_SOLTU	P93784	solanum tub	327	6	0.8	305	1	SOHB_BUCSC	Q44600	buchnera ap
255	6	0.8	259	1	1436_LVCES	P93211	lycopersico	328	6	0.8	307	1	T2RA_HUMAN	Q9nyw0	homo sapien
256	6	0.8	258	1	1437_TOBAC	O49998	nicotiana t	329	6	0.8	308	1	ARGC_RHILO	Q982x3	rhizobium l
257	6	0.8	258	1	UBIE_RHIME	Q928k7	rhizobium m	330	6	0.8	308	1	PYRB_BACCL	P41008	bacillus ca
258	6	0.8	259	1	1432_ARATH	Q01525	arabidopsis	331	6	0.8	310	1	ARGC_BRUME	Q8ygi8	brucella me
259	6	0.8	259	1	1433_LILLO	Q9SP07	lilium long	332	6	0.8	310	1	ARGC_BRUSE	P53114	brucella su
260	6	0.8	259	1	RB34_MOUSE	Q64008	mus musculus	333	6	0.8	310	1	ARGC_RHIME	Q92qr7	rhizobium m
261	6	0.8	259	1	UBIE_AGR5T	Q8u1h5	agrobacteri	334	6	0.8	310	1	FAH1_BACAA	Q81j90	bacillus an
262	6	0.8	260	1	1433_LVCES	P93209	lycopersico	335	6	0.8	310	1	FAH1_BACCR	Q81gm0	bacillus ce
263	6	0.8	260	1	1433_OENHO	P29307	oenothera h	336	6	0.8	311	1	KHSE_SULSO	Q97w70	sulfolobus
264	6	0.8	260	1	1433_ORISA	Q06967	oryza sativ	337	6	0.8	311	1	RUVB_UREPA	Q9pq42	ureaplasma
265	6	0.8	260	1	1433_PEA	P46266	pisum sativ	338	6	0.8	313	1	MRAN_ECOL6	Q8f168	escherichia
266	6	0.8	260	1	143C_TOBAC	P93343	nicotiana t	339	6	0.8	313	1	ZS11_HUMAN	Q9y6i9	homo sapien
267	6	0.8	261	1	143A_VICFA	P42653	vicia faba	340	6	0.8	315	1	Y209_AQUAE	Q66403	aquifex aeo
268	6	0.8	261	1	SPRE_MOUSE	Q64105	mus musculus	341	6	0.8	320	1	Y013_NPVOP	P65361	orgyia pseu
269	6	0.8	261	1	YRBE_HAEIN	P45030	haemophilus	342	6	0.8	322	1	Y348_MYCGE	P47590	mycoplasma
270	6	0.8	262	1	143A_HORVU	P29305	hordeum vul	343	6	0.8	323	1	FLIM_PSEAE	Q51465	pseudomonas
271	6	0.8	262	1	143B_HORVU	Q43470	hordeum vul	344	6	0.8	325	1	HMGL_HUMAN	P35914	homo sapien
272	6	0.8	262	1	COX3_BRALA	O47425	branchiosto	345	6	0.8	325	1	HMGL_MOUSE	P38060	mus musculus
273	6	0.8	264	1	HB21_MOUSE	P04230	mus musculus	346	6	0.8	325	1	HMGL_RAT	P97519	rattus norv
274	6	0.8	264	1	HB22_MOUSE	P01915	mus musculus	347	6	0.8	326	1	FSTL_ARATH	P52839	arabidopsis
275	6	0.8	264	1	HB24_MOUSE	P20040	mus musculus	348	6	0.8	326	1	PER1_ORISA	P37834	oryza sativ
276	6	0.8	264	1	Y547_METJA	Q57967	methanococc	349	6	0.8	326	1	RLUC_PASMA	Q9cm51	pasteurella
277	6	0.8	265	1	NUSM_ANOON	Q31696	anopheles g	350	6	0.8	326	1	YIE1_YEAST	P40531	saccharomyc
278	6	0.8	266	1	ELH1_ACICA	Q59093	acinetobact	351	6	0.8	330	1	LRHD_STAEP	Q8cn22	staphylococ
279	6	0.8	267	1	1431_ARATH	P42643	arabidopsis	352	6	0.8	330	1	PRC2_FORGI	P33437	porphyromon
280	6	0.8	267	1	1434_ARATH	P46077	arabidopsis	353	6	0.8	331	1	FHR4_HUMAN	Q92496	homo sapien
281	6	0.8	267	1	PPN1_OCEIH	Q8er9	oceanobacil	354	6	0.8	333	1	Y808_METJA	Q58218	methanococc
282	6	0.8	267	1	TRY7_ANGOA	P35041	anopheles g	355	6	0.8	334	1	PRC1_PORGI	P59916	porphyromon
283	6	0.8	268	1	ET1B_XENIA	P18756	xenopus lae	356	6	0.8	334	1	SIR6_MOUSE	P59941	mus musculus
284	6	0.8	268	1	TRPA_HAEIN	P43759	haemophilus	357	6	0.8	335	1	GCP_AQUAE	Q66986	aquifex aeo
285	6	0.8	269	1	IL1B_TRIVU	O9xs77	trichosurus	358	6	0.8	335	1	OXAA_BIFLO	Q896j6	bifidobacte
286	6	0.8	269	1	UBIE_BRUME	Q8yde4	brucella me	359	6	0.8	335	1	YJ89_PYRHO	O57713	pyrococcus
287	6	0.8	269	1	UBIE_BRUSU	Q8fuz3	brucella su	360	6	0.8	337	1	RFPI_SALTY	P19816	salmonella
288	6	0.8	270	1	Y166_LISMO	Q8v634	listeria mo	361	6	0.8	339	1	GPDA_YERPE	Q8zjm6	yersinia pe
289	6	0.8	270	1	YJ80_LISMO	Q92ae2	listeria in	362	6	0.8	339	1	YH96_CIOAB	Q97157	clostridium
290	6	0.8	271	1	YLBF_ECOLI	P77518	escherichia	363	6	0.8	340	1	GPDA_SERMA	Q8km1	serratia ma
291	6	0.8	271	1	RR2_NEPOL	Q9t103	nephroselm	364	6	0.8	340	1	EFTS_LACLA	Q9cd5	lactococcus
292	6	0.8	275	1	UPK1_BACHD	Q9kf15	bacillus ha	365	6	0.8	344	1	DHAS_CORFL	P41400	corynebacte
293	6	0.8	275	1	BPBH_PSEPS	P08694	p cis-2,3-d	366	6	0.8	344	1	DHAS_CORGL	P26511	corynebacte
294	6	0.8	275	1	TRY3_ANGOA	P35037	anopheles g	367	6	0.8	345	1	MURB_BUCAP	Q8ka63	buchnera ap
295	6	0.8	275	1	TRY4_ANGOA	P35038	anopheles g	368	6	0.8	345	1	AMIE_RHOER	Q01360	rhodococcus
296	6	0.8	277	1	ZWIN_HUMAN	Q95229	homo sapien	369	6	0.8	345	1	YE38_MYCPN	P75340	mycoplasma
297	6	0.8	278	1	KDUI_YERPE	Q8zfh8	yersinia pe	370	6	0.8	346	1	EFTS_STRP3	Q8e389	streptococc
298	6	0.8	278	1	PHAZ_PSEFL	Q51718	pseudomonas	371	6	0.8	346	1	EFTS_STRP8	P53383	synchocyst
299	6	0.8	279	1	DAPF_AQUAE	Q67693	aquifex aeo	372	6	0.8	346	1	EFTS_STRP8	Q8n243	streptococc
300	6	0.8	279	1	MURI_SYNY3	P73737	synchocyst	373	6	0.8	346	1	EFTS_STRPY	Q99xq7	streptococc
301	6	0.8	280	1	MDCB_PSEPU	Q92452	pseudomonas	374	6	0.8	346	1	PR22_USTMA	P31303	ustilago ma
302	6	0.8	281	1	AAC9_MICCH	P29810	micromonosp	375	6	0.8	352	1	FAS_ARSAN	P36189	anser anser
303	6	0.8	285	1	CNO7_HUMAN	Q9u1v1	homo sapien	376	6	0.8	352	1	NADA_PSEAE	Q914w9	pseudomonas
304	6	0.8	285	1	CNO7_MOUSE	Q60809	mus musculus	377	6	0.8	353	1	MRP_SYNY3	P53383	synchocyst
305	6	0.8	285	1	LPXC_SYNEL	Q8di02	synchococc	378	6	0.8	356	1	MURB_BUCAI	P57153	buchnera ap
306	6	0.8	286	1	TRUA_MYCLE	Q9x796	mycobacteri	379	6	0.8	356	1	TORS_CABEL	Q95nu5	caenorhabdi
307	6	0.8	286	1	YO18_PSEAE	Q9i163	pseudomonas	380	6	0.8	357	1	LEU3_XANAC	Q8ph05	xanthomonas
308	6	0.8	286	1	YTFG_ECOLI	P39315	escherichia	381	6	0.8	357	1	LEU3_XANCP	Q8p511	xanthomonas
309	6	0.8	287	1	DMSC_ECOLI	P18777	escherichia	382	6	0.8	357	1	Y303_MYCGE	P47545	mycoplasma
310	6	0.8	287	1	YICC_ECOLI	P23839	escherichia	383	6	0.8	360	1	AROC_ECOLI	Q8xcq4	escherichia
311	6	0.8	288	1	CDSA_HAEIN	P44937	h phosphati	384	6	0.8	360	1	AROC_ECOLI	P12808	escherichia
312	6	0.8	288	1	VP30_EBOZM	Q05323	ebola virus	385	6	0.8	360	1	AROC_SALTI	P16280	salmonella
313	6	0.8	288	1	BCHL_RHORU	Q31815	rhodospiril	386	6	0.8	360	1	AROC_SALTY	P58729	salmonella
314	6	0.8	291	1	FSBO_CHLRE	P12835	chlamydomon	387	6	0.8	360	1	LEU3_AZOVI	P61197	azotobacter
315	6	0.8	292	1	CNT8_HUMAN	Q9uif9	homo sapien	388	6	0.8	360	1	LEU3_PSEAE	Q51375	pseudomonas
316	6	0.8	292	1	RM07_YEAST	P36519	saccharomyc	389	6	0.8	360	1	LEU3_PSEPK	Q881e5	pseudomonas
317	6	0.8	293	1	VU26_HSVJ7	P52445	human herpe	390	6	0.8	360	1	NUIC_ABRATH	Q37165	arabidopsis
318	6	0.8	297	1	NLPD_PSEAE	P45682	pseudomonas	391	6	0.8	361	1	AROC_VIBAN	P39198	vibrio angu
319	6	0.8	297	1	TRUA_MYCTU	O06322	mycobacteri	392	6	0.8	361	1	AROC_VIBCH	Q9kq85	vibrio chol
320	6	0.8	298	1	YIHV_ECOLI	P32143	escherichia	393	6	0.8	361	1	AROC_VIBPA	Q87mm9	vibrio para
321	6	0.8	299	1	YE05_YEAST	P32643	saccharomyc	394	6	0.8	361	1	AROC_VIBVU	Q8db42	vibrio vuln
322	6	0.8	300	1	VLE3_VIBPA	Q87fd6	vibrio para	395	6	0.8	361	1	BMP_TREPA	P29725	treponema p
323	6	0.8	303	1	LIP2_SYNY3	Q73572	synchocyst	396	6	0.8	363	1	NUIC_LOTJA	Q9bbn9	lotus japon
324	6	0.8	304	1	CYSD_XYLFA	Q9pd79	xyella fas	397	6	0.8	364	1	YM28_MYCTU	Q10512	mycobacteri
325	6	0.8	304	1	CYSD_XYLFT	Q87d98	xyella fas	398	6	0.8	365	1	PENR_MESSR	P41343	mesembryant

399	6	0.8	365	1	NU1C SPIOL	Q9m316	spinacia ol	472	6	0.8	411	1	C1W3_RAT	O54912	rattus norv
400	6	0.8	365	1	RECA SPIPL	P48293	spirulina p	473	6	0.8	412	1	C1S1_RICBE	Q59734	rickettsia
401	6	0.8	366	1	RF2_BACSU	P28367	bacillus su	474	6	0.8	412	1	PGK_MYCTU	O06821	mycobacteri
402	6	0.8	366	1	TORV_ECO57	P58361	escherichia	475	6	0.8	413	1	ALM5_TAMSI	O54757	tamias sibi
403	6	0.8	366	1	TORY_ECOLI	P52005	escherichia	476	6	0.8	413	1	ALM5_TAMSI	O54758	tamias sibi
404	6	0.8	367	1	MK12_ECOLI	O08911	mus musculus	477	6	0.8	413	1	ALST_TAMSI	O54760	tamias sibi
405	6	0.8	367	1	MK12_RAT	Q63538	rattus norv	478	6	0.8	413	1	ALST_TAMSI	O54759	tamias sibi
406	6	0.8	368	1	YBHR_ECOLI	P75774	escherichia	479	6	0.8	413	1	HP55_TAMSI	Q09055	tamias sibi
407	6	0.8	369	1	CYCH BRAJA	P45399	bradyrhizob	480	6	0.8	413	1	LOLC_XYLFA	Q87eif5	xyella fas
408	6	0.8	369	1	PENR SPIOL	P00455	spinacia ol	481	6	0.8	413	1	LOLC_XYLFT	Q97eif5	xyella fas
409	6	0.8	370	1	CYB_EPICE	Q48043	epicrates c	482	6	0.8	415	1	CRF1_RAT	P35353	rattus norv
410	6	0.8	370	1	EGSR_AERPE	Q894r2	aeropyrum p	483	6	0.8	415	1	LOLC_NEIMA	P57061	neisseria m
411	6	0.8	370	1	RECF LISMO	Q8yav8	listeria mo	484	6	0.8	415	1	LOLC_NEIMB	P57062	neisseria m
412	6	0.8	371	1	CYB_BORAC	P92848	boa constri	485	6	0.8	415	1	TRSA_STRAM	Q07197	streptomyce
413	6	0.8	371	1	MNCP_OXYFA	P15798	oxytricha f	486	6	0.8	416	1	CRTC_MOUSE	P14211	mus musculu
414	6	0.8	371	1	MNCP_OXYTR	Q27151	oxytricha t	487	6	0.8	416	1	SVY_TREPA	O83806	treponema p
415	6	0.8	375	1	ADH4_KLULA	P49385	kluyveromyc	488	6	0.8	419	1	ARGJ_SYNY3	P74122	s arginine
416	6	0.8	375	1	HIS7_XYLFA	Q9p0c7	xyella fas	489	6	0.8	419	1	PSG7_HUMAN	Q13046	homo sapien
417	6	0.8	375	1	ISCS_BACHD	Q9kdj6	bacillus ha	490	6	0.8	421	1	SYTC_HUMAN	Q8iv01	homo sapien
418	6	0.8	375	1	LEUI_BUCTS	Q31287	buchnera ap	491	6	0.8	421	1	SYTC_MOUSE	Q920n7	mus musculu
419	6	0.8	375	1	YBJF_ECO57	Q8x6g5	escherichia	492	6	0.8	421	1	SYTC_RAT	P87610	rattus norv
420	6	0.8	375	1	YBJF_ECOLI	P75817	escherichia	493	6	0.8	424	1	LE22_METJA	P81291	methanococc
421	6	0.8	377	1	DNAJ BRAJA	P94319	bradyrhizob	494	6	0.8	426	1	ALFA_BACSU	P71006	bacillus su
422	6	0.8	379	1	DNAJ RHOSP	O08356	rhodopseudo	495	6	0.8	427	1	ALFB_BACSU	Q8rk22	bacillus su
423	6	0.8	379	1	AGLJ RHIME	Q923r7	rhizobium m	496	6	0.8	427	1	HISX_LEPIN	Q8f393	leptospira
424	6	0.8	380	1	OPRK CAVPO	P41144	cavia porce	497	6	0.8	427	1	YF05_METTH	O27549	methanobact
425	6	0.8	381	1	CYK MYOME	Q35038	myoictis me	498	6	0.8	428	1	CKKR_HUMAN	P32238	homo sapien
426	6	0.8	381	1	RSAL_YEAST	O08932	saccharomyc	499	6	0.8	428	1	ELK1_HUMAN	P19419	homo sapien
427	6	0.8	382	1	ADH2_ZYMO	P06758	zymomonas m	500	6	0.8	428	1	FIXC_ECOLI	P31575	escherichia
428	6	0.8	382	1	SPGN_MOUSE	P16546	mus musculus	501	6	0.8	428	1	GLYA_AQUAE	O46776	aquifex aeo
429	6	0.8	382	1	YAM3_SCHPO	Q10058	schizosacch	502	6	0.8	429	1	ELKT_MOUSE	P96881	mycobacteri
430	6	0.8	382	1	YSYF_CABEL	Q8ta81	caenorhabdi	503	6	0.8	429	1	PURK_MYCTU	Q821q3	chlamydophi
431	6	0.8	384	1	NUMM_ANOAR	P51899	anopheles a	504	6	0.8	431	1	NQRF_CHLCV	Q940q1	arabidopsis
432	6	0.8	386	1	RB87_DROME	P48810	drosophila	505	6	0.8	431	1	PELI_ARATH	Q940q1	arabidopsis
433	6	0.8	387	1	CEAN_ECOLI	P08083	escherichia	506	6	0.8	431	1	UROK_HUMAN	P00749	homo sapien
434	6	0.8	387	1	RT05_SCHPO	Q10234	schizosacch	507	6	0.8	431	1	URTB_DSERO	P98121	desmodus ro
435	6	0.8	388	1	ALR_BACHD	Q9kff9	bacillus ha	508	6	0.8	433	1	UROK_BOVIN	Q05589	bos taurus
436	6	0.8	388	1	CU55_HUMAN	Q9nx36	homo sapien	509	6	0.8	433	1	UROK_PAPCY	P16227	papio cynoc
437	6	0.8	389	1	AL44_PSEAE	Q9yh69	pseudomonas	510	6	0.8	435	1	PNCB_VIBCH	Q9kn67	vibrio chol
438	6	0.8	389	1	WN2B_MOUSE	Q70283	mus musculus	511	6	0.8	436	1	CKKR_MOUSE	O08786	mus musculu
439	6	0.8	391	1	WN2B_HUMAN	Q93097	homo sapien	512	6	0.8	436	1	NPT3_HUMAN	O00624	homo sapien
440	6	0.8	392	1	HIS2_LISIN	Q92682	listeria in	513	6	0.8	436	1	YINS_YEAST	P40463	saccharomyc
441	6	0.8	393	1	HIS2_LISMO	Q8y9f9	listeria mo	514	6	0.8	437	1	KICM_MOUSE	P08730	mus musculu
442	6	0.8	394	1	AV71_ACAVI	Q17107	acanthochei	515	6	0.8	438	1	ETIA_XENLA	P18755	xenopus lae
443	6	0.8	394	1	C1W3_HUMAN	O14649	homo sapien	516	6	0.8	438	1	MYC_CALJA	P49032	callithrix
444	6	0.8	394	1	URTG_DSERO	P49150	desmodus ro	517	6	0.8	439	1	ENO_RHORB	Q870b9	rhodotorula
445	6	0.8	394	1	YWFF_BACSU	P39642	bacillus su	518	6	0.8	439	1	MYC_CANPA	Q28350	canis famil
446	6	0.8	395	1	FLD2_RHIME	Q52942	rhizobium m	519	6	0.8	439	1	MYC_FELCA	P06877	felis silve
447	6	0.8	395	1	YHAC_ECOLI	P11864	escherichia	520	6	0.8	439	1	MYC_MARMO	P22555	marmota mon
448	6	0.8	396	1	NASR_KLEOX	P18664	escherichia	521	6	0.8	439	1	MYC_MOUSE	P01108	mus musculu
449	6	0.8	397	1	ACKA_OCEIH	Q48468	klebsiella	522	6	0.8	439	1	MYC_SHEEP	Q28566	ovis aries
450	6	0.8	399	1	LHX5_BRABE	O8ebp9	oceanobacil	523	6	0.8	439	1	NH97_CABEL	Q9bjks	caenorhabdi
451	6	0.8	400	1	APC3_ARATH	P52889	brachydanio	524	6	0.8	439	1	BRNO_BACSU	Q94499	bacillus su
452	6	0.8	400	1	DFP_HASIN	P51568	arabidopsis	525	6	0.8	440	1	ENO_CLARE	P42040	cladoporiu
453	6	0.8	401	1	FLD1_RHIME	P44953	haemophilus	526	6	0.8	440	1	ETSI_MOUSE	P27577	mus musculu
454	6	0.8	402	1	ILV5_NEUCR	P38674	neurospora	527	6	0.8	440	1	YDJN_HABIN	P45079	haemophilus
455	6	0.8	402	1	KLUC_MOUSE	Q9v6x7	drosophila	528	6	0.8	440	1	YJZ6_YEAST	P47097	saccharomyc
456	6	0.8	403	1	LFH1_XENLA	P19001	mus musculus	529	6	0.8	440	1	YJZ6_YEAST	P47099	saccharomyc
457	6	0.8	403	1	MGLB_TREPA	P29674	xenopus lae	530	6	0.8	440	1	YME5_YEAST	Q04705	saccharomyc
458	6	0.8	403	1	P37_MYCHR	Q08255	treponema p	531	6	0.8	440	1	YMO1_YEAST	Q12231	saccharomyc
459	6	0.8	403	1	ILV5_SCHPO	P15363	mycoplasma	532	6	0.8	440	1	YTY1_YEAST	P08405	saccharomyc
460	6	0.8	404	1	LHX1_HUMAN	P78827	schizosacch	533	6	0.8	441	1	DBNT_TAXCA	Q81169	taxus canad
461	6	0.8	404	1	PEX9_YARLI	P48742	homo sapien	534	6	0.8	441	1	ETSI_HUMAN	P14921	homo sapien
462	6	0.8	406	1	LHX1_CHICK	P54817	yarrowia li	535	6	0.8	441	1	ETSI_RAT	P41156	rattus norv
463	6	0.8	406	1	LHX1_MOUSE	P53411	gallus gall	536	6	0.8	441	1	ETSA_CHICK	P13474	rattus gall
464	6	0.8	406	1	LHX1_MOUSE	P36199	mus musculus	537	6	0.8	442	1	LEU2_BUCUH	Q9evh7	buchnera ap
465	6	0.8	408	1	SEPR_THESR	P80146	thermus sp.	538	6	0.8	442	1	UROK_PIG	P04185	sus scrofa
466	6	0.8	409	1	C1W3_MOUSE	Q35111	mus musculus	539	6	0.8	443	1	AMYA_AERHY	P41131	aeromonas h
467	6	0.8	410	1	ASSY_PYRFU	Q8u484	pyrococcus	540	6	0.8	444	1	CKCR_RAT	P30551	rattus norv
468	6	0.8	410	1	CGEI_HUMAN	P24864	homo sapien	541	6	0.8	448	1	YKA3_CABEL	P34255	caenorhabdi
469	6	0.8	410	1	SAHH_THEAC	Q248x4	thermoplas	542	6	0.8	451	1	PTKC_ECOLI	P37189	escherichia
470	6	0.8	410	1	YCF1_MESVI	Q9um00	mesoigima	543	6	0.8	452	1	KICO_MOUSE	P61414	mus musculu
471	6	0.8	411	1	C1S1_RICTY	P51043	rickettsia	544	6	0.8	453	1	Y081_METMA	Q8q0q5	methanosarc

545	1	Y856	METTH	026944	methanobact	618	6	0.8	504	1	NRFL_BRARE	Q90x44	brachydanio
546	1	Y855	MOUSE	Q9er04	mus musculus	619	6	0.8	505	1	ATPA_SYN6	P08449	synecococc
547	1	Y854	YEAST	P40161	saccharomyc	620	6	0.8	506	1	MOT6_HUMAN	O15375	homo sapien
548	1	K1CO	HUMAN	P19012	homo sapien	621	6	0.8	507	1	ATPA_ANASP	P12405	anabaena sp
549	1	M6A1	YEAST	P53050	saccharomyc	622	6	0.8	508	1	CPY7_MOUSE	P27786	mus musculus
550	1	MLP1	ECOLI	P37773	escherichia	623	6	0.8	509	1	COBI_MYCTU	P42118	xenopus lae
551	1	Y853	HUMAN	Q9h383	homo sapien	624	6	0.8	510	1	HUTH_BACSU	Q10677	mycobacteri
552	1	CD4_CERAE	CD4_CERAE	Q08338	cercopithe	625	6	0.8	511	1	MATK_SCHTR	Q10944	bacillus su
553	1	CD4_HUMAN	CD4_HUMAN	P01730	homo sapien	626	6	0.8	512	1	PR12_HUMAN	Q95e84	schlumberge
554	1	CD4_MACEA	CD4_MACEA	P79185	macaca fasc	627	6	0.8	513	1	D7A1_HUMAN	P49643	homo sapien
555	1	CD4_MACFU	CD4_MACFU	P79184	macaca fusc	628	6	0.8	514	1	D7A1_MOUSE	P49419	homo sapien
556	1	CD4_MACMU	CD4_MACMU	P16003	macaca mulla	629	6	0.8	515	1	ACCD_TOBAC	Q9dbf1	mus musculus
557	1	CD4_MACNE	CD4_MACNE	Q08340	macaca neme	630	6	0.8	516	1	ATPA_MOUSE	P12219	nicotiana t
558	1	CD4_PANTR	CD4_PANTR	P16004	pan troglod	631	6	0.8	517	1	ATPA_MOUSE	P05439	rhodopseudo
559	1	NU4M_STRCA	NU4M_STRCA	Q21406	struthio ca	632	6	0.8	518	1	ZRFL_MOUSE	P54103	mus musculus
560	1	NU4M_CHICK	NU4M_CHICK	P18939	gallus gall	633	6	0.8	519	1	CP11_PAGMA	P98181	pagrus majo
561	1	NU4M_FELCA	NU4M_FELCA	P48916	felis silve	634	6	0.8	520	1	LEUI_BUCDN	O85070	buchnera ap
562	1	NU4M_RH1UN	NU4M_RH1UN	Q96088	rhinoceros	635	6	0.8	521	1	ATPA_MYCGE	P47641	mycoplasma
563	1	TRME_STAAN	TRME_STAAN	Q93161	staphylococ	636	6	0.8	522	1	LEUI_CANBF	Q7VQ16	candidatus
564	1	TRME_STAEP	TRME_STAEP	Q99qt3	staphylococ	637	6	0.8	523	1	SYH_FUGRU	P70076	fugu rubrip
565	1	LIP8_CANAL	LIP8_CANAL	Q8cmu5	staphylococ	638	6	0.8	524	1	CP11_LIZSAU	O42231	liza aurata
566	1	HGD_ARATH	HGD_ARATH	Q9p8v9	candida alb	639	6	0.8	525	1	CP11_LIZSAU	Q9w683	liza salien
567	1	KRM2_MOUSE	KRM2_MOUSE	Q9zra2	arabidopsis	640	6	0.8	526	1	CP11_ONCMY	Q92110	oncorhynch
568	1	Y852	YEAST	Q8k187	mus musculus	641	6	0.8	527	1	GUAA_CORGL	Q92109	oncorhynch
569	1	Y851	YEAST	O42941	schizosacch	642	6	0.8	528	1	RORA_MOUSE	Q8nsr1	corynebacte
570	1	Y850	YEAST	Q8tq61	methanosarc	643	6	0.8	529	1	GUAA_CORAM	P51448	mus musculus
571	1	Y849	YEAST	P56176	helicobacte	644	6	0.8	530	1	ATLI_HUMAN	O52831	corynebacte
572	1	Y848	YEAST	P30847	escherichia	645	6	0.8	531	1	GUAA_MOUSE	Q8n666	homo sapien
573	1	Y847	YEAST	Q9y512	homo sapien	646	6	0.8	532	1	GUAA_MOUSE	O50729	mycobacteri
574	1	Y846	YEAST	P33213	rhizobium f	647	6	0.8	533	1	Y487_TREPA	O83500	treponema p
575	1	Y845	YEAST	Q91280	pleuronecte	648	6	0.8	534	1	GUAA_STRCO	Q91082	streptomyce
576	1	Y844	YEAST	Q05309	clostridium	649	6	0.8	535	1	PUR9_BUCAP	Q8ka70	bifunctio
577	1	Y843	YEAST	P37391	mycobacteri	650	6	0.8	536	1	PUR9_NEIMB	Q9jzm7	n bifunctio
578	1	Y842	YEAST	O6250	mycobacteri	651	6	0.8	537	1	GUAA_MYCLE	P46810	mycobacteri
579	1	Y841	YEAST	Q9pax0	xylella fas	652	6	0.8	538	1	LNT_RHILO	Q8bji6	rhizobium l
580	1	Y840	YEAST	Q87bp9	xylella fas	653	6	0.8	539	1	PGPL_MOUSE	Q8vca0	mus musculus
581	1	Y839	YEAST	Q42586	arabidopsis	654	6	0.8	540	1	PUR9_NEIMA	Q9ju88	n bifunctio
582	1	Y838	YEAST	O75674	homo sapien	655	6	0.8	541	1	NAB1_RALSO	Q8xwm7	raistonia s
583	1	Y837	YEAST	P98119	desmodus ro	656	6	0.8	542	1	NAB8_YERPE	Q8zd80	yerisinia pe
584	1	Y836	YEAST	P15638	desmodus ro	657	6	0.8	543	1	PUR9_PASMU	P57828	p bifunctio
585	1	Y835	YEAST	P41342	nicotiana t	658	6	0.8	544	1	VIE2_AGRU	P07544	agrobacteri
586	1	Y834	YEAST	P95297	methanobact	659	6	0.8	545	1	YEO9_MYCPN	P75375	mycoplasma
587	1	Y833	YEAST	P17454	oryctolagus	660	6	0.8	546	1	COX1_RICPR	O54069	rickettia
588	1	Y832	YEAST	P24214	escherichia	661	6	0.8	547	1	IF2P_SULAC	P95691	sulfolobus
589	1	Y831	YEAST	Q83rel	shigella fl	662	6	0.8	548	1	PUR9_PSESM	Q87v99	p bifunctio
590	1	Y830	YEAST	P15062	gallus gall	663	6	0.8	549	1	NAB8_VIBCH	Q9kpa4	vibrio chol
591	1	Y829	YEAST	O6491	bacillus su	664	6	0.8	550	1	SCD2_SCHPO	P40996	schizosacch
592	1	Y828	YEAST	Q87893	vibrio para	665	6	0.8	551	1	NAB8_ECOLI	O8xa23	escherichia
593	1	Y827	YEAST	Q9kpg8	vibrio chol	666	6	0.8	552	1	NAB8_ECOLI	P10920	escherichia
594	1	Y826	YEAST	Q8del1	vibrio vuln	667	6	0.8	553	1	NAB8_SALTY	Q8z4k0	salmonella
595	1	Y825	YEAST	Q8z1e8	yerisinia pe	668	6	0.8	554	1	NAB8_SALTY	Q8zmx9	salmonella
596	1	Y824	YEAST	Q07263	bos taurus	669	6	0.8	555	1	CH60_COREQ	Q93q12	corynebacte
597	1	Y823	YEAST	P07729	oryza sativ	670	6	0.8	556	1	CH60_NOCFA	O9afae	nocardia fa
598	1	Y822	YEAST	P09481	gallus gall	671	6	0.8	557	1	P20A_MOUSE	Q8ci30	mus musculus
599	1	Y821	YEAST	Q9fh66	arabidopsis	672	6	0.8	558	1	LCPT_BACSU	P55910	bacillus su
600	1	Y820	YEAST	Q9p197	chlamydia m	673	6	0.8	559	1	CH60_NOCAS	Q9afes	nocardia as
601	1	Y819	YEAST	P17972	drosophila	674	6	0.8	560	1	ZYX_CHICK	Q04584	gallus gall
602	1	Y818	YEAST	P04757	rattus norv	675	6	0.8	561	1	GCH2_ARATH	P47924	arabidopsis
603	1	Y817	YEAST	P35962	human immun	676	6	0.8	562	1	TCPH_MOUSE	Q99832	homo sapien
604	1	Y816	YEAST	P07728	oryza sativ	677	6	0.8	563	1	TCPH_MOUSE	P80313	mus musculus
605	1	Y815	YEAST	P08717	rhodobacter	678	6	0.8	564	1	TCPA_SCHMA	Q94757	schistosoma
606	1	Y814	YEAST	P33041	homo sapien	679	6	0.8	565	1	YQ44_CAEEL	Q09460	caenorhabdi
607	1	Y813	YEAST	Q60676	mus musculus	680	6	0.8	566	1	AMYG_YEAST	P08019	saccharomyc
608	1	Y812	YEAST	P33042	rattus norv	681	6	0.8	567	1	NCAP_MUMPM	P21186	mumps virus
609	1	Y811	YEAST	Q65979	synecococc	682	6	0.8	568	1	TCPH_YEAST	P42943	saccharomyc
610	1	Y810	YEAST	P95646	rhodobacter	683	6	0.8	569	1	YCHM_ECOLI	P40877	escherichia
611	1	Y809	YEAST	Q35132	r 25-hydrox	684	6	0.8	570	1	LLDP_ECOLI	Q8x4d9	escherichia
612	1	Y808	YEAST	Q9ev18	buchnera ap	685	6	0.8	571	1	LLDP_ECOLI	P33231	escherichia
613	1	Y807	YEAST	P37966	bacillus su	686	6	0.8	572	1	TREC_ECOLI	P28904	escherichia
614	1	Y806	YEAST	P32297	homo sapien	687	6	0.8	573	1	Y900_METJA	Q58310	methanococc
615	1	Y805	YEAST	Q9evh0	buchnera ap	688	6	0.8	574	1	NCAP_MUMPM	Q9v666	drosophila
616	1	Y804	YEAST	Q16656	homo sapien	689	6	0.8	575	1	C791_SORBI	P21277	mumps virus
617	1	Y803	YEAST	Q9wu00	mus musculus	690	6	0.8	576	1	C791_SORBI	Q43135	georghum bic

691 6 0.8 557 1 MERA SHEPU Q54465 shewanella
 692 6 0.8 558 1 Y561_CHLMU Q9pka6 chlamydia m
 693 6 0.8 559 1 TPA_MOUSE P11214 mus musculus
 694 6 0.8 559 1 TPA_RAT P19637 rattus norv
 695 6 0.8 560 1 EFS_MOUSE Q64355 mus musculu
 696 6 0.8 560 1 HCYG_SEPOF P58626 sepiia offic
 697 6 0.8 560 1 POTM_MYCPN P75059 mycoplasma
 698 6 0.8 560 1 YECO_YEAST P39994 saccharomyc
 699 6 0.8 561 1 EFS_HUMAN O43281 homo sapien
 700 6 0.8 562 1 TPA_HUMAN P00750 homo sapien

ALIGNMENTS

RESULT 1
 Y836_AQUAE
 ID Y836_AQUAE STANDARD; PRT; 232 AA.
 AC O67008;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Hypothetical protein AQ_836.
 GN AQ_836.
 OS Aquifox acolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 acolicus";
 RL Nature 392:353-358(1998).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC
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 CC
 CC EMBL; A5000709; AAC06970.1; -
 DR PIR; E70372; E70372.
 KW Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 4 24 POTENTIAL.
 FT TRANSMEM 42 62 POTENTIAL.
 FT TRANSMEM 100 120 POTENTIAL.
 FT TRANSMEM 145 165 POTENTIAL.
 FT TRANSMEM 171 191 POTENTIAL.
 SQ SEQUENCE 232 AA; 26317 MW; B934B56FEA35B183 CRC64;

Query Match 1.2%; Score 9; DB 1; Length 232;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 FENCKSCRN 96
 |||||
 DB 23 FENCKSCRN 31

RESULT 2
 BMPH_STRPU STANDARD; PRT; 639 AA.
 ID BMPH_STRPU
 AC F98069;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Bone morphogenetic protein 1 homolog precursor (EC 3.4.24.-) (SUBMP).
 OS Strongylocentrotus purpuratus (Purple sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
 OC Strongylocentrotus.
 OX NCBI_TaxID=7668;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=94215496; PubMed=8162855;
 RA Hwang S.P.L., Partin J.S., Lennarz W.J.;
 RT "Characterization of a homolog of human bone morphogenetic protein 1
 in the embryo of the sea urchin, Strongylocentrotus purpuratus";
 RL Development 120:559-568(1994).
 CC -1- TISSUE SPECIFICITY: Ectodermal and primary mesenchym cells in
 CC hatched blastula.
 CC -1- DEVELOPMENTAL STAGE: Embryo; highest level before spiculogenesis.
 CC -1- SIMILARITY: Belongs to peptidase family M12A.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 2 CUB domains.
 CC
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 CC
 CC EMBL; L23838; AAA30081.1; -
 DR HSP; P00736; 1APQ.
 DR MEROPS; M12.005; -
 DR InterPro; IPR000152; Asx_hydroxyl_1.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR001506; Peptidase_M12A.
 DR Pfam; PF01400; Astacin; 1.
 DR Pfam; PF00431; CUB; 2.
 DR PRINTS; PR00480; ASTACIN.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00235; ZnMG; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo;
 KW Metalloprotease; EGF-like domain; Calcium; Signal.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 109 POTENTIAL.
 FT CHAIN 110 639 BONE MORPHOGENETIC PROTEIN 1 HOMOLOG.
 FT DOMAIN 110 306 METALLOPROTEASE.
 FT DOMAIN 307 419 CUB 1.
 FT DOMAIN 420 531 CUB 2.
 FT DOMAIN 532 573 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
 FT METAL 137 197 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 198 198 BY SIMILARITY.
 FT METAL 201 201 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 207 207 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 536 548 BY SIMILARITY.
 FT DISULFID 544 557 BY SIMILARITY.
 FT DISULFID 559 572 BY SIMILARITY.
 FT CARBOHYD 122 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 317 317 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 639 AA; 71893 MW; 59307B265B7894AD CRC64;
 Query Match 1.2%; Score 9; DB 1; Length 639;
 Best Local Similarity 100.0%; Pred.No. 0.56;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 179 YDYVEVRDG 187
 Db 475 YDYVEVRDG 483

RESULT 3
 BMP1_HUMAN
 ID BMP1_HUMAN STANDARD; PRT; 986 AA.
 AC P13497; Q13872; Q14874; Q99421; Q99423; Q9UL38;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
 DE (Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
 GN BMP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BMP1-3).
 RC TISSUE=Skin;
 RX MEDLINE=96209868; PubMed=8643539;
 RA Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V.,
 Prockop D.J.;
 RT "The C-proteinase that processes procollagens to fibrillar collagens
 is identical to the protein previously identified as bone morphogenic
 protein-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130 (1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM BMP1-1).
 RX MEDLINE=89072730; PubMed=3201241;
 RA Wosney J.M., Rosen V., Celeste A.J., Mitsuoka L.M., Whitters M.J.,
 Kriz R.W., Hewick R.M., Wang E.A.;
 RT "Novel regulators of bone formation: molecular clones and
 activities.";
 RL Science 242:1528-1534 (1988).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).
 RC TISSUE=Placenta;
 RX MEDLINE=98160316; PubMed=9500680;
 RA Janitz M., Heiser V., Boettcher U., Landt O., Lauener R.;
 RT "Three alternatively spliced variants of the gene coding for the human
 bone morphogenetic protein-1.";
 RL J. Mol. Med. 76:141-146 (1998).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).
 RC TISSUE=Placenta;
 RX MEDLINE=95096114; PubMed=7798260;
 RA Takahara K., Lyons G.E., Greenspan D.S.;
 RT "Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld)
 are encoded by alternatively spliced transcripts which are
 differentially expressed in some tissues.";
 RL J. Biol. Chem. 269:32572-32578 (1994).
 RN [5]
 RP DISULFIDE BOND IN METALLOPROTEINASE DOMAIN.
 RX MEDLINE=21336528; PubMed=11283002;
 RA Garrigue-Antar L., Barker C., Kadler K.E.;
 RT "Identification of amino acid residues in bone morphogenetic
 protein-1 important for procollagen C-proteinase activity.";
 RL J. Biol. Chem. 276:26237-26242 (2001).
 CC -1- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
 and III. Induces cartilage and bone formation.
 CC -1- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
 Ala-I-Asp in type I and II procollagens and at Arg-I-Asp in type
 III.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC

CC -1- ENZYME REGULATION: Activity is increased by the procollagen C-
 endopeptidase enhancer protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=7;
 CC Name=BMP1-3;
 CC IsoId=P13497-1; Sequence=Displayed;
 CC Name=BMP1-1;
 CC IsoId=P13497-2; Sequence=VSP_005461, VSP_005462;
 CC Name=BMP1-2;
 CC IsoId=P13497-7; Sequence=Not described;
 CC Name=BMP1-4;
 CC IsoId=P13497-3; Sequence=VSP_005463, VSP_005464;
 CC Name=BMP1-5;
 CC IsoId=P13497-4; Sequence=VSP_005465, VSP_005466;
 CC Name=BMP1-6;
 CC IsoId=P13497-5; Sequence=VSP_005467, VSP_005468;
 CC Name=BMP1-7;
 CC IsoId=P13497-6; Sequence=VSP_005469, VSP_005470;
 CC -1- TISSUE SPECIFICITY: Ubiquitous
 CC -1- SIMILARITY: Belongs to peptidase family M12A.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -1- SIMILARITY: Contains 5 CUB domains.
 CC

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 CC

CC EMBL; U50330; AAA93462.1; -;
 CC EMBL; M22488; AAA51833.1; -;
 CC EMBL; Y08723; CAA69973.1; -;
 CC EMBL; Y08724; CAA69974.1; -;
 CC EMBL; Y08725; CAA69975.1; -;
 CC EMBL; L35278; AAC41703.1; -;
 CC EMBL; L35279; AAC41710.1; -;
 CC PIR; A37278; B58788.
 CC HSP; P00736; IAPQ.
 CC MEROPS; M12.005; -;
 CC Genew; HGNC:1067; BMP1.
 CC MIM; 112264; -;
 CC GO; GO:0005576; C:extracellular; NAS.
 CC GO; GO:0008237; F:metallopeptidase activity; NAS.
 CC GO; GO:0001502; P:cartilage condensation; TAS.
 CC GO; GO:0007275; P:development; TAS.
 CC InterPro; IPR000152; Asx hydroxyl S.
 CC InterPro; IPR000859; CUB.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR006209; EGF_Like.
 CC InterPro; IPR006025; Peptidase M.
 CC InterPro; IPR001506; Peptidase M12A.
 CC Pfam; PF01400; Astacin; 1.
 CC Pfam; PF00431; CUB; 5.
 CC Pfam; PF00008; EGF; 2.
 CC PRINTS; PR00480; ASTACIN.
 CC SMART; SM00042; CUB; 5.
 CC SMART; SM00179; EGF_CA; 2.
 CC SMART; SM00235; ZnMG; 1.
 CC PROSITE; PS00010; ASX_HYDROXYL; 2.
 CC PROSITE; PS01180; CUB; 5.
 CC PROSITE; PS00022; EGF_1; FALSE_NEG.
 CC PROSITE; PS01186; EGF_2; 2.
 CC PROSITE; PS50026; EGF_3; 2.
 CC PROSITE; PS01187; EGF_CA; 2.
 CC PROSITE; PS01142; ZINC_PROTEASE; 1.
 CC Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;
 CC Hydrolase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
 CC Glycoprotein; Zymogen; Alternative splicing.
 CC SIGNAL 1 22 POTENTIAL.
 CC PROPEP 23 120 POTENTIAL.
 CC

FT	CHAIN	121	986	BONE MORPHOGENETIC PROTEIN 1.
FT	DOMAIN	121	321	METALLOPROTEINASE.
FT	DOMAIN	322	434	CUB 1.
FT	DOMAIN	435	546	CUB 2.
FT	DOMAIN	547	588	EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	591	703	CUB 3.
FT	DOMAIN	704	743	EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	747	859	CUB 4.
FT	DOMAIN	860	976	CUB 5.
FT	METAL	213	213	ZINC (CATALYTIC) (BY SIMILARITY).
FT	ACT SITE	214	214	BY SIMILARITY.
FT	METAL	217	217	ZINC (CATALYTIC) (BY SIMILARITY).
FT	METAL	223	223	ZINC (CATALYTIC) (BY SIMILARITY).
FT	DISULFID	183	186	BY SIMILARITY.
FT	DISULFID	322	348	BY SIMILARITY.
FT	DISULFID	375	397	BY SIMILARITY.
FT	DISULFID	435	461	BY SIMILARITY.
FT	DISULFID	488	510	BY SIMILARITY.
FT	DISULFID	551	563	BY SIMILARITY.
FT	DISULFID	559	572	BY SIMILARITY.
FT	DISULFID	574	587	BY SIMILARITY.
FT	DISULFID	591	617	BY SIMILARITY.
FT	DISULFID	644	666	BY SIMILARITY.
FT	DISULFID	707	718	BY SIMILARITY.
FT	DISULFID	714	727	BY SIMILARITY.
FT	DISULFID	729	742	BY SIMILARITY.
FT	CARBOHYD	91	91	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	142	142	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	363	363	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	599	599	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	703	730	KDCEKSDNGGQQDQVNTGSEYECQR -> EKRPALQPP
FT				RGRPHQKFRVQRNRTPQ (in isoform BMP1-1).
FT				Missing (in isoform BMP1-1).
FT	VARSPLIC	731	986	/FTid=VSP_005461.
FT				Missing (in isoform BMP1-1).
FT	VARSPLIC	245	302	/FTid=VSP_005462.
FT				IKVNFQWQEVESIGETVDFDSIMHYARNTSRGIFLDT
FT				QYKVEYGVKPIGOR -> VLSHSLILSCSRNGASFP
FT				CSLESSTHQAICWTGLFLRSPFPRLPLAAPTILRAGV
FT				(in isoform BMP1-4).
FT				/FTid=VSP_005463.
FT				Missing (in isoform BMP1-4).
FT	VARSPLIC	303	986	/FTid=VSP_005464.
FT				AACGGFLTKNGITSPTGMPKVEPPNKNCTIWLQV -> GCY
FT	VARSPLIC	589	622	DLQVQKELLDNRGCFRLSTHGPEMLGTALRG (in
FT				isoform BMP1-5).
FT				/FTid=VSP_005465.
FT	VARSPLIC	623	986	Missing (in isoform BMP1-5).
FT				/FTid=VSP_005466.
FT	VARSPLIC	703	717	KDCEKSDNGGQQD -> GGELFGLLGHPPRP (in
FT				isoform BMP1-6).
FT				/FTid=VSP_005467.
FT	VARSPLIC	718	986	Missing (in isoform BMP1-6).
FT				/FTid=VSP_005468.
FT	VARSPLIC	703	823	KDCEKSDNGGQQDQVNTGSEYECQRCRQSVLHKNHDKCK
FT				EGCDHKVTSSTISPTSNWPKYPSKCTWALISPTGHR
FT				VKLTFTMWDIESPECAYDHLVDFDGRDAXAPVLGRFCG
FT				-> VLEGADRHSLSGLLELLCHALVDVTPAPPALHGD
FT				THARTHTVHTPIAQCTCGPLGASRLSPQPGHLLTIA
FT				PQEGSYLDFTDTHRGDPKPRRRKSLTKTFLSLTPATFRGIWA
FT				L (in isoform BMP1-7).
FT				/FTid=VSP_005469.
FT	VARSPLIC	824	986	Missing (in isoform BMP1-7).
FT				/FTid=VSP_005470.
FT	CONFLICT	748	748	D -> N (IN REF. 4).
FT	CONFLICT	934	934	R -> S (IN REF. 4).
FT	SEQUENCE	986 AA;	111248 MW;	P89201913AC3CBEA CRC64;

Query Match
Best Local Similarity 1.2%; Score 9; DB 1; Length 986;
Matches 9; Conservative 0; Mismatches 0; Indels 0;
179 YDYVEVRDG 187

QY

Db	377 YDYVEVRDG 385
RESULT 4	
BMP1_MOUSE	
ID_BMP1_MOUSE	STANDARD; PRT; 991 AA.
AC	P98063;
DT	01-FEB-1996 (Rel. 33, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
DE	(procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mtld).
GN	BMP1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;	
OX	[1]
RN	SEQUENCE FROM N.A.
RP	STRAIN=CS7BL/6; TISSUE=Embryo;
RC	MEDLINE=94229342; PubMed=8174772;
RX	Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.;
RA	"Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1),
RT	which is related to the Drosophila dorsoventral gene tolloid and
RT	encodes a putative astacin metalloendopeptidase.";
RT	Dev. Biol. 163:175-183(1994).
RT	-I- FUNCTION: Cleaves the C-terminal propeptides of procollagen I, II
CC	and III. Induces cartilage and bone formation.
CC	-I- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
CC	Ala- -Asp in type I and II procollagens and at Arg- -Asp in type
CC	III.
CC	-I- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC	-I- ENZYME REGULATION: Activity is increased by the procollagen C-
CC	endopeptidase enhancer protein.
CC	-I- TISSUE SPECIFICITY: At high levels in embryonic maternal deciduum
CC	and floor plate region of the neural tube. Less in developing
CC	membranous and endochondral bone, submucosa of intestine, dermis
CC	of skin and the mesenchyme of spleen and lung.
CC	-I- SIMILARITY: Belongs to peptidase family M12A.
CC	-I- SIMILARITY: Contains 2 EGF-like domains.
CC	-I- SIMILARITY: Contains 5 CUB domains.
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; L24755; AAA37306.1; -.
DR	PIR; I49540; I49540.
DR	HSSP; P00736; IAPQ.
DR	MEROPS; M12.005; -.
DR	MGI; 88176; Bmp1.
DR	InterPro; IPR00152; Asx_hydroxyl_s.
DR	InterPro; IPR000859; CUB.
DR	InterPro; IPR001881; EGF_Ca.
DR	InterPro; IPR006209; EGF_like.
DR	InterPro; IPR006025; Pept_M_Zn_BS.
DR	InterPro; IPR006026; Peptidase_M.
DR	InterPro; IPR001506; Peptidase_M12A.
DR	Pfam; PF01400; Astacin; 1.
DR	Pfam; PF00431; CUB; 5.
DR	Pfam; PF00008; EGF; 2.
DR	PRINTS; PR00480; ASTACIN.
DR	SMART; SM00042; CUB; 5.
DR	SMART; SM00179; EGF_CA; 2.
DR	SMART; SM00235; ZmC; 1.
DR	PROSITE; PS00010; ASX_HYDROXYL; 2.
DR	PROSITE; PS01180; CUB; 5.
DR	PROSITE; PS00022; EGF_1; FALSE_NEG.

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DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Growth factor; Cytokine; Repeat; Osteogenesis; Chondrogenesis;
KW Hydrolyase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
KW Glycoprotein; Zymogen.
FT SIGNAL 1 25
FT PROPEP 26 125
FT CHAIN 126 991
FT DOMAIN 126 326
FT DOMAIN 327 439
FT DOMAIN 440 551
FT DOMAIN 552 593
FT DOMAIN 596 707
FT DOMAIN 708 748
FT DOMAIN 752 864
FT DOMAIN 865 981
FT METAL 218 219
FT ACT_SITE 219 219
FT METAL 222 222
FT METAL 228 228
FT METAL 228 228
FT DISULFID 188 191
FT DISULFID 327 353
FT DISULFID 380 402
FT DISULFID 440 466
FT DISULFID 493 515
FT DISULFID 556 568
FT DISULFID 564 577
FT DISULFID 579 592
FT DISULFID 596 622
FT DISULFID 649 671
FT DISULFID 712 723
FT DISULFID 719 732
FT DISULFID 734 747
FT CARBOHYD 96 96
FT CARBOHYD 147 147
FT CARBOHYD 337 337
FT CARBOHYD 368 368
FT CARBOHYD 604 604
SQ SEQUENCE 991 AA; 111607 MW; 68A1847783A0BB9E CRC64;

Query Match 1.2%; Score 9; DB 1; Length 991;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 179 YDVEVRDG 187
DB 382 YDVEVRDG 390

RESULT 5
ID Y260 AQUAE STANDARD; PRT; 158 AA.
AC Q86619;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0090 protein AQ_260.
GN AQ_260.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus";
RL Nature 392:353-358 (1998).
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CC -!- SIMILARITY: Belongs to the UPF0090 family.
CC -----
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CC -----
CC EMBL; AE000681; AAC06588.1; -.
DR PIR; G70323; G70323.
DR HAMAP; MF_01077; -. 1.
DR InterPro; IPR003728; DUF150.
DR Pfam; PF02576; DUF150; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 158 AA; 18147 MW; 6F9869AB382FE734 CRC64;

Query Match 1.1%; Score 8; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GKREVVGY 64
DB 114 GKREVVGY 121

RESULT 6
ID WTSB LACLC STANDARD; PRT; 360 AA.
AC P34878;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Modification methylase ScrFIB (EC 2.1.1.73) (Cytosine-specific
DE methyltransferase ScrFIB) (M.ScrFIB) (M.ScrFI-B).
GN SCRFBM.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UC503;
RA Twomey D.P., Davis R., Daly C., Fitzgerald G.F.;
RT "Sequence of the gene encoding a second ScrFI m5C methyltransferase
RT of Lactococcus lactis.";
RL Gene 136:205-209 (1993).
CC -!- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE
CC CCNGG. CAUSES SPECIFIC METHYLATION ON C-2 ON BOTH STRANDS, AND
CC PROTECTS THE DNA FROM CLEAVAGE BY THE SCRFI ENDONUCLEASE.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA cytosine = S-
CC adenosyl-L-homocysteine + DNA 5-methylcytosine.
CC -!- SIMILARITY: Belongs to the C5-methyltransferase family.
CC -----
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CC -----
DR EMBL; LI2227; AAA16838.1; -.
DR EMBL; U89998; AAB66694.1; -.
DR HSSP; P05102; 6MHT.
DR REBASE; 3682; M.ScrFIB.
DR InterPro; IPR001525; C5_DNA_meth.
DR Pfam; PF00145; DNA_methylase; 1.
DR PRINTS; PR00105; C5METTRFRASE.
DR TIGRFAMs; TIGR00675; dcm; 1.
DR PROSITE; PS00094; C5_MTASE_1; 1.
DR PROSITE; PS00095; C5_MTASE_2; 1.
DR Transferase; Methyltransferase; Restriction system.
KW
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FT ACT_SITE 127 127 BY SIMILARITY.
SQ SEQUENCE 360 AA; 41844 MW; B51D60F72A22A7D7 CRC64;

Query Match 1.1%; Score 8; DB 1; Length 360;
Best Local Similarity 100.0%; Pred.No. 4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 272 ENLLEARN 279
DB 46 ENLLEARN 53

RESULT 7
VIBC_VIBC STANDARD; PRT; 395 AA.
AC 007898; Q9JQ09;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vibriobactin-specific isochorismate synthase (EC 5.4.99.6)
DE (isochorismate mutase).
GN VIBC OR VC0773.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=El Tor Lou15;
RX MEDLINE=98037504; PubMed=9371453;
RA Wyckoff E.E., Stobner J.A., Reed K.E., Payne S.M.;
RT "Cloning of a Vibrio cholerae vibriobactin gene cluster:
RT identification of genes required for early steps in siderophore
RT biosynthesis."
RL J. Bacteriol. 179:7055-7062 (1997).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406933; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483 (2000).
CC -!- CATALYTIC ACTIVITY: Chorismate = isochorismate.
CC -!- PATHWAY: Vibriobactin biosynthesis.
CC -!- SIMILARITY: Belongs to the isochorismate synthase family.
CC -!- CAUTION: It is uncertain whether Met-1 or Met-3 is the initiator.
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-----
CC EMBL; U52150; AAC45925.1; -.
CC EMBL; AE004162; AAF93938.1; -.
CC F1R; A82283; A82283.
CC TIGR; VC0773; -.
CC InterPro; IPR005801; Anth synth chor.
CC InterPro; IPR004561; Isochor synth.
CC Pfam; PF00425; chorismate bind; 1.
CC ProDom; PD000779; Anth synth chor; 1.
CC TIGRFAMs; TIGR00543; isochor_syn; 1.
CC Iron transport; Isomerase; Complete proteome.
SQ SEQUENCE 395 AA; 43594 MW; 2FFAF87DD948C78B CRC64;

Query Match 1.1%; Score 8; DB 1; Length 395;
Best Local Similarity 100.0%; Pred.No. 4.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 58 KREVVGYT 65
DB 4 KREVVGYT 11

RESULT 8
FA7_BOVIN STANDARD; PRT; 407 AA.
AC F22457;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coagulation factor VII (EC 3.4.21.21) (Serum prothrombin conversion
DE accelerator).
GN F7.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE.
RP MEDLINE=89008362; PubMed=3049594;
RA Takeya H., Kawabata S., Nakagawa K., Yamamichi Y., Miyata T.,
RA Iwanaga S.;
RT "Bovine factor VII. Its purification and complete amino acid
RT sequence."
RL J. Biol. Chem. 263:14868-14877 (1988).
RN [2]
STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=89213999; PubMed=3149637;
RA Hase S., Kawabata S., Nishimura H., Takeya H., Sueyoshi T.,
RA Miyata T., Iwanaga S., Takao T., Shimonishi Y., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in bovine
RT blood coagulation factors VII and IX."
RL J. Biochem. 104:867-868 (1988).
RN [3]
STRUCTURE OF CARBOHYDRATE ON SER-52.
RX MEDLINE=91344709; PubMed=2129367;
RA Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
RT "A new trisaccharide sugar chain linked to a serine residue in the
RT first EGF-like domain of clotting factors VII and IX and protein Z."
RL Adv. Exp. Med. Biol. 281:121-131 (1990).
CC -!- FUNCTION: Circulates in the blood in a zymogen form. Factor VII is
CC converted to factor VIIa by factor Xa, factor XIIa, factor IXa, or
CC thrombin by minor proteolysis. In the presence of tissue factor
CC and calcium ions, factor VIIa then converts factor X to factor Xa
CC by limited proteolysis. Factor VIIa will also convert factor IX to
CC factor IXa in the presence of tissue factor and calcium.
CC -!- CATALYTIC ACTIVITY: Hydrolyzes one Arg-|-Ile bond in factor X to
CC form factor Xa.
CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
CC a disulfide bond.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some
CC glutamate residues allows the modified protein to bind calcium.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC F1R; A31979; KFB07.
CC HSP; P08709; IBF9.
CC MEROPS; S01.215; -.
CC InterPro; IPR00152; Abx hydroxyl S.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR002383; GLA_blood.

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DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR000294; VitK_dep_GLA.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00594; Gla; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0010; EGFLOOD.
 DR PRINTS; PRO0001; GLABLOOD.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00069; GLA; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS00022; EGF_2; 1.
 DR PROSITE; PS00026; EGF_3; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR Hydroxylase; Serine protease; Blood coagulation; Zymogen; Glycoprotein;
 KW Liver; Plasma; Vitamin K; Calcium-binding; Gamma-carboxyglutamic acid;
 KW EGF-like domain; Repeat.
 FT CHAIN 1 152
 FT CHAIN 153 407
 FT DOMAIN 6 35
 FT DOMAIN 46 82
 FT DOMAIN 87 128
 FT DOMAIN 153 407
 FT SITE 152 153
 FT ACT SITE 193 193
 FT ACT SITE 242 242
 FT ACT SITE 344 344
 FT BINDING 338 338
 FT DISULFID 17 22
 FT DISULFID 50 61
 FT DISULFID 55 70
 FT DISULFID 72 81
 FT DISULFID 91 102
 FT DISULFID 98 112
 FT DISULFID 114 127
 FT DISULFID 135 262
 FT DISULFID 159 164
 FT DISULFID 178 194
 FT DISULFID 310 329
 FT DISULFID 340 368
 FT MOD_RES 6 6
 FT MOD_RES 7 7
 FT MOD_RES 14 14
 FT MOD_RES 16 16
 FT MOD_RES 19 19
 FT MOD_RES 20 20
 FT MOD_RES 25 25
 FT MOD_RES 26 26
 FT MOD_RES 29 29
 FT MOD_RES 35 35
 FT CARBOHYD 52 52
 FT CARBOHYD 145 145
 FT CARBOHYD 203 203
 SQ SEQUENCE 407 AA; 44431 MW; 703E1FE0636F7F10 CRC64;
 Query Match 1.1%; Score 8; DB 1; Length 407;
 Best Local Similarity 100.0%; Pred. No. 4.4;
 Matched 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 643 VTDNMFECA 650
 DB 323 VTDNMFECA 330
 RESULT 9

YDBH SCHPO
 ID YDBH SCHPO STANDARD; PRT; 486 AA.
 AC Q10367;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein C22E12.17c in chromosome I.
 GN SPAC22E12.17C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Welter J., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moescl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves J.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Dega R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.;
 RL "The genome sequence of Schizosaccharomyces pombe."
 Nature 415:871-880(2002).
 CC -!- FUNCTION: GTPase-activating protein for the ADP ribosylation
 CC factor family (potential).
 CC -!- SIMILARITY: Contains 1 Arf-GAP domain.
 CC
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 CC
 CC EMBL; Z70043; CAA93904.1; -;
 DR PIR; T38174; T38174.
 DR GeneDB Spombe; SPAC22E12.17c; -;
 DR InterPro; IPR001164; hRIP_like.
 DR Pfam; PF01412; ArfGAP; 1.
 DR PRINTS; PRO0405; REVINTRACTING.
 DR SMART; SM00105; ArfGAP; 1.
 DR PROSITE; PS00115; ARFGAP; 1.
 DR Hypothetical protein; GTPase activation; Zinc-finger.
 KW DOMAIN 9 131
 FT ZN FING 24 47
 FT ZN FING 24 47
 SQ SEQUENCE 486 AA; 53000 MW; 3A6ED366C04F8105 CRC64;
 Query Match 1.1%; Score 8; DB 1; Length 486;
 Best Local Similarity 100.0%; Pred. No. 5.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 386 SAPTKKPA 393

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Db          279 S8PTKKPA 286
|||||
RESULT 10
CATB_STRRE  STANDARD;      PRT;    740 AA.
AC   C87864;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
GN CPB.
OS Streptomyces reticuli.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1926;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tu45;
RX MEDLINE=99231840; PubMed=10217488;
RA Zou P., Borovok I., Ortiz de Orue Lucana D., Muller D., Schrempf H.;
RT "The mycelium-associated Streptomyces reticuli catalase-peroxidase,
its gene and regulation by PURS.";
RL Microbiology 145:549-559(1999).
CC -!- FUNCTION: Bifunctional, exhibiting both a catalase and broad-
spectrum peroxidase activities (By similarity).
CC -!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
CC -!- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per
dimer (By similarity).
CC -!- SIMILARITY: Belongs to the peroxidase family. Bacterial
peroxidase/catalase subfamily.
CC -----
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CC -----
CC EMBL; Y14317; CAA74698.1; -.
CC HSSP; P00431; LCCA.
CC InterPro; IPR000763; Bac_ctase/prase.
CC InterPro; IPR020216; Peroxidase.
CC Pfam; PF00141; Peroxidase; 1.
CC PRINTS; PR00458; PEROXIDASE.
CC TIGRfam; TIGR00198; cat_per_HPI; 1.
CC PROSITE; PS00435; PEROXIDASE_1; 1.
CC PROSITE; PS00436; PEROXIDASE_2; 1.
CC PROSITE; PS00873; PEROXIDASE_4; 1.
CC Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
KW ACT SITE 105 105 BY SIMILARITY.
FT ACT SITE 109 109 BY SIMILARITY.
FT METAL 272 272 IRON (HEME AXIAL LIGAND).
SQ SEQUENCE 740 AA; 81345 MW; E21860AEE4B4A0E CRC64;

Query Match 1.1%; Score 8; DB 1; Length 740;
Best Local Similarity 100.0%; Pred.No. 7.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 558 DADIATLK 565
DB 453 DADIATLK 460
|||||

RESULT 11
LFC_CARRO  STANDARD;      PRT;    1019 AA.
AC Q26422;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

```

```

DE Limulus clotting factor C precursor (EC 3.4.21.84) (FC).
OS Carinoscorpius rotundicauda (Southeast Asian horseshoe crab).
OX Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OX Limulidae; Carinoscorpius.
OX NCBI_TaxID=6848;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95268506; PubMed=7538401;
RA Ding J.L., Navas M.A. III, Ho B.;
RT "Molecular cloning and sequence analysis of factor C cDNA from the
Singapore horseshoe crab, Carinoscorpius rotundicauda.";
RL Mol. Mar. Biol. Biotechnol. 4:90-103(1995).
CC -!- FUNCTION: This enzyme is closely associated with an endotoxin-
sensitive hemolymph coagulation system which may play important
roles in both hemostasis and host defense mechanisms. Its active
form catalyzes the activation of factor B.
CC -!- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-|-Ser-104 and
124-Ile-|-Ile-125 bonds in Limulus clotting factor B to form
activated factor B. Cleavage of Pro-Arg-|-Xaa bonds in synthetic
substrates.
CC -!- ENZYME REGULATION: Activated by Gram-negative bacterial
lipopolysaccharides and chymotrypsin (By similarity).
CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
a disulfide bond (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 LCCL domain.
CC -!- SIMILARITY: Contains 5 Sushi (SCR) domains.
CC -----
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CC -----
CC EMBL; S77063; AAB34361.1; -.
CC HSSP; P00763; LDPO.
CC MEROPS; S01.219; -.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR004043; LCCL_dom.
CC InterPro; IPR001304; Lectin C.
CC InterPro; IPR001254; Peptidase S1.
CC InterPro; IPR001314; Peptidase S1A.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF03815; LCCL; 1.
CC Pfam; PF00059; lectin_C; 1.
CC Pfam; PF00084; sushi; 5.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00032; CCP; 5.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00603; LCCL; 1.
CC SMART; SM00020; TRYSP; 1.
CC PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
CC PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PS00026; EGF_3; 1.
CC PROSITE; PS00820; LCCL; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Signal; Lectin; Hemolymph clotting;
KW Glycoprotein; Cell adhesion; EGF-like domain; Sushi; Repeat.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 1019 LIMULUS CLOTTING FACTOR C.

```

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FT CHAIN 26 690 LIMULUS CLOTTING FACTOR C, HEAVY CHAIN.
FT CHAIN 691 1019 LIMULUS CLOTTING FACTOR C, LIGHT CHAIN.
FT CHAIN 691 762 LIMULUS CLOTTING FACTOR C, A CHAIN.
FT CHAIN 763 1019 LIMULUS CLOTTING FACTOR C, B CHAIN.
FT DOMAIN 102 137 EGF-LIKE.
FT DOMAIN 142 195 SUSHI 1.
FT DOMAIN 200 254 SUSHI 2.
FT DOMAIN 260 321 SUSHI 3.
FT DOMAIN 325 421 LCCL.
FT DOMAIN 436 568 C-TYPE LECTIN.
FT DOMAIN 576 634 SUSHI 4.
FT DOMAIN 685 748 SUSHI 5.
FT DOMAIN 763 1019 SERINE PROTEASE.
FT ACT SITE 809 809 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 865 865 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 966 966 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT BINDING 960 960 SUBSTRATE (BY SIMILARITY).
FT DOMAIN 643 689 PRO-RICH.
FT DISULFID 106 118 BY SIMILARITY.
FT DISULFID 112 125 BY SIMILARITY.
FT DISULFID 127 136 BY SIMILARITY.
FT DISULFID 436 447 BY SIMILARITY.
FT DISULFID 464 564 BY SIMILARITY.
FT DISULFID 538 556 BY SIMILARITY.
FT DISULFID 794 810 BY SIMILARITY.
FT DISULFID 932 951 BY SIMILARITY.
FT DISULFID 962 966 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 740 760 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 767 767 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 912 912 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1019 AA; 112429 MW; 918A1ED8B817B6C3 CRC64;

Query Match 1.1%; Score 8; DB 1; Length 1019;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 574 TRVQPICL 581
DB 879 TRVQPICL 886
|||||

RESULT 12
LPC_TACTR STANDARD; PRT; 1019 AA.
AC P28175;1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DS Limulus clotting factor C precursor (EC 3.4.21.84) (FC).
OS Tachyplesus tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Lamulidae; Tachyplesus.
OX NCBI_TaxID=6853;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.
RX MEDLINE=91177916; PubMed=2007602;
RA Muta T., Miyata T., Misumi Y., Tokunaga F., Nakamura T., Toh Y.,
RA Ikehara Y., Iwanaga S.;
RT "Limulus factor C. An endotoxin-sensitive serine protease zymogen
RT with a mosaic structure of complement-like, epidermal growth
RT factor-like, and lectin-like domains."
RL J. Biol. Chem. 266:6554-6561(1991).
CC -1- FUNCTION: This enzyme is closely associated with an endotoxin-
CC sensitive hemolymph coagulation system which may play important
CC roles in both hemostasis and host defense mechanisms. Its active
CC form catalyzes the activation of factor B.
CC -1- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-Ser-104 and
CC 124-Ile-Ile-125 bonds in Limulus clotting factor B to form
CC activated factor B. Cleavage of Pro-Arg-Xaa bonds in synthetic
CC substrates.
```

```
CC -1- ENZYME REGULATION: Activated by Gram-negative bacterial
CC lipopolysaccharides and chymotrypsin.
CC -1- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
CC a disulfide bond.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P28175-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P28175-2; Sequence=VSP_005413, VSP_005414;
CC -1- SIMILARITY: Belongs to peptidase family S1_
CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 LCCL domain.
CC -1- SIMILARITY: Contains 5 Sushi (SCR) domains.
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CC -----
CC EMBL; D90271; BAA14315.1; -
CC EMBL; D90272; BAA14316.1; -
CC PIR; A38738; A38738.
CC HSP; P00763; IDPO.
CC MEROPS; S01.219; -.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR004043; LCCL dom.
CC InterPro; IPR001304; Lectin C.
CC InterPro; IPR001254; Peptidase S1.
CC InterPro; IPR001314; Peptidase S1A.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF03815; LCCL; 1.
CC Pfam; PF00059; lectin_c; 1.
CC Pfam; PF00084; sushi; 5.
CC PRINTS; PR00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC SMART; SM00032; CCF; 5.
CC SMART; SM00034; CLECT; 1.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00603; LCCL; 1.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
CC PROSITE; PS00041; C-TYPE LECTIN_2; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PS50026; EGF_3; 1.
CC PROSITE; PS50820; LCCL; 1.
CC PROSITE; PS50240; TRYPSIN DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Serine protease; Signal; Alternative splicing; Lectin;
CC Hemolymph clotting; Glycoprotein; Cell adhesion; EGF-like domain;
CC SUSHI; Repeat.
CC SIGNAL 1 25
CC CHAIN 26 1019 LIMULUS CLOTTING FACTOR C.
CC CHAIN 26 690 LIMULUS CLOTTING FACTOR C, HEAVY CHAIN.
CC CHAIN 691 1019 LIMULUS CLOTTING FACTOR C, LIGHT CHAIN.
CC CHAIN 691 762 LIMULUS CLOTTING FACTOR C, A CHAIN.
CC CHAIN 763 1019 LIMULUS CLOTTING FACTOR C, B CHAIN.
CC DOMAIN 102 137 EGF-LIKE.
CC DOMAIN 142 195 SUSHI 1.
CC DOMAIN 200 254 SUSHI 2.
CC DOMAIN 260 321 SUSHI 3.
CC DOMAIN 325 421 LCCL.
CC DOMAIN 436 568 C-TYPE LECTIN.
CC DOMAIN 576 634 SUSHI 4.
CC DOMAIN 685 748 SUSHI 5.
```

FT DOMAIN 763 1019 SERINE PROTEASE.
FT ACT_SITE 809 865 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 865 966 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT BINDING 966 966 SUBSTRATE (BY SIMILARITY).
FT DOMAIN 643 689 PRO-RICH.
FT DISULFID 106 118 BY SIMILARITY.
FT DISULFID 112 125 BY SIMILARITY.
FT DISULFID 127 136 BY SIMILARITY.
FT DISULFID 436 447 BY SIMILARITY.
FT DISULFID 464 564 BY SIMILARITY.
FT DISULFID 538 586 BY SIMILARITY.
FT DISULFID 794 810 BY SIMILARITY.
FT DISULFID 932 951 BY SIMILARITY.
FT DISULFID 962 996 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 740 767 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 912 912 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 492 498 LTTWTG -> TDNVVAT (in isoform Short).
FT VARSPLIC 499 1019 /FTId=VSP 005413.
FT VARSPLIC 499 1019 Missing (In isoform Short).
FT SEQUENCE 1019 AA; 112346 MW; 58C2864C6715289B CRC64;
SQ SEQUENCE 1019 AA; 112346 MW; 58C2864C6715289B CRC64;
Query Match 1.1%; Score 8; DB 1; Length 1019;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 574 TRVQICL 581
DB 879 TRVQICL 886
RESULT 13
ID YPA2_ASCIM STANDARD; PRT; 167 AA.
AC P22375;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 13.7 kDa protein (ORF2).
OS Ascobolus immersus.
OG Mitochondrion.
CG Plasmid pA12.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
OC Pezizales; Ascobolaceae; Ascobolus.
OX NCBI_TaxID=5191;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2/I;
RX MEDLINE=90066356; PubMed=2573821;
RA Kompen F., Meinhardt F., Esser K.;
RT "In organollo replication and viral affinity of linear,
RL Mol. Gen. Genet. 218:523-530(1989).
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CC -----
CC EMBL; X15982; CAA34107.1; --
DR PIR; S05364; S05364.
KW Hypothetical protein; Plasmid; Mitochondrion.
SQ SEQUENCE 167 AA; 19762 MW; 2A6EC8ADD91E8D93 CRC64;
Query Match 1.0%; Score 7; DB 1; Length 167;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 LLLJSSL 22
DB 106 LLLJSSL 112
RESULT 14
ID Y377_MYCGE STANDARD; PRT; 193 AA.
AC P47617;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG377.
GN MG377.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
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CC -----
CC EMBL; U39719; AAC71604.1; --
DR PIR; G64241; G64241.
DR TIGR; MG377; --
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 193 AA; 22649 MW; A85E543E6BD281DF CRC64;
Query Match 1.0%; Score 7; DB 1; Length 193;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 534 DEKTIQS 540
DB 102 DEKTIQS 108
RESULT 15
ID CRBD_CHICK STANDARD; PRT; 196 AA.
AC P49152;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta crystallin A4.
GN CRBA4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White leghorn; TISSUE=Lens;


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RX MEDLINE=96032342; PubMed=7557428;
RA Duncan M.K., Haynes J.I. II, Piatigorsky J.;
RT "The chicken beta A4- and beta B1-crystallin-encoding genes are
RT tightly linked";
RL Gene 162:189-196(1995).
CC -!- FUNCTION: Crystallins are the dominant structural components of
CC the vertebrate eye lens.
CC -!- SUBUNIT: Homo/heterodimer, or complexes of higher order. The
CC structure of beta-crystallin oligomers seems to be stabilized
CC through interactions between the N-terminal arms (By similarity).
CC -!- DOMAIN: Has a two-domain beta-structure, folded into four very
CC similar greek key motifs.
CC -!- SIMILARITY: Belongs to the beta/gamma-crystallin family.
CC -!- SIMILARITY: Contains 4 beta/gamma crystallin 'greek key' domains.
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CC -----
DR EMBL; U18261; AAB60607.1; -.
DR EMBL; U18260; AAB62669.1; -.
DR HSSP; P02522; 2BB2.
DR InterPro; IPR001064; Crystallin.
DR Pfam; PF00030; Crystall; 2.
DR PRINTS; PR01367; BGCYSTALLIN.
DR SMART; SM00247; XTALbg; 2.
DR PROSITE; PS00915; CRYSTALLIN_BETAGAMMA; 4.
DR Eyo lens protein; Repeat.
FT DOMAIN 1 11 N-TERMINAL ARM.
FT DOMAIN 12 51 BETA/GAMMA CRYSTALLIN 'GREEK KEY' 1.
FT DOMAIN 52 98 BETA/GAMMA CRYSTALLIN 'GREEK KEY' 2.
FT DOMAIN 99 104 CONNECTING PEPTIDE.
FT DOMAIN 105 146 BETA/GAMMA CRYSTALLIN 'GREEK KEY' 3.
FT DOMAIN 147 195 BETA/GAMMA CRYSTALLIN 'GREEK KEY' 4.
FT VARIANT 103 103 G -> R.
SQ SEQUENCE 196 AA; 22416 MW; BC0787DC8FCBC8D5 CRC64;

Query Match 1.0%; Score 7; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 486 FLVCSGA 492
Db 142 FLVCSGA 148

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Search completed: August 18, 2004, 16:32:40
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:17:08 ; Search time 57 Seconds
(without alignments)
3569.021 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MELGCTGLTFLQLLLS.....LSTFTKVLVFPKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database : A_Geneseq_23Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3945	100.0	720	3	Aay66695 Membrane-
2	3945	100.0	720	4	Aau29108 Human PRO
3	3945	100.0	720	4	Aab87544 Human PRO
4	3945	100.0	720	4	Aab87544 Human PRO
5	3945	100.0	720	5	Aab65218 Human PRO
6	3945	100.0	720	5	Abg95869 Human sec
7	3945	100.0	720	6	Abu58484 Human PRO
8	3945	100.0	720	6	Abu88032 Human PRO
9	3945	100.0	720	6	Abu84347 Human sec
10	3945	100.0	720	6	Abu86221 Human sec
11	3945	100.0	720	6	Abu865611 Human sec
12	3945	100.0	720	6	Abu599551 Human sec
13	3945	100.0	720	6	Abu58033 Human PRO
14	3945	100.0	720	6	Abu59111 Novel hum
15	3945	100.0	720	6	Abu82623 Human sec
16	3945	100.0	720	6	Abu82790 Human PRO
17	3945	100.0	720	6	Abu89911 Novel hum
18	3945	100.0	720	6	Abu86160 Human sec
19	3945	100.0	720	6	Abu60542 Human sec
20	3945	100.0	720	6	Abu96213 Novel hum
21	3945	100.0	720	6	Abu92644 Human sec
22	3945	100.0	720	6	Abu08721 Human sec
23	3945	100.0	720	6	Abu02773 Human sec
24	3945	100.0	720	6	Abu74927 Human sec
25	3945	100.0	720	6	Abu94689 Human sec
26	3945	100.0	720	6	Abu13924 Human PRO
27	3945	100.0	720	6	Abu85662 Human PRO
28	3945	100.0	720	6	Abu98822 Novel hum
29	3945	100.0	720	6	Abu98037 Novel hum
30	3945	100.0	720	6	Abu91743 Novel hum
31	3945	100.0	720	6	Abu89436 Human PRO
32	3945	100.0	720	6	Abu86277 Human sec
33	3945	100.0	720	6	Abu67490 Human sec
34	3945	100.0	720	6	Abu80518 Human PRO
35	3945	100.0	720	6	Abu72509 Novel hum
36	3945	100.0	720	6	Abu90894 Novel hum
37	3945	100.0	720	6	Abu33953 Human sec
38	3945	100.0	720	6	Abu99436 Human sec
39	3945	100.0	720	6	Abu98826 Human sec
40	3945	100.0	720	6	Abu16349 Human sec
41	3945	100.0	720	6	Abu92249 Human sec
42	3945	100.0	720	6	Abu18890 Human sec
43	3945	100.0	720	6	Abu78311 Human sec
44	3945	100.0	720	6	Abu71970 Human hum
45	3945	100.0	720	6	Abu85047 Novel hum
46	3945	100.0	720	6	Abu00186 Novel hum
47	3945	100.0	720	6	Abu11518 Human sec
48	3945	100.0	720	6	Abu02163 Human sec
49	3945	100.0	720	6	Abu88737 Novel hum
50	3945	100.0	720	6	Abu83432 Human sec
51	3945	100.0	720	6	Abu06233 Novel hum
52	3945	100.0	720	6	Abu59269 Human sec
53	3945	100.0	720	6	Abu09331 Human sec
54	3945	100.0	720	6	Abu19195 Novel hum
55	3945	100.0	720	6	Abu11213 Human sec
56	3945	100.0	720	6	Abu66831 Human sec
57	3945	100.0	720	6	Abu16044 Human sec
58	3945	100.0	720	6	Abu13750 Human sec
59	3945	100.0	720	6	Abu71524 Human sec
60	3945	100.0	720	6	Abu65653 Human sec
61	3945	100.0	720	6	Abu07501 Human PRO
62	3945	100.0	720	6	Abu03688 Human sec
63	3945	100.0	720	6	Abu67136 Human sec
64	3945	100.0	720	6	Abu15739 Human sec
65	3945	100.0	720	6	Abu56020 Human sec
66	3945	100.0	720	6	Abu72305 Human PRO
67	3945	100.0	720	6	Abu65348 Human PRO
68	3945	100.0	720	6	Abu95293 Novel hum
69	3945	100.0	720	6	Abu71196 Human PRO
70	3945	100.0	720	6	Abu07806 Human PRO
71	3945	100.0	720	6	Abu70047 Human sec
72	3945	100.0	720	6	Abu69380 Human sec
73	3945	100.0	720	6	Abu01521 Human PRO
74	3945	100.0	720	6	Abu81323 Human PRO
75	3945	100.0	720	6	Abu60120 Human sec
76	3945	100.0	720	6	Abu90878 Human PRO
77	3945	100.0	720	6	Abu67855 Human sec
78	3945	100.0	720	6	Abu65243 Human sec
79	3945	100.0	720	6	Abu68465 Human sec
80	3945	100.0	720	6	Abu71877 Human sec
81	3945	100.0	720	6	Abu59258 Human sec
82	3945	100.0	720	6	Abu85357 Human PRO
83	3945	100.0	720	6	Abu89047 Human sec
84	3945	100.0	720	6	Abu83127 Human sec
85	3945	100.0	720	6	Abu94983 Novel hum
86	3945	100.0	720	6	Abu90531 Novel hum
87	3945	100.0	720	6	Abu84042 Human sec
88	3945	100.0	720	6	Abu93693 Novel hum
89	3945	100.0	720	6	Abu25955 Human PRO
90	3945	100.0	720	6	Abu64938 Human sec
91	3945	100.0	720	6	Abu68770 Human sec
92	3945	100.0	720	6	Abu06586 Human sec
93	3945	100.0	720	6	Abu99131 Human sec
94	3945	100.0	720	6	Abu57015 Human PRO
95	3945	100.0	720	6	Abu85967 Novel hum
96	3945	100.0	720	6	Abu82254 Human PRO
97	3945	100.0	720	6	Abu87265 Human PRO
98	3945	100.0	720	6	Abu83737 Human sec

99	3945	100.0	720	6	ABO08111	AbO08111 Human PRO	172	3945	100.0	720	6	ABR90334	AbR90334 Human sec
100	3945	100.0	720	6	ABU92494	AbU92494 Human sec	173	3945	100.0	720	6	ABM17248	AbM17248 Human sec
101	3945	100.0	720	6	ABU1822	AbU1822 Novel hum	174	3945	100.0	720	6	ABR94994	AbR94994 Human sec
102	3945	100.0	720	6	ABU65986	AbU65986 Novel hum	175	3945	100.0	720	6	ABR95299	AbR95299 Human sec
103	3945	100.0	720	6	ABU81164	AbU81164 Human sec	176	3945	100.0	720	6	ADB17095	AdB17095 Human tra
104	3945	100.0	720	6	ABR59815	AbR59815 Human sec	177	3945	100.0	720	6	ABO21537	AbO21537 Human sec
105	3945	100.0	720	6	ABU94003	AbU94003 Novel hum	178	3945	100.0	720	6	ABR97801	AbR97801 Human sec
106	3945	100.0	720	6	ABU99856	AbU99856 Novel hum	179	3945	100.0	720	6	ABR87589	AbR87589 Human sec
107	3945	100.0	720	6	ABR66526	AbR66526 Human sec	180	3945	100.0	720	6	ABM77630	AbM77630 Human sec
108	3945	100.0	720	6	ABR90944	AbR90944 Human sec	181	3945	100.0	720	6	ABM7860	AbM7860 Human sec
109	3945	100.0	720	6	ABO53279	AbO53279 Novel hum	182	3945	100.0	720	6	ABM06141	AbM06141 Human sec
110	3945	100.0	720	6	ABU58964	AbU58964 Human sec	183	3945	100.0	720	6	ABM03647	AbM03647 Human sec
111	3945	100.0	720	6	ABU94371	AbU94371 Human PRO	184	3945	100.0	720	6	ABM35098	AbM35098 Human sec
112	3945	100.0	720	6	ABU79253	AbU79253 Human PRO	185	3945	100.0	720	6	ABM26335	AbM26335 Human sec
113	3945	100.0	720	6	ABU86582	AbU86582 Human PRO	186	3945	100.0	720	6	ABO48117	AbO48117 Human sec
114	3945	100.0	720	6	ABU86887	AbU86887 Novel hum	187	3945	100.0	720	6	ABR92859	AbR92859 Human sec
115	3945	100.0	720	6	ABU94676	AbU94676 Human PRO	188	3945	100.0	720	6	ABO24620	AbO24620 Human sec
116	3945	100.0	720	6	ABO04603	AbO04603 Human PRO	189	3945	100.0	720	6	ADA37742	AdA37742 Human sec
117	3945	100.0	720	6	ABR70352	AbR70352 Human sec	190	3945	100.0	720	6	ABM11631	AbM11631 Human sec
118	3945	100.0	720	6	ABU92342	AbU92342 Novel hum	191	3945	100.0	720	6	ABM02732	AbM02732 Human sec
119	3945	100.0	720	6	ABU98517	AbU98517 Human PRO	192	3945	100.0	720	6	ABM16028	AbM16028 Human sec
120	3945	100.0	720	6	ABR65916	AbR65916 Human sec	193	3945	100.0	720	6	ABO27589	AbO27589 Human sec
121	3945	100.0	720	6	ABR64633	AbR64633 Human sec	194	3945	100.0	720	6	ABM29080	AbM29080 Human sec
122	3945	100.0	720	6	ABU59407	AbU59407 Novel hum	195	3945	100.0	720	6	ABM07056	AbM07056 Human sec
123	3945	100.0	720	6	ABU79558	AbU79558 Human PRO	196	3945	100.0	720	6	ABM21150	AbM21150 Human sec
124	3945	100.0	720	6	ABU92949	AbU92949 Human sec	197	3945	100.0	720	6	ABM09496	AbM09496 Human sec
125	3945	100.0	720	6	ABU95508	AbU95508 Human PRO	198	3945	100.0	720	6	ABO41366	AbO41366 Human sec
126	3945	100.0	720	6	ABU91128	AbU91128 Novel hum	199	3945	100.0	720	6	ABO36181	AbO36181 Human PRO
127	3945	100.0	720	6	ABU90221	AbU90221 Novel hum	200	3945	100.0	720	6	ABO43710	AbO43710 Human PRO
128	3945	100.0	720	6	ABO09636	AbO09636 Human sec	201	3945	100.0	720	6	ABM76410	AbM76410 Human sec
129	3945	100.0	720	6	ABO10908	AbO10908 Human sec	202	3945	100.0	720	6	ABM76106	AbM76106 Human sec
130	3945	100.0	720	6	ABR70962	AbR70962 Human sec	203	3945	100.0	720	6	ABM25725	AbM25725 Human sec
131	3945	100.0	720	6	ABU98281	AbU98281 Novel hum	204	3945	100.0	720	6	ABM26030	AbM26030 Human sec
132	3945	100.0	720	6	ABU87570	AbU87570 Human PRO	205	3945	100.0	720	6	ADA21428	AdA21428 Human sec
133	3945	100.0	720	6	ABU91438	AbU91438 Human PRO	206	3945	100.0	720	6	ABO03383	AbO03383 Human sec
134	3945	100.0	720	6	ABU89286	AbU89286 Novel hum	207	3945	100.0	720	6	ABO02468	AbO02468 Human sec
135	3945	100.0	720	6	ABU84552	AbU84552 Human sec	208	3945	100.0	720	6	ABO44257	AbO44257 Human sec
136	3945	100.0	720	6	ABR69742	AbR69742 Human PRO	209	3945	100.0	720	6	ABR90639	AbR90639 Human sec
137	3945	100.0	720	6	ABU80119	AbU80119 Human PRO	210	3945	100.0	720	6	ABR73707	AbR73707 Human sec
138	3945	100.0	720	6	ABU82493	AbU82493 Novel hum	211	3945	100.0	720	6	ABO16959	AbO16959 Human sec
139	3945	100.0	720	6	ABU92173	AbU92173 Novel hum	212	3945	100.0	720	6	ABR94384	AbR94384 Human sec
140	3945	100.0	720	6	ABU93388	AbU93388 Human PRO	213	3945	100.0	720	6	ABR75891	AbR75891 Human sec
141	3945	100.0	720	6	ABO09941	AbO09941 Human sec	214	3945	100.0	720	6	ABR71267	AbR71267 Human sec
142	3945	100.0	720	6	ABO09026	AbO09026 Human sec	215	3945	100.0	720	6	ABR93164	AbR93164 Human sec
143	3945	100.0	720	6	ABU96457	AbU96457 Human PRO	216	3945	100.0	720	6	ABR93469	AbR93469 Human sec
144	3945	100.0	720	6	ABU10879	AbU10879 Human PRO	217	3945	100.0	720	6	ADA10215	AdA10215 Human sec
145	3945	100.0	720	6	ABU10594	AbU10594 Human sec	218	3945	100.0	720	6	ABR87894	AbR87894 Human sec
146	3945	100.0	720	6	ABU81631	AbU81631 Novel hum	219	3945	100.0	720	6	ABO27894	AbO27894 Human sec
147	3945	100.0	720	6	ABU72127	AbU72127 Human PRO	220	3945	100.0	720	6	ABO30029	AbO30029 Human sec
148	3945	100.0	720	6	ABU95603	AbU95603 Human PRO	221	3945	100.0	720	6	ABO33238	AbO33238 Human PRO
149	3945	100.0	720	6	ABU96812	AbU96812 Novel hum	222	3945	100.0	720	6	ABM04926	AbM04926 Human sec
150	3945	100.0	720	6	ABR70657	AbR70657 Human sec	223	3945	100.0	720	6	ABM08886	AbM08886 Human sec
151	3945	100.0	720	6	ABO05008	AbO05008 Novel hum	224	3945	100.0	720	6	ABO36486	AbO36486 Human sec
152	3945	100.0	720	6	ABO08416	AbO08416 Human sec	225	3945	100.0	720	6	ABO35571	AbO35571 Human PRO
153	3945	100.0	720	6	ABU88570	AbU88570 Human sec	226	3945	100.0	720	6	ABO39536	AbO39536 Human sec
154	3945	100.0	720	6	ABO34084	AbO34084 Human PRO	227	3945	100.0	720	6	ABM10411	AbM10411 Human sec
155	3945	100.0	720	6	ABO05623	AbO05623 Human sec	228	3945	100.0	720	6	ABM11936	AbM11936 Human sec
156	3945	100.0	720	6	ABR74012	AbR74012 Human sec	229	3945	100.0	720	6	ABO52082	AbO52082 Human PRO
157	3945	100.0	720	6	ABR95604	AbR95604 Human sec	230	3945	100.0	720	6	ABO52387	AbO52387 Human PRO
158	3945	100.0	720	6	ABR80901	AbR80901 Human sec	231	3945	100.0	720	6	ADA19900	AdA19900 Novel hum
159	3945	100.0	720	6	ABR81206	AbR81206 Human sec	232	3945	100.0	720	6	ADA23705	AdA23705 Human sec
160	3945	100.0	720	6	ABM00902	AbM00902 Human sec	233	3945	100.0	720	6	ADB17283	AdB17283 Human tra
161	3945	100.0	720	6	ABR88504	AbR88504 Human sec	234	3945	100.0	720	6	ADA17759	AdA17759 Human PRO
162	3945	100.0	720	6	ABM77325	AbM77325 Human sec	235	3945	100.0	720	6	ABR97191	AbR97191 Human sec
163	3945	100.0	720	6	ABO28809	AbO28809 Human sec	236	3945	100.0	720	6	ABR86979	AbR86979 Human sec
164	3945	100.0	720	6	ABO31554	AbO31554 Human sec	237	3945	100.0	720	6	ABM11021	AbM11021 Human sec
165	3945	100.0	720	6	ABM07971	AbM07971 Human sec	238	3945	100.0	720	6	ABM28165	AbM28165 Human sec
166	3945	100.0	720	6	ABO40451	AbO40451 Human sec	239	3945	100.0	720	6	ABM32164	AbM32164 Human sec
167	3945	100.0	720	6	ABO35876	AbO35876 Human PRO	240	3945	100.0	720	6	ABM15291	AbM15291 Human sec
168	3945	100.0	720	6	ABO44015	AbO44015 Human PRO	241	3945	100.0	720	6	ABM06446	AbM06446 Human sec
169	3945	100.0	720	6	ADA77922	AdA77922 Human sec	242	3945	100.0	720	6	ABM04257	AbM04257 Human sec
170	3945	100.0	720	6	ABM24810	AbM24810 Human sec	243	3945	100.0	720	6	ABM22370	AbM22370 Human sec
171	3945	100.0	720	6	ABO03078	AbO03078 Human sec	244	3945	100.0	720	6	ABM07666	AbM07666 Human sec

245	3945	100.0	720	6	ABO40756	Human sec
246	3945	100.0	720	6	ABM35403	Human sec
247	3945	100.0	720	6	ABM33166	Human sec
248	3945	100.0	720	6	ABO52692	Human PRO
249	3945	100.0	720	6	ABO50252	Human sec
250	3945	100.0	720	6	ABU99246	Human sec
251	3945	100.0	720	6	ABO404298	Human sec
252	3945	100.0	720	6	ABO05928	Human sec
253	3945	100.0	720	6	ABM18468	Human sec
254	3945	100.0	720	6	ADA27867	Human sec
255	3945	100.0	720	6	ABR97496	Human sec
256	3945	100.0	720	6	ABR80596	Human sec
257	3945	100.0	720	6	ABM01207	Human sec
258	3945	100.0	720	6	ABR88809	Human sec
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268	3945	100.0	720	6	ADA79714	Human sec
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289	3945	100.0	720	6	ADA20072	Novel hum
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303	3945	100.0	720	6	ABO16654	Human sec
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364	3945	100.0	720	6	ABR96581	Human sec
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367	3945	100.0	720	6	ABR99741	Human sec
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373	3945	100.0	720	6	ABO38316	Human sec
374	3945	100.0	720	6	ABO45616	Human PRO
375	3945	100.0	720	6	ADA81441	Human sec
376	3945	100.0	720	6	ABO16654	Human sec
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378	3945	100.0	720	6	ABO18280	Human PRO
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381	3945	100.0	720	6	ABR92554	Human sec
382	3945	100.0	720	6	ABR81511	Human sec
383	3945	100.0	720	6	ABM77935	Human sec
384	3945	100.0	720	6	ABR89724	Human sec
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392	3945	100.0	720	6	ABM35403	Human sec
393	3945	100.0	720	6	ABM33166	Human sec
394	3945	100.0	720	6	ABO52692	Human PRO
395	3945	100.0	720	6	ABO50252	Human sec
396	3945	100.0	720	6	ABU99246	Human sec
397	3945	100.0	720	6	ABO404298	Human sec
398	3945	100.0	720	6	ABO05928	Human sec
399	3945	100.0	720	6	ABM18468	Human sec
400	3945	100.0	720	6	ADA27867	Human sec
401	3945	100.0	720	6	ABR97496	Human sec
402	3945	100.0	720	6	ABR80596	Human sec
403	3945	100.0	720	6	ABM01207	Human sec
404	3945	100.0	720	6	ABR88809	Human sec
405	3945	100.0	720	6	ABM13461	Human sec
406	3945	100.0	720	6	ABM20845	Human sec
407	3945	100.0	720	6	ABO41976	Human sec
408	3945	100.0	720	6	ABO42586	Human sec
409	3945	100.0	720	6	ABM10106	Human sec
410	3945	100.0	720	6	ABO38621	Human sec
411	3945	100.0	720	6	ABM32861	Human sec
412	3945	100.0	720	6	ABM22675	Human sec
413	3945	100.0	720	6	ABM74886	Human sec
414	3945	100.0	720	6	ADA79714	Human sec
415	3945	100.0	720	6	ABR96276	Human sec
416	3945	100.0	720	6	ABM02427	Human sec
417	3945	100.0	720	6	ABR86369	Human sec
418	3945	100.0	720	6	ABR86674	Human sec
419	3945	100.0	720	6	ABM16638	Human sec
420	3945	100.0	720	6	ABM29690	Human sec
421	3945	100.0	720	6	ABO29114	Human sec
422	3945	100.0	720	6	ABM23895	Human sec
423	3945	100.0	720	6	ABM23285	Human sec
424	3945	100.0	720	6	ABM22065	Human sec
425	3945	100.0	720	6	ABO37706	Human sec
426	3945	100.0	720	6	ABM28470	Human sec
427	3945	100.0	720	6	ABM28775	Human sec
428	3945	100.0	720	6	ABM66419	Human sec
429	3945	100.0	720	6	ABM75801	Human sec
430	3945	100.0	720	6	ABM34081	Human sec
431	3945	100.0	720	6	ABM34386	Human sec
432	3945	100.0	720	6	ABO20317</	

391	3945	100.0	720	7	ABM17858	Human sec	464	3945	100.0	720	7	ABM14986	Human sec
392	3945	100.0	720	7	ABR95909	Human sec	465	3945	100.0	720	7	ABO41061	Human sec
393	3945	100.0	720	7	ABO21842	Human sec	466	3945	100.0	720	7	ABO36791	Human sec
394	3945	100.0	720	7	ABO20012	Human sec	467	3945	100.0	720	7	ABO37401	Human sec
395	3945	100.0	720	7	ABO24315	Human sec	468	3945	100.0	720	7	ABM75191	Human sec
396	3945	100.0	720	7	ABR86064	Human sec	469	3945	100.0	720	7	ABM33471	Human sec
397	3945	100.0	720	7	ABM10716	Human sec	470	3945	100.0	720	7	ABO46226	Human sec
398	3945	100.0	720	7	ABM76715	Human sec	471	3945	100.0	720	7	ADA82605	Human sec
399	3945	100.0	720	7	ABR89419	Human sec	472	3945	100.0	720	7	ADB85611	Novel hum
400	3945	100.0	720	7	ABM12546	Human sec	473	3945	100.0	720	7	ADB96239	Human PRO
401	3945	100.0	720	7	ABM05836	Human sec	474	3945	100.0	720	7	ABM31825	Human sec
402	3945	100.0	720	7	ABO34961	Human PRO	475	3945	100.0	720	7	ABM31215	Human sec
403	3945	100.0	720	7	ABM03037	Human sec	476	3945	100.0	720	7	ADB85913	Human sec
404	3945	100.0	720	7	ABM19015	Human sec	477	3945	100.0	720	7	ABM32130	Human sec
405	3945	100.0	720	7	ABM19320	Human sec	478	3945	100.0	720	7	ABM32435	Human sec
406	3945	100.0	720	7	ABO46531	Human PRO	479	3945	100.0	720	7	ADB868290	Human PRO
407	3945	100.0	720	7	ABO49032	Human sec	480	3945	100.0	720	7	ADB68097	Human PRO
408	3945	100.0	720	7	ABR69075	Human sec	481	3945	100.0	720	7	ABM31520	Human sec
409	3945	100.0	720	7	ABR89114	Human sec	482	3945	100.0	720	7	ABM30910	Human sec
410	3945	100.0	720	7	ABR74317	Human sec	483	3945	100.0	720	7	ADB90914	Novel hum
411	3945	100.0	720	7	ABR74317	Human sec	484	3945	100.0	720	7	ADC57711	Human PRO
412	3945	100.0	720	7	ABO18585	Human sec	485	3945	100.0	720	7	ADC55075	Human PRO
413	3945	100.0	720	7	ABR80291	Human sec	486	3945	100.0	720	7	ADC11942	Human sec
414	3945	100.0	720	7	ABM01512	Human sec	487	3945	100.0	720	7	ADC06994	Human PRO
415	3945	100.0	720	7	ABM02122	Human sec	488	3945	100.0	720	7	ADC56364	Human PRO
416	3945	100.0	720	7	ABR87284	Human sec	489	3945	100.0	720	7	ADC17173	Mammalian
417	3945	100.0	720	7	ABM12851	Human sec	490	3945	100.0	720	7	ADC07419	Human sec
418	3945	100.0	720	7	ABM30605	Human sec	491	3945	100.0	720	7	ADC11409	Human sec
419	3945	100.0	720	7	ABM24505	Human sec	492	3945	100.0	720	7	ADC14871	Novel hum
420	3945	100.0	720	7	ABO29419	Human sec	493	3945	100.0	720	7	ADC52366	Novel hum
421	3945	100.0	720	7	ABO31249	Human sec	494	3945	100.0	720	7	ADC14531	Novel hum
422	3945	100.0	720	7	ABM14376	Human sec	495	3945	100.0	720	7	ADC08063	Novel hum
423	3945	100.0	720	7	ABM09801	Human sec	496	3945	100.0	720	7	ADC81888	Human PRO
424	3945	100.0	720	7	ABO38926	Human sec	497	3945	100.0	720	7	ADD07530	Novel hum
425	3945	100.0	720	7	ABM34691	Human sec	498	3945	100.0	720	7	ADC82421	Human PRO
426	3945	100.0	720	7	ABO51167	Human sec	499	3945	100.0	720	7	ADD05643	Human sec
427	3945	100.0	720	7	ABO03993	Human sec	500	3945	100.0	720	7	ADD08601	Novel hum
428	3945	100.0	720	7	ABO10463	Human PRO	501	3945	100.0	720	7	ADD06850	Novel hum
429	3945	100.0	720	7	ABG53170	Human sec	502	3945	100.0	720	7	ADC83097	Human PRO
430	3945	100.0	720	7	ABR77706	Human sec	503	3945	100.0	720	7	ADD55204	Human PRO
431	3945	100.0	720	7	ABR78916	Human sec	504	3945	100.0	720	7	ADD36042	Novel hum
432	3945	100.0	720	7	ABO24010	Human sec	505	3945	100.0	720	7	ADD56162	Human PRO
433	3945	100.0	720	7	ABR93774	Human sec	506	3945	100.0	720	7	ADD54600	Human PRO
434	3945	100.0	720	7	ABM01817	Human sec	507	3945	100.0	720	7	AD26754	Novel hum
435	3945	100.0	720	7	ABM78240	Human sec	508	3945	100.0	720	7	AD26221	Novel hum
436	3945	100.0	720	7	ABR90029	Human sec	509	3945	100.0	720	7	AD52176	Novel hum
437	3945	100.0	720	7	ADA22354	Human sec	510	3945	100.0	720	7	AD74307	Human sec
438	3945	100.0	720	7	ABM27555	Human sec	511	3945	100.0	720	7	AD74919	Human sec
439	3945	100.0	720	7	ABM13156	Human sec	512	3945	100.0	720	7	AB70532	Human PRO
440	3945	100.0	720	7	ABO31859	Human sec	513	3939	99.8	720	4	AAU00401	Human sec
441	3945	100.0	720	7	ABM14071	Human sec	514	3936	99.8	720	3	AAU00401	Human sec
442	3945	100.0	720	7	ABM08276	Human sec	515	3921.5	99.4	737	4	AAU00401	Human sec
443	3945	100.0	720	7	ABO40146	Human sec	516	3921.5	99.4	737	4	AAU00401	Human sec
444	3945	100.0	720	7	ABM74581	Human sec	517	3921.5	99.4	762	4	AAU00401	Human sec
445	3945	100.0	720	7	ABM33776	Human sec	518	3612	91.6	720	4	AAU00401	Human sec
446	3945	100.0	720	7	ABM20235	Human sec	519	3602.5	91.6	719	3	AAU00401	Human sec
447	3945	100.0	720	7	ABO48727	Human sec	520	3500.5	88.7	649	5	AAU00401	Human sec
448	3945	100.0	720	7	ABO22540	Human sec	521	3089.5	78.3	567	4	AAU00401	Human sec
449	3945	100.0	720	7	ABO22540	Human sec	522	2946.5	74.7	570	3	AAU00401	Human sec
450	3945	100.0	720	7	ABO15434	Human sec	523	2577.5	65.3	499	4	AAU00401	Human sec
451	3945	100.0	720	7	ABO15129	Human sec	524	2413	61.2	455	5	AAU00401	Human sec
452	3945	100.0	720	7	ABO15129	Human sec	525	2413	61.2	455	5	AAU00401	Human sec
453	3945	100.0	720	7	ABO17264	Human sec	526	1909	48.4	359	4	AAU00401	Human sec
454	3945	100.0	720	7	ABM17553	Human sec	527	1909	48.4	359	4	AAU00401	Human sec
455	3945	100.0	720	7	ADA06520	Human sec	528	1708.5	43.3	323	5	AAU00401	Human sec
456	3945	100.0	720	7	ADA39213	Human sec	529	1708.5	43.3	323	5	AAU00401	Human sec
457	3945	100.0	720	7	ABR85454	Human sec	530	1175.5	29.8	234	4	AAU00401	Human sec
458	3945	100.0	720	7	ABM77020	Human sec	531	672	17.0	1019	6	AAU00401	Human sec
459	3945	100.0	720	7	ABO28199	Human sec	532	665	16.9	1019	2	AAU00401	Human sec
460	3945	100.0	720	7	ABM22980	Human sec	533	665	16.9	1019	2	AAU00401	Human sec
461	3945	100.0	720	7	ABM30300	Human sec	534	665	16.9	1019	2	AAU00401	Human sec
462	3945	100.0	720	7	ABM21760	Human sec	535	665	16.9	1019	3	AAU00401	Human sec
463	3945	100.0	720	7	ABM21455	Human sec	536	665	16.9	1019	4	AAU00401	Human sec

537	665	16.9	1019	6	ABP72334	Abp72334	Horsehoe	610	315.5	8.0	419	5	AAU99071	Aau99071	Human Pro
538	665	16.9	1083	2	AAW43393	Aaw43393	Singapore	611	315.5	8.0	419	5	AAU99087	Aau99087	Human Pro
539	665	16.9	1083	2	AYO5749	Ayo5749	Horsehoe	612	315.5	8.0	419	5	AAU99079	Aau99079	Human Pro
540	665	16.9	1083	2	AAW4301	Aaw4301	Horsehoe	613	315.5	8.0	461	2	AAR62653	Aar62653	Human Pro
541	665	16.9	1083	2	AAW4289	Aaw4289	Horsehoe	614	314.5	8.0	419	2	AAR35760	Aar35760	Protein C
542	665	16.9	1083	3	AAW4289	Aaw4289	Horsehoe	615	314.5	8.0	419	5	AAU99053	Aau99053	Human Pro
543	665	16.9	1083	6	ABP72333	Abp72333	Horsehoe	616	314.5	8.0	419	5	AAU99007	Aau99007	Human Pro
544	662	16.8	146	4	AAW41743	Aam41743	Human pol	617	314.5	8.0	419	5	AAU99077	Aau99077	Human Pro
545	580	14.7	1033	7	ADH87459	Ade87459	Human MBL	618	314.5	8.0	419	5	AAU99043	Aau99043	Human Pro
546	476	12.1	699	7	ADH87459	Ade87459	Human MBL	619	314	8.0	855	5	AAE23083	Aae23083	Epithin p
547	471	11.9	728	4	ABH85060	Abh85060	Human ser	620	313.5	7.9	419	2	AAW72753	Aaw72753	Primary s
548	468	11.9	728	7	ADH87461	Ade87461	Human MBL	621	313.5	7.9	419	5	AAU99005	Aau99005	Human Pro
549	461	11.7	728	4	AAH47559	Aag47559	Protease	622	313.5	7.9	419	5	AAU99025	Aau99025	Human Pro
550	429	10.9	707	5	ABH80756	Abh80756	Murine C1	623	313.5	7.9	419	5	AAU99065	Aau99065	Human Pro
551	403.5	10.2	705	4	ABH80756	Abh80756	Murine C1	624	313.5	7.9	419	5	AAU99016	Aau99016	Human Pro
552	401.5	10.2	686	5	ABH80756	Abh80756	Murine C1	625	313.5	7.9	419	5	AAU99023	Aau99023	Human Pro
553	401.5	10.2	686	5	ABH80756	Abh80756	Murine C1	626	313	7.9	509	2	AAR13083	Aar13083	PAP-I pro
554	401.5	10.2	686	5	ABH80756	Abh80756	Murine C1	627	312.5	7.9	419	5	AAU99072	Aau99072	Human Pro
555	401.5	10.2	686	5	ABH80756	Abh80756	Murine C1	628	312.5	7.9	419	5	AAU99097	Aau99097	Human Pro
556	401.5	10.2	686	5	ABH80756	Abh80756	Murine C1	629	312.5	7.9	419	5	AAU99009	Aau99009	Human Pro
557	400.5	10.2	686	5	ABH80756	Abh80756	Murine C1	630	312.5	7.9	419	5	AAU99064	Aau99064	Human Pro
558	398.5	10.1	671	5	AAE14565	Aae14565	Human mat	631	312.5	7.9	419	5	AAU99069	Aau99069	Human Pro
559	340.5	8.6	694	7	ADH87462	Ade87462	Rat Prote	632	312.5	7.9	419	5	AAU99082	Aau99082	Human Pro
560	340.5	8.6	694	7	ADH87462	Ade87462	Rat Prote	633	312.5	7.9	419	5	AAU99096	Aau99096	Human Pro
561	340.5	8.6	695	7	ADH87462	Ade87462	Rat Prote	634	312.5	7.9	419	5	AAU99091	Aau99091	Human Pro
562	340.5	8.6	695	7	ADH87462	Ade87462	Rat Prote	635	312.5	7.9	419	5	AAU99024	Aau99024	Human Pro
563	336	8.5	760	3	ADH87462	Ade87462	Rat Prote	636	312.5	7.9	419	5	AAU99048	Aau99048	Human Pro
564	334	8.5	688	7	ADH87462	Ade87462	Rat Prote	637	312.5	7.9	419	5	AAU99067	Aau99067	Human Pro
565	334	8.5	688	7	ADH87462	Ade87462	Rat Prote	638	312.5	7.9	419	5	AAU99075	Aau99075	Human Pro
566	331.5	8.4	1019	4	AAE06940	Aae06940	Human ent	639	312.5	7.9	419	5	AAU99092	Aau99092	Human Pro
567	331.5	8.4	1019	6	ADH87462	Ade87462	Rat Prote	640	312.5	7.9	419	5	AAU99011	Aau99011	Human Pro
568	329	8.3	460	2	AAU13623	Aau13623	Human Pro	641	312.5	7.9	419	5	AAU99032	Aau99032	Human Pro
569	328.5	8.3	1274	5	ABG76507	Abg76507	DNA encod	642	312	7.9	419	4	AAH82677	Aah82677	Human Pro
570	328.5	8.3	1783	5	AAU11815	Aau11815	Cancer an	643	312	7.9	460	2	AAR13537	Aar13537	Human Pro
571	328.5	8.3	1800	5	AAU11812	Aau11812	Cancer an	644	312	7.9	1031	5	ABP60993	Abp60993	Novel hum
572	328.5	8.3	1826	5	AAU11812	Aau11812	Cancer an	645	311.5	7.9	419	5	AAU99008	Aau99008	Human Pro
573	328.5	8.3	2008	5	AAU11814	Aau11814	Cancer an	646	311.5	7.9	419	5	AAU99039	Aau99039	Human Pro
574	328.5	8.3	2306	5	AAU11817	Aau11817	Cancer an	647	311.5	7.9	419	5	AAU99047	Aau99047	Human Pro
575	328.5	8.3	2352	5	AAU11816	Aau11816	Cancer an	648	311.5	7.9	419	5	AAU99070	Aau99070	Human Pro
576	328.5	8.3	683	3	AAU19551	Aau19551	Human mat	649	311.5	7.9	419	5	AAU99017	Aau99017	Human Pro
577	328.5	8.3	762	3	AAU90284	Aay90284	Human pep	650	311.5	7.9	419	5	AAU99044	Aau99044	Human Pro
578	328.5	8.3	851	4	ABH11428	Abh11428	Human pro	651	311.5	7.9	419	5	AAU99014	Aau99014	Human Pro
579	328.5	8.3	851	4	ABH11428	Abh11428	Human pro	652	311.5	7.9	419	5	AAU99031	Aau99031	Human Pro
580	328.5	8.3	855	3	AAU19552	Aau19552	Human mem	653	311.5	7.9	419	5	AAU99057	Aau99057	Human Pro
581	328.5	8.3	855	3	AAU19552	Aau19552	Human mem	654	311.5	7.9	419	5	AAU99054	Aau99054	Human Pro
582	327.5	8.3	449	3	AAH35465	Aah35465	Human mem	655	311.5	7.9	419	5	AAU99095	Aau99095	Human Pro
583	327.5	8.3	855	2	AAU06671	Aay06671	Tumour an	656	311.5	7.9	419	5	AAU99015	Aau99015	Human Pro
584	327.5	8.3	855	4	AAH98500	Aah98500	Human TAD	657	311.5	7.9	461	1	AAH81205	Aah81205	Human Pro
585	327.5	8.3	855	5	AAO22929	Aao22929	Type II t	658	311.5	7.9	461	2	AAR13539	Aar13539	Human Pro
586	327.5	8.3	855	5	AAO22929	Aao22929	Type II t	659	311.5	7.9	461	2	AAR13997	Aar13997	Human Pro
587	327.5	8.3	855	5	AAO22929	Aao22929	Type II t	660	311	7.9	419	4	AAH82678	Aah82678	Human Pro
588	327.5	8.3	855	6	AAO30146	Aao30146	Human mem	661	311	7.9	419	4	AAH82675	Aah82675	Human Pro
589	327.5	8.3	855	6	AAO30146	Aao30146	Human mem	662	310.5	7.9	409	7	ADC40013	Adc40013	Human act
590	327.5	8.3	855	6	AAO30146	Aao30146	Human mem	663	310.5	7.9	410	7	ADC40012	Adc40012	Human act
591	327.5	8.3	855	6	AAO30146	Aao30146	Human mem	664	310.5	7.9	415	3	AAU56803	Aay56803	Truncated
592	327.5	8.3	855	6	AAO30146	Aao30146	Human mem	665	310.5	7.9	419	4	AAH82673	Aah82673	Wild-type
593	324	8.2	3095	7	ADH87462	Ade87462	Rat Prote	666	310.5	7.9	419	4	AAH82673	Aah82673	Wild-type
594	320.5	8.1	3069	5	AAE20788	Aae20788	Rat C3b/C	667	310.5	7.9	419	4	AAH82673	Aah82673	Wild-type
595	320.5	8.1	3100	5	AAE20789	Aae20789	Human C3b	668	310.5	7.9	419	4	AAH82673	Aah82673	Wild-type
596	319.5	8.1	419	5	AAU99088	Aau99088	Human Pro	669	310.5	7.9	419	5	AAU99063	Aau99063	Human mat
597	319.5	8.1	419	5	AAU99088	Aau99088	Human Pro	670	310.5	7.9	419	5	AAU99012	Aau99012	Human Pro
598	318.5	8.1	419	5	AAU99078	Aau99078	Human Pro	671	310.5	7.9	419	5	AAU99050	Aau99050	Human Pro
599	318.5	8.1	2669	5	ABG79169	Abg79169	Human cub	672	310.5	7.9	419	5	AAU99010	Aau99010	Human Pro
600	318.5	8.1	3104	5	ABG79168	Abg79168	Human cub	673	310.5	7.9	419	5	AAU99040	Aau99040	Human Pro
601	317.5	8.0	419	5	AAU99006	Aau99006	Human Pro	674	310.5	7.9	419	5	AAU99060	Aau99060	Human Pro
602	317.5	8.0	419	5	AAU99066	Aau99066	Human Pro	675	310.5	7.9	419	5	AAU99055	Aau99055	Human Pro
603	317.5	8.0	788	2	AAR57283	Aar57283	Bovine en	676	310.5	7.9	419	5	AAU99056	Aau99056	Human Pro
604	317.5	8.0	3069	5	AAE20900	Aae20900	Human C3b	677	310.5	7.9	419	5	AAU99059	Aau99059	Human Pro
605	317.5	8.0	3100	5	AAE20901	Aae20901	Human C3b	678	310.5	7.9	419	5	AAU99002	Aau99002	Human Pro
606	316.5	8.0	419	5	AAU99076	Aau99076	Human Pro	679	310.5	7.9	419	5	AAU99051	Aau99051	Human Pro
607	316.5	8.0	419	5	AAU99022	Aau99022	Human Pro	680	310.5	7.9	419	5	AAU99052	Aau99052	Human Pro
608	315.5	8.0	419	5	AAU99026	Aau99026	Human Pro	681	310.5	7.9	419	6	ABR55547	Abx55547	Amino aci
609	315.5	8.0	419	5	AAU99081	Aau99081	Human Pro	682	310.5	7.9	419	7	ADC40014	Adc40014	Human act

683 310.5 7.9 460 1 AAp81104 Sequence
 684 310.5 7.9 460 2 AAw25086 Human pro
 685 310.5 7.9 461 1 AAp60001 Sequence
 686 310.5 7.9 461 1 AAp70855 Human Pro
 687 310.5 7.9 461 1 AAp90401 Zymogen f
 688 310.5 7.9 461 2 AAr13622 Human pro
 689 310.5 7.9 461 2 AAr13081 Human pro
 690 310.5 7.9 461 2 AAr13074 Protein C
 691 310.5 7.9 461 2 AAr34295 Protein C
 692 310.5 7.9 461 2 AAw02600 Human pro
 693 310.5 7.9 461 2 AAv49561 Human lec
 694 310.5 7.9 461 2 AAb82674 Wild-type
 695 310.5 7.9 461 4 AAb36895 Human pro
 696 310.5 7.9 461 4 AAw08626 Human wil
 697 310.5 7.9 461 5 AAw99001 Human pro
 698 310 7.9 419 4 AAb82676 Human pro
 699 310 7.9 419 4 AAw08630 Human pro
 700 310 7.9 460 2 AAr13538 Human Pro

ALIGNMENTS

RESULT 1

AAy66695
 ID AAY66695 standard; protein; 720 AA.

XX AC AAY66695;
 XX DT 05-APR-2000 (first entry)
 XX DE Membrane-bound protein PRO1344.
 XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
 KW pharmacutical; receptor immunoadhesin; gene mapping.
 XX OS Homo sapiens.

XX PN WO9963088-A2.
 XX PD 09-DEC-1999.

XX PF 02-JUN-1999; 99WO-US012252.

XX PR 02-JUN-1998; 98US-0087607P.
 PR 02-JUN-1998; 98US-0087609P.
 PR 02-JUN-1998; 98US-0087759P.
 PR 03-JUN-1998; 98US-0087827P.
 PR 04-JUN-1998; 98US-0088021P.
 PR 04-JUN-1998; 98US-0088025P.
 PR 04-JUN-1998; 98US-0088028P.
 PR 04-JUN-1998; 98US-0088029P.
 PR 04-JUN-1998; 98US-0088033P.
 PR 04-JUN-1998; 98US-0088326P.
 PR 05-JUN-1998; 98US-0088167P.
 PR 05-JUN-1998; 98US-0088202P.
 PR 05-JUN-1998; 98US-0088212P.
 PR 05-JUN-1998; 98US-0088217P.
 PR 09-JUN-1998; 98US-0088655P.
 PR 10-JUN-1998; 98US-0088722P.
 PR 10-JUN-1998; 98US-0088730P.
 PR 10-JUN-1998; 98US-0088734P.
 PR 10-JUN-1998; 98US-0088738P.
 PR 10-JUN-1998; 98US-0088740P.
 PR 10-JUN-1998; 98US-0088741P.
 PR 10-JUN-1998; 98US-0088742P.
 PR 10-JUN-1998; 98US-0088810P.
 PR 10-JUN-1998; 98US-0088811P.
 PR 10-JUN-1998; 98US-0088824P.
 PR 10-JUN-1998; 98US-0088825P.
 PR 10-JUN-1998; 98US-0088826P.
 PR 11-JUN-1998; 98US-0088858P.

PR 11-JUN-1998; 98US-0088861P.
 PR 11-JUN-1998; 98US-0088863P.
 PR 11-JUN-1998; 98US-0088876P.
 PR 12-JUN-1998; 98US-0089090P.
 PR 12-JUN-1998; 98US-0089105P.
 PR 16-JUN-1998; 98US-0089440P.
 PR 16-JUN-1998; 98US-0089512P.
 PR 16-JUN-1998; 98US-0089514P.
 PR 17-JUN-1998; 98US-0089532P.
 PR 17-JUN-1998; 98US-0089538P.
 PR 17-JUN-1998; 98US-0089598P.
 PR 17-JUN-1998; 98US-0089599P.
 PR 17-JUN-1998; 98US-0089600P.
 PR 17-JUN-1998; 98US-0089653P.
 PR 18-JUN-1998; 98US-0089801P.
 PR 18-JUN-1998; 98US-0089907P.
 PR 18-JUN-1998; 98US-0089908P.
 PR 19-JUN-1998; 98US-0089947P.
 PR 19-JUN-1998; 98US-0089948P.
 PR 19-JUN-1998; 98US-0089952P.
 PR 22-JUN-1998; 98US-0090246P.
 PR 22-JUN-1998; 98US-0090252P.
 PR 22-JUN-1998; 98US-0090254P.
 PR 23-JUN-1998; 98US-0090349P.
 PR 23-JUN-1998; 98US-0090355P.
 PR 24-JUN-1998; 98US-0090429P.
 PR 24-JUN-1998; 98US-0090431P.
 PR 24-JUN-1998; 98US-0090435P.
 PR 24-JUN-1998; 98US-0090444P.
 PR 24-JUN-1998; 98US-0090445P.
 PR 24-JUN-1998; 98US-0090461P.
 PR 24-JUN-1998; 98US-0090472P.
 PR 24-JUN-1998; 98US-0090535P.
 PR 24-JUN-1998; 98US-0090538P.
 PR 24-JUN-1998; 98US-0090540P.
 PR 24-JUN-1998; 98US-0090557P.
 PR 25-JUN-1998; 98US-0090676P.
 PR 25-JUN-1998; 98US-0090678P.
 PR 25-JUN-1998; 98US-0090688P.
 PR 25-JUN-1998; 98US-0090690P.
 PR 25-JUN-1998; 98US-0090691P.
 PR 25-JUN-1998; 98US-0090694P.
 PR 25-JUN-1998; 98US-0090695P.
 PR 25-JUN-1998; 98US-0090696P.
 PR 26-JUN-1998; 98US-0090862P.
 PR 26-JUN-1998; 98US-0090863P.
 PR 01-JUL-1998; 98US-0091358P.
 PR 01-JUL-1998; 98US-0091360P.
 PR 02-JUL-1998; 98US-0091478P.
 PR 02-JUL-1998; 98US-0091486P.
 PR 02-JUL-1998; 98US-0091519P.
 PR 02-JUL-1998; 98US-0091544P.
 PR 02-JUL-1998; 98US-0091626P.
 PR 02-JUL-1998; 98US-0091628P.
 PR 02-JUL-1998; 98US-0091633P.
 PR 02-JUL-1998; 98US-0091646P.
 PR 02-JUL-1998; 98US-0091673P.
 PR 07-JUL-1998; 98US-0091978P.
 PR 09-JUL-1998; 98US-0091982P.
 PR 10-JUL-1998; 98US-0092472P.
 PR 20-JUL-1998; 98US-0093339P.
 PR 30-JUL-1998; 98US-0094651P.
 PR 04-AUG-1998; 98US-0095282P.
 PR 04-AUG-1998; 98US-0095285P.
 PR 04-AUG-1998; 98US-0095301P.
 PR 04-AUG-1998; 98US-0095302P.
 PR 04-AUG-1998; 98US-0095318P.
 PR 04-AUG-1998; 98US-0095321P.
 PR 04-AUG-1998; 98US-0095325P.
 PR 10-AUG-1998; 98US-0095916P.
 PR 10-AUG-1998; 98US-0095929P.
 PR 10-AUG-1998; 98US-0096012P.

PR 11-AUG-1998; 98US-0096143P.
PR 11-AUG-1998; 98US-0096146P.
PR 12-AUG-1998; 98US-0096329P.
PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.
PR 17-AUG-1998; 98US-0096768P.
PR 17-AUG-1998; 98US-0096773P.
PR 17-AUG-1998; 98US-0096791P.
PR 17-AUG-1998; 98US-0096867P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 17-AUG-1998; 98US-0096895P.
PR 17-AUG-1998; 98US-0096897P.
PR 18-AUG-1998; 98US-0096949P.
PR 18-AUG-1998; 98US-0096950P.
PR 18-AUG-1998; 98US-0096959P.
PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097954P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX (GETH) GENENTECH INC.
XX Baker K, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX WPI; 2000-072883/06.
DR N-PSDB; AA265034.
XX
PT Membrane-bound proteins and related nucleotide sequences.
XX Claim 12; Fig 159; 822pp; English.
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
SQ Sequence 720 AA;
Query Match 100.0%; Score 3945; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.2e-204;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MELGCWTQLGLTFLQLLSSLPREYTVINEACPGAENIMCRECCYDQIECVCGKRE 60
DB 1 MELGCWTQLGLTFLQLLSSLPREYTVINEACPGAENIMCRECCYDQIECVCGKRE 60
QY 61 VVGTYIPCCRNEECDSCLIHPGCTIFENCKSCRNGSWGGLTDDPFYVKGFCACRAGW 120

Db 61 VVGTYIPCCRNEECDSCLIHPGCTIFENCKSCRNGSWGGLTDDPFYVKGFCACRAGW 120
QY 121 YGGDCMCGQVLRAPKGOILLESYPLNAHCBSWTTHAKPGFVIQLRFVWLSLEFDMCOYD 180
Db 121 YGGDCMCGQVLRAPKGOILLESYPLNAHCBSWTTHAKPGFVIQLRFVWLSLEFDMCOYD 180
QY 181 YVEVRDGNDRDQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNFGDFHAIYEITACS 240
Db 181 YVEVRDGNDRDQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNFGDFHAIYEITACS 240
QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDDPGVPNGYQKITGGPGLI 300
Db 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDDPGVPNGYQKITGGPGLI 300
QY 301 NGRHAKIGTVVSFFCNNSYVLSGNEKTCQNGSWGSKQPICIKACREPKISDLVRRVL 360
Db 301 NGRHAKIGTVVSFFCNNSYVLSGNEKTCQNGSWGSKQPICIKACREPKISDLVRRVL 360
QY 361 PMQVQSRETPHLQLYSAAFSKQLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPPYR 420
Db 361 PMQVQSRETPHLQLYSAAFSKQLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPPYR 420
QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLWPMQAAIYRSTSGVHDGSL 480
Db 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLWPMQAAIYRSTSGVHDGSL 480
QY 481 HKGAWFLVCSGALVNERTVVVAACHVTDGLKVMTIKTADLKVLGKFRDDEKTKTQS 540
Db 481 HKGAWFLVCSGALVNERTVVVAACHVTDGLKVMTIKTADLKVLGKFRDDEKTKTQS 540
QY 541 LQISAILHPNYDPILLDADIAILKLDKARISTRVQPICLAASRDISTSTQESHITVAG 600
Db 541 LQISAILHPNYDPILLDADIAILKLDKARISTRVQPICLAASRDISTSTQESHITVAG 600
QY 601 WNVLADVRSPGFKNDTLRSVGVSVDLSLICEQHDHGIPIVSVTDNMFCASWEPTAPSDI 660
Db 601 WNVLADVRSPGFKNDTLRSVGVSVDLSLICEQHDHGIPIVSVTDNMFCASWEPTAPSDI 660
QY 661 CTAETGGIAAVSFFPGRASPEPRWHLMLVSNYSYDKTCSHRLSTAFKVLPFKDWIERNNK 720
Db 661 CTAETGGIAAVSFFPGRASPEPRWHLMLVSNYSYDKTCSHRLSTAFKVLPFKDWIERNNK 720
RESULT 2
AAU29108
ID AAU29108 standard; protein; 720 AA.
XX AC AAU29108;
XX DT 18-DEC-2001 (first entry)
XX DE Human PRO polypeptide sequence #85.
XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
XX KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
XX KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
XX KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
XX OS Homo sapiens.
XX PN WO200168848-A2.
XX PD 20-SEP-2001.
XX PF 28-FEB-2001; 2001WO-US0006520.
XX PR 01-MAR-2000; 2000WO-US005601.
XX PR 02-MAR-2000; 2000WO-US005841.
XX PR 03-MAR-2000; 2000US-0187202P.
XX PR 06-MAR-2000; 2000US-0186968P.
XX PR 14-MAR-2000; 2000US-0189320P.
XX PR 14-MAR-2000; 2000US-0189328P.

PR 15-MAR-2000; 2000WO-US006884.
 PR 21-MAR-2000; 2000US-0190828P.
 PR 21-MAR-2000; 2000US-0191007P.
 PR 21-MAR-2000; 2000US-0191048P.
 PR 21-MAR-2000; 2000US-0191314P.
 PR 28-MAR-2000; 2000US-0192655P.
 PR 29-MAR-2000; 2000US-0193032P.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 04-APR-2000; 2000US-0194449P.
 PR 04-APR-2000; 2000US-0194647P.
 PR 11-APR-2000; 2000US-0195975P.
 PR 11-APR-2000; 2000US-0196000P.
 PR 11-APR-2000; 2000US-0196187P.
 PR 11-APR-2000; 2000US-0196690P.
 PR 11-APR-2000; 2000US-0196820P.
 PR 18-APR-2000; 2000US-0198121P.
 PR 18-APR-2000; 2000US-0198585P.
 PR 25-APR-2000; 2000US-0199397P.
 PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PA (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Deanovers L, Goddard A, Godowski PJ, Gurney AL;
 XX Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2001-602746/68.
 DR N-PSDB; AAS46009.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX Claim 11; Fig 170; 774pp; English.
 XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX Sequence 720 AA;
 Query Match 100.0%; Score 3945; DB 4; Length 720;
 Match Local Similarity 100.0%; Pred. No. 1.2e-204; Indels 0; Gaps 0;
 Matches 720; Conservative 0; Mismatches 0;
 QY 1 MELGWTQLGLTFLQLLLISSLPREYTVINEACPGAENWIMCRECCYDQIEVCVPGKRE 60
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MELGWTQLGLTFLQLLLISSLPREYTVINEACPGAENWIMCRECCYDQIEVCVPGKRE 60
 QY 61 VVGVTTPCCNEENECDSCLIHPGCTIFENCKSCRNGSWGTTLDDFVXKGFYCAECRAGW 120
 Db 61 VVGVTTPCCNEENECDSCLIHPGCTIFENCKSCRNGSWGTTLDDFVXKGFYCAECRAGW 120
 QY 121 YGGDCMRCQGVLRAPKQIILLESYPINAHCEWTIHAKPGFVIQIRFVWLSLEFDYMCQYD 180
 Db 121 YGGDCMRCQGVLRAPKQIILLESYPINAHCEWTIHAKPGFVIQIRFVWLSLEFDYMCQYD 180
 QY 181 YVEVRDGNDRDGOIKRVCGNERPAPIQISGSLHLVFLHSDGSKNFDGPHAIYEETIACS 240
 Db 181 YVEVRDGNDRDGOIKRVCGNERPAPIQISGSLHLVFLHSDGSKNFDGPHAIYEETIACS 240
 QY 241 SSPCFHDGTCLVDKAGSYKACIAGYTQRCENLLEERNCSDFGPGVNGYQKITGGPGLI 300
 Db 241 SSPCFHDGTCLVDKAGSYKACIAGYTQRCENLLEERNCSDFGPGVNGYQKITGGPGLI 300
 QY 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWGSKQPICIKACREPKISDLVRRVL 360
 Db 301 NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWGSKQPICIKACREPKISDLVRRVL 360
 QY 361 PMOVQSRRETPHLQYSAAPSKOKLQAPTKKPPALPGDLPNGYQHLHLTQYECISPFYR 420
 Db 361 PMOVQSRRETPHLQYSAAPSKOKLQAPTKKPPALPGDLPNGYQHLHLTQYECISPFYR 420
 QY 421 RLGSRRRTCLRTQKWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSL 480
 Db 421 RLGSRRRTCLRTQKWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSL 480
 QY 481 HKGAWFLVCSGALVNERTVVAACHVTDLGKVTMIKTADLKVVLGKPYRDDDRDEKTIQS 540
 Db 481 HKGAWFLVCSGALVNERTVVAACHVTDLGKVTMIKTADLKVVLGKPYRDDDRDEKTIQS 540
 QY 541 LOISAILHPNYPILLDDADIALKLLDKARISTRVQPICLAASRDISTSFQESHITVAG 600
 Db 541 LOISAILHPNYPILLDDADIALKLLDKARISTRVQPICLAASRDISTSFQESHITVAG 600
 QY 601 WNVLDVRSFGKNDTLRSQVSVVDSLLCEQHEHDGIPVSVTDNMFCASWBPAPSIDI 660
 Db 601 WNVLDVRSFGKNDTLRSQVSVVDSLLCEQHEHDGIPVSVTDNMFCASWBPAPSIDI 660
 QY 661 CTATGTGIAAVSPFGRASPEPRWHLNGLVSWSDYDKTCSHRLSTAFTKVLPFKDWIERNMK 720
 Db 661 CTATGTGIAAVSPFGRASPEPRWHLNGLVSWSDYDKTCSHRLSTAFTKVLPFKDWIERNMK 720
 RESULT 3
 AAB87544
 ID AAB87544 standard; protein; 720 AA.
 XX AC AAB87544;
 XX DT 15-MAY-2001 (first entry)
 XX DE Human PRO1344.
 XX KW Human; PRO protein; mapping.
 XX OS Homo sapiens.
 XX PN W0200116318-A2.
 XX PD 08-MAR-2001.
 XX PF 24-AUG-2000; 2000WO-US023328.
 XX PR 01-SEP-1999; 99WO-US020111.
 XX PR 15-SEP-1999; 99WO-US021090.
 XX PR 07-DEC-1999; 99US-0169495P.
 XX PR 09-DEC-1999; 99US-0170262P.
 XX PR 11-JAN-2000; 2000US-0175481P.
 XX PR 18-FEB-2000; 2000WO-US004341.

PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000WO-US005601.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.
XX (GETH) GENENTECH INC.
XX Eaton DL, Filvaroff B, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;
XX N-PSDB; AAP92076.
XX WPI; 2001-183260/18.
XX
XX Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
XX biology, including use as hybridization probes, and in chromosome and
XX gene mapping.
XX
XX Claim 12; Fig 38; 278pp; English.
XX
XX The present sequence is a human PRO polypeptide (secreted and
XX transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
XX anti-PRO antibodies are useful for preparation of a medicament useful in
XX the treatment of a condition which is responsive to the PRO protein,
XX agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
XX employed as molecular weight markers for protein electrophoresis. The PRO
XX coding sequence has applications in molecular biology, including use as
XX hybridisation probes, and in chromosome and gene mapping
XX
XX Sequence 720 AA;
Query Match 100.0%; Score 3945; DB 4; Length 720;
Best Local Similarity 100.0%; Pred. No. 1.2e-204;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MELGCTQLGLTFLQLLSSLPREYTVINEACPGAENWIMCRECCEDYDQIECVCPGRE 60
DB 1 MELGCTQLGLTFLQLLSSLPREYTVINEACPGAENWIMCRECCEDYDQIECVCPGRE 60
QY 61 VVGTYTPCCNEENECDSCLIHFGCTTFENCKSCRNCSWGGLTDDFFVYGFYCAECRAGW 120
DB 61 VVGTYTPCCNEENECDSCLIHFGCTTFENCKSCRNCSWGGLTDDFFVYGFYCAECRAGW 120
QY 121 YGGDCMRCGOVLAPKQGIILLESYPLNAHCEWTTHAKPGFVIOLRFVWLSLEFDYMCQYD 180
DB 121 YGGDCMRCGOVLAPKQGIILLESYPLNAHCEWTTHAKPGFVIOLRFVWLSLEFDYMCQYD 180
QY 181 YVEVRDGNRDGQIIKRVCGNERPAPISGSSHLVLFHSDGSKNFDGPHAIYEEITACS 240
DB 181 YVEVRDGNRDGQIIKRVCGNERPAPISGSSHLVLFHSDGSKNFDGPHAIYEEITACS 240
QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDPGPGVNGYKQTGGPGLI 300
DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTGQRCENLLEERNCSDPGPGVNGYKQTGGPGLI 300
QY 301 NGRHAKITGVVSPFCNNYSYVLSGNEKRTCOQNGSWGSKQPIKACREPKISDLVRRVL 360
DB 301 NGRHAKITGVVSPFCNNYSYVLSGNEKRTCOQNGSWGSKQPIKACREPKISDLVRRVL 360
QY 361 PMQVQSRETPHLQLYSAFQKQLQSAPTKKPALPFGDLPNGYQHLTLQYECISPFYR 420
DB 361 PMQVQSRETPHLQLYSAFQKQLQSAPTKKPALPFGDLPNGYQHLTLQYECISPFYR 420
QY 421 RLSSRRRTCLRTGKWSGRAPSCPIPCGKIENITAPKTQGLRWPAQAIYVRTSGVHDGSL 480
DB 421 RLSSRRRTCLRTGKWSGRAPSCPIPCGKIENITAPKTQGLRWPAQAIYVRTSGVHDGSL 480
QY 481 HKGAWFLVCSGALVNERVTVAACHVTDLGKVTMIKTADLKVVLGKFRDDEKTIQS 540

DB 481 HKGAWFLVCSGALVNERVTVAACHVTDLGKVTMIKTADLKVVLGKFRDDEKTIQS 540
QY 541 LOISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSSTFQESHITVAG 600
DB 541 LOISAIILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSSTFQESHITVAG 600
QY 601 WNVLADVRSPGFKNDTLRSQVSVVVDLSLLCEQHEDHGIPVSVTDNMFCASWEPTAPSDI 660
DB 601 WNVLADVRSPGFKNDTLRSQVSVVVDLSLLCEQHEDHGIPVSVTDNMFCASWEPTAPSDI 660
QY 661 CTAETGGIAAASFPGGRASPEPRWHLMLGLVMSYDKTCSHRLSTAFTKVLPFKDWIERNNK 720
DB 661 CTAETGGIAAASFPGGRASPEPRWHLMLGLVMSYDKTCSHRLSTAFTKVLPFKDWIERNNK 720
RESULT 4
AAB65218
ID AAB65218 standard; protein; 720 AA.
XX AAB65218;
XX 02-APR-2001 (first entry)
XX Human PRO1344 (UNQ699) protein sequence SEQ ID NO:231.
XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
XX cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay.
XX Homo sapiens.
XX WO200073454-A1.
XX 07-DEC-2000.
XX 30-MAR-2000; 2000WO-US008439.
XX 02-JUN-1999; 99WO-US012252.
XX 23-JUN-1999; 99US-0141037P.
XX 07-JUL-1999; 99US-0143048P.
XX 20-JUL-1999; 99US-0144758P.
XX 26-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 17-AUG-1999; 99US-0149396P.
XX 15-SEP-1999; 99WO-US021090.
XX 15-SEP-1999; 99WO-US021547.
XX 08-OCT-1999; 99US-0158663P.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 05-JAN-2000; 2000WO-US000219.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 22-FEB-2000; 2000WO-US004414.
XX 24-FEB-2000; 2000WO-US004914.
XX 02-MAR-2000; 2000WO-US005004.
XX 15-MAR-2000; 2000WO-US005841.
XX 20-MAR-2000; 2000WO-US006884.
XX 20-MAR-2000; 2000WO-US007377.
XX (GETH) GENENTECH INC.
XX Ashkenazi AV, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gurney AL, KJavin IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
XX Zhang Z;
XX WPI; 2001-032160/04.
XX N-PSDB; AAP44180.
XX

PT PRO polynucleotides used to produce polypeptides used to target bioactive
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.

PS Claim 12; Fig 159; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins can
XX be used for targeted delivery of bioactive molecules, such as toxins,
XX radiolabels or antibodies, that cause cell death. PRO nucleotide
XX sequences, and their fragments, can be used as hybridisation probes, in
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and
XX DNA. They may also be used to produce transgenic animals which are used
XX to develop and screen therapeutically useful reagents. The PRO nucleotide
XX and protein sequence can be used for tissue typing and in treating
XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
XX AAF44470 represent PCR primers and hybridisation probes used in the
XX isolation of human PRO sequences. AAF44087 to AAF44269 and AAF5151 to
XX AAF5300 represent human PRO polynucleotide and protein sequences given
XX in the exemplification of the present invention

SQ Sequence 720 AA;

Query Match	100.0%; Score 3945; DB 4; Length 720;
Best Local Similarity	100.0%; Pred. No. 1.28-204;
Matched 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MELGWTQLGLTFLQLLISLIPREYTVINEACPGAENWIMCRECEYDIECVCPGRRE 60	
DB 1 MELGWTQLGLTFLQLLISLIPREYTVINEACPGAENWIMCRECEYDIECVCPGRRE 60	
QY 61 VVGTYTPCRNEENECDSCLIHGCTTIFENCKSCRNCSGWTGTLDDPYKGYFCACRAGW 120	
DB 61 VVGTYTPCRNEENECDSCLIHGCTTIFENCKSCRNCSGWTGTLDDPYKGYFCACRAGW 120	
QY 121 YGDCMRGCGOVLRAKPGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMSLEFDMCYD 180	
DB 121 YGDCMRGCGOVLRAKPGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMSLEFDMCYD 180	
QY 181 YVEVDGDNRDGQIIKRVCGNERPAPIQISGSLHVLPHSDGSKNPDGFHAIYEITACS 240	
DB 181 YVEVDGDNRDGQIIKRVCGNERPAPIQISGSLHVLPHSDGSKNPDGFHAIYEITACS 240	
QY 241 SSPCFHDTGTCVLDKAGSKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI 300	
DB 241 SSPCFHDTGTCVLDKAGSKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLI 300	
QY 301 NGRHAKIGTVSVFFCNNSVYLSGNEKRTCCQNGEMSGKQPCIKACREPKISDLVRRVL 360	
DB 301 NGRHAKIGTVSVFFCNNSVYLSGNEKRTCCQNGEMSGKQPCIKACREPKISDLVRRVL 360	
QY 361 PMQVQSRTPHLQLYSAAFSKQLQSAPTKPKPALPFGDLPMGYQHLHTQLQYECISPFYR 420	
DB 361 PMQVQSRTPHLQLYSAAFSKQLQSAPTKPKPALPFGDLPMGYQHLHTQLQYECISPFYR 420	
QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHDGSL 480	
DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRTSGVHDGSL 480	
QY 481 HKGAFVLCSGALVNERTVVAACHVCTDLGKVTMTKTADLKVLGKPYRDDDRDEKTIQS 540	
DB 481 HKGAFVLCSGALVNERTVVAACHVCTDLGKVTMTKTADLKVLGKPYRDDDRDEKTIQS 540	
QY 541 LQISAILHPNVDPIILLADIAILKLLKARISTRVQPICLAASRDLSSTQESHITVAG 600	
DB 541 LQISAILHPNVDPIILLADIAILKLLKARISTRVQPICLAASRDLSSTQESHITVAG 600	
QY 601 MNVLADVRSPGKNDTLRSVVVSDSLCEQHDHGIPIVSVTDNMFCASWEPTAPSDI 660	
DB 601 MNVLADVRSPGKNDTLRSVVVSDSLCEQHDHGIPIVSVTDNMFCASWEPTAPSDI 660	
QY 661 CTAETGGIAAVSPGRASPEPRWHLMLGVLVSWSDYKTCSHRLSTAFTKVLFPKDWIERNMK 720	

661 CTAETGGIAAVSPGRASPEPRWHLMLGVLVSWSDYKTCSHRLSTAFTKVLFPKDWIERNMK 720

RESULT 5

ABG95869
ID ABG95869 standard; protein; 720 AA.

XX AC ABG95869;

XX DT 10-DEC-2002 (first entry)

XX DE Human secreted/transmembrane protein PRO1344.

XX KW Human; secreted protein; transmembrane protein; antirheumatic;
XX antiarthritic; osteopathic; sports-related joint problem;
XX articular cartilage defect; osteoarthritis; rheumatoid arthritis.

XX OS Homo sapiens.

XX PN US2002119130-A1.

XX PD 29-AUG-2002.

XX PF 06-DEC-2001; 2001US-00006867.

XX PR 29-OCT-1997; 97US-0063435P.

XX PR 29-OCT-1997; 97US-0064215P.

XX PR 22-APR-1998; 98US-0082797P.

XX PR 29-APR-1998; 98US-0083495P.

XX PR 15-MAY-1998; 98US-0085579P.

XX PR 02-JUN-1998; 98US-0087759P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088029P.

XX PR 04-JUN-1998; 98US-0088030P.

XX PR 10-JUN-1998; 98US-0088734P.

XX PR 10-JUN-1998; 98US-0088740P.

XX PR 10-JUN-1998; 98US-0088811P.

XX PR 10-JUN-1998; 98US-0088824P.

XX PR 10-JUN-1998; 98US-0088825P.

XX PR 11-JUN-1998; 98US-0088863P.

XX PR 12-JUN-1998; 98US-0089105P.

XX PR 16-JUN-1998; 98US-0089514P.

XX PR 17-JUN-1998; 98US-0089653P.

XX PR 19-JUN-1998; 98US-0089952P.

XX PR 22-JUN-1998; 98US-0090246P.

XX PR 24-JUN-1998; 98US-0090444P.

XX PR 25-JUN-1998; 98US-0090688P.

XX PR 25-JUN-1998; 98US-0090696P.

XX PR 26-JUN-1998; 98US-0090862P.

XX PR 02-JUL-1998; 98US-0091628P.

XX PR 10-AUG-1998; 98US-0096012P.

XX PR 17-AUG-1998; 98US-0096757P.

XX PR 18-AUG-1998; 98US-0096949P.

XX PR 18-AUG-1998; 98US-0096959P.

XX PR 26-AUG-1998; 98US-0097954P.

XX PR 26-AUG-1998; 98US-0097971P.

XX PR 26-AUG-1998; 98US-0097979P.

XX PR 01-SEP-1998; 98US-0098749P.

XX PR 10-SEP-1998; 98US-0099741P.

XX PR 10-SEP-1998; 98US-0099763P.

XX PR 10-SEP-1998; 98US-0099792P.

XX PR 10-SEP-1998; 98US-0099812P.

XX PR 10-SEP-1998; 98US-0099815P.

XX PR 16-SEP-1998; 98US-0100627P.

XX PR 16-SEP-1998; 98US-0100662P.

XX PR 16-SEP-1998; 98US-0100683P.

XX PR 17-SEP-1998; 98US-0100684P.

XX PR 17-SEP-1998; 98US-0100684P.

XX PR 17-SEP-1998; 98US-0100930P.

XX PR 22-SEP-1998; 98US-0101279P.

XX PR 23-SEP-1998; 98US-0101475P.

XX PR 24-SEP-1998; 98US-0101738P.

XX PR 24-SEP-1998; 98US-0101743P.

PR 24-SEP-1998; 98US-0101916P.
 PR 30-SEP-1998; 98US-0102570P.
 PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012852.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 22-DEC-1999; 99WO-US021194.
 PR 18-FEB-2000; 99WO-US030720.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 22-FEB-2000; 2000WO-US004342.
 PR 01-MAR-2000; 2000WO-US004414.
 PR 30-MAR-2000; 2000WO-US005601.
 PR 02-MAY-2000; 2000WO-US008439.
 PR 22-JUN-2000; 2000WO-US014042.
 PR 23-AUG-2000; 2000WO-US015264.
 PR 24-AUG-2000; 2000WO-US023522.
 PR 10-NOV-2000; 2000WO-US023328.
 PR 01-DEC-2000; 2000WO-US030873.
 PR 20-DEC-2000; 2000WO-US032378.
 PR 28-FEB-2001; 2000WO-US034956.
 PR 01-MAR-2001; 2001WO-US006520.
 PR 30-MAY-2001; 2001WO-US006666.
 PR 01-JUN-2001; 2001WO-US017443.
 PR 20-JUN-2001; 2001WO-US017800.
 PR 29-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021066.
 PR 2001WO-US021735.
 XX

(GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;
 XX

DR WPI; 2002-731348/79.

DR N-PSDB; ABS74396.

XX New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.

XX Claim 20; Fig 38; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95851-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5801
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC PRO20233 polypeptide and I is a PRO1890 polypeptide. The sample comprises
 CC a cell suspected of expressing the A, B, C or D polypeptide. The E, F, G,
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis

CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid
 CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence represents a novel secreted or transmembrane protein of the
 CC invention

XX SQ Sequence 720 AA;

Query Match 100.0%; Score 3945; DB 5; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.2e-204;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MELGWTQLGLTFLQLLLISSLPREYTVINACPGAENIMCRECEYDQIECVCPGKRE 60
 DB 1 MELGWTQLGLTFLQLLLISSLPREYTVINACPGAENIMCRECEYDQIECVCPGKRE 60
 QY 61 VGYTIPCRNEECDSCLIHPCGCTIIFENCKSCNCSWGGLTDDFYVKGFCACRAGW 120
 DB 61 VGYTIPCRNEECDSCLIHPCGCTIIFENCKSCNCSWGGLTDDFYVKGFCACRAGW 120
 QY 121 YGGDCMRGQVLRAPKGQILLESYPLNAHCWTHAKPGFVIQLRFVWMLSEFDYWCQVD 180
 DB 121 YGGDCMRGQVLRAPKGQILLESYPLNAHCWTHAKPGFVIQLRFVWMLSEFDYWCQVD 180
 QY 181 YVEVRDGNRDGQIIKRVCGNERPAPIQISGLSHLVFHSKGNFDFGFAIYEITACS 240
 DB 181 YVEVRDGNRDGQIIKRVCGNERPAPIQISGLSHLVFHSKGNFDFGFAIYEITACS 240
 QY 241 SSPCFHDCVLDKAGSYKCAKLAGYTGRCENLLEERNCSDDPGPVNGYQKITGGGLI 300
 DB 241 SSPCFHDCVLDKAGSYKCAKLAGYTGRCENLLEERNCSDDPGPVNGYQKITGGGLI 300
 QY 301 NGRHAKIGTVWSFFCNNSYVLSGNEKRTCCQNGWSGKQPIKACREPKISDLVRRVRL 360
 DB 301 NGRHAKIGTVWSFFCNNSYVLSGNEKRTCCQNGWSGKQPIKACREPKISDLVRRVRL 360
 QY 361 PMQVOSRETPHLQLYSAAFSKQKLOSAPTKPKALPFGDLPMGYQHLTQLQYECISPFYR 420
 DB 361 PMQVOSRETPHLQLYSAAFSKQKLOSAPTKPKALPFGDLPMGYQHLTQLQYECISPFYR 420
 QY 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRRTSGVHDGSL 480
 DB 421 RLGSRRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRRTSGVHDGSL 480
 QY 481 HKGAWFLVCSGALVNERVTWVAACHCVTDLGKVTMIKTADLKVLGKPYRDDDDREKTIQS 540
 DB 481 HKGAWFLVCSGALVNERVTWVAACHCVTDLGKVTMIKTADLKVLGKPYRDDDDREKTIQS 540
 QY 541 LOISAILHPNVDPIILLDADITAILKLLDKARISTRVQPICLAASRDLSSTFOESHITVAG 600
 DB 541 LOISAILHPNVDPIILLDADITAILKLLDKARISTRVQPICLAASRDLSSTFOESHITVAG 600
 QY 601 MNVLADVRSFGPKNDTLRSVVVSDSLLCBEQHDHGI PVSVTDNMFCASWEPTAPSDI 660
 DB 601 MNVLADVRSFGPKNDTLRSVVVSDSLLCBEQHDHGI PVSVTDNMFCASWEPTAPSDI 660
 QY 661 CTATGGIAAASFPGRASPEPRWHLMLGLSVSYDKTCSHRLSTAFTKVLFPFKDWIERNMK 720
 DB 661 CTATGGIAAASFPGRASPEPRWHLMLGLSVSYDKTCSHRLSTAFTKVLFPFKDWIERNMK 720

RESULT 6

ABU58484

ID ABU58484 standard; protein; 720 AA.

XX

AC ABU58484;

XX 15-APR-2003 (first entry) PR 22-MAY-1998; 98US-0086486P.
DT 28-MAY-1998; 98US-0087098P.
TX 28-MAY-1998; 98US-0087208P.
DE 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
KW 03-JUN-1998; 98US-0087827P.
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT; 98US-0088025P.
KW antibody-dependent enzyme mediated prodrug therapy. 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.
OS Homo sapiens. 98US-0088033P.
XX 04-JUN-1998; 98US-0088326P.
XX 04-JUN-1998; 98US-0088167P.
PN 05-JUN-1998; 98US-0088202P.
XX 05-JUN-1998; 98US-0088212P.
XX 05-JUN-1998; 98US-0088217P.
XX 09-JUN-1998; 98US-0088655P.
XX 10-JUN-1998; 98US-0088722P.
XX 10-JUN-1998; 98US-0088738P.
XX 10-JUN-1998; 98US-0088740P.
XX 10-JUN-1998; 98US-0088811P.
XX 10-JUN-1998; 98US-0088824P.
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XX 22-JUN-1998; 98US-0090252P.
XX 22-JUN-1998; 98US-0090254P.
XX 24-JUN-1998; 98US-0090429P.
XX 24-JUN-1998; 98US-0090435P.
XX 24-JUN-1998; 98US-0090444P.
XX 24-JUN-1998; 98US-0090461P.
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XX 24-JUN-1998; 98US-0090540P.
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XX 25-JUN-1998; 98US-0090694P.
XX 25-JUN-1998; 98US-0090695P.
XX 25-JUN-1998; 98US-0090696P.
XX 26-JUN-1998; 98US-00105413.
XX 26-JUN-1998; 98US-0090862P.
XX 26-JUN-1998; 98US-0090863P.
XX 26-JUN-1998; 98US-0091010P.
XX 01-JUL-1998; 98US-0091359P.
XX 01-JUL-1998; 98US-0091544P.
XX 02-JUL-1998; 98US-0091478P.
XX 02-JUL-1998; 98US-0091486P.
XX 02-JUL-1998; 98US-0091626P.
XX 02-JUL-1998; 98US-0091628P.
XX 02-JUL-1998; 98US-0091632P.
XX 24-JUL-1998; 98US-0094006P.
XX 04-AUG-1998; 98US-0095282P.
XX 10-AUG-1998; 98US-0095998P.
XX 10-AUG-1998; 98US-0096012P.
XX 17-AUG-1998; 98US-0096757P.
XX 17-AUG-1998; 98US-0096766P.
XX 17-AUG-1998; 98US-0096867P.
XX 17-AUG-1998; 98US-0096891P.
XX 17-AUG-1998; 98US-0096897P.
XX 18-AUG-1998; 98US-0096949P.
XX 18-AUG-1998; 98US-0096959P.

PR 11-DEC-1997; 97US-00693335P.
PR 12-DEC-1997; 97US-00694252P.
PR 17-DEC-1997; 97US-00698707P.
PR 18-DEC-1997; 97US-00680177P.
PR 10-MAR-1998; 98US-00774507P.
PR 11-MAR-1998; 98US-00776322P.
PR 11-MAR-1998; 98US-00778499P.
PR 20-MAR-1998; 98US-00788866P.
PR 20-MAR-1998; 98US-00789399P.
PR 27-MAR-1998; 98US-00796642P.
PR 27-MAR-1998; 98US-00797866P.
PR 31-MAR-1998; 98US-00801077P.
PR 31-MAR-1998; 98US-00801942P.
PR 01-APR-1998; 98US-00803277P.
PR 01-APR-1998; 98US-00803333P.
PR 08-APR-1998; 98US-00810499P.
PR 08-APR-1998; 98US-00810707P.
PR 09-APR-1998; 98US-00811959P.
PR 15-APR-1998; 98US-00818388P.
PR 21-APR-1998; 98US-00825688P.
PR 21-APR-1998; 98US-00825699P.
PR 22-APR-1998; 98US-00827042P.
PR 22-APR-1998; 98US-00827977P.
PR 28-APR-1998; 98US-00833222P.
PR 29-APR-1998; 98US-00834959P.
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PR 29-APR-1998; 98US-00834999P.
PR 29-APR-1998; 98US-00835599P.
PR 05-MAY-1998; 98US-00843666P.
PR 06-MAY-1998; 98US-00844142P.
PR 07-MAY-1998; 98US-00846399P.
PR 07-MAY-1998; 98US-00846402P.
PR 07-MAY-1998; 98US-00846433P.
PR 15-MAY-1998; 98US-00855799P.
PR 15-MAY-1998; 98US-00855802P.
PR 15-MAY-1998; 98US-00855822P.
PR 18-MAY-1998; 98US-00860232P.
PR 22-MAY-1998; 98US-00865922P.
PR 22-MAY-1998; 98US-00866486P.
PR 28-MAY-1998; 98US-00870988P.
PR 28-MAY-1998; 98US-00872088P.
PR 02-JUN-1998; 98US-00876099P.
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PR 04-JUN-1998; 98US-00880333P.
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PR 05-JUN-1998; 98US-00884122P.
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PR 10-JUN-1998; 98US-00887222P.
PR 10-JUN-1998; 98US-00887388P.
PR 10-JUN-1998; 98US-00887402P.
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PR 10-JUN-1998; 98US-00888242P.
PR 10-JUN-1998; 98US-00888259P.
PR 10-JUN-1998; 98US-00888262P.
PR 11-JUN-1998; 98US-00888612P.
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PR 12-JUN-1998; 98US-00890909P.
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PR 18-JUN-1998; 98US-00899088P.
PR 19-JUN-1998; 98US-00899522P.
PR 22-JUN-1998; 98US-00902466P.
PR 22-JUN-1998; 98US-00902522P.
PR 22-JUN-1998; 98US-00902542P.
PR 24-JUN-1998; 98US-00904292P.
PR 24-JUN-1998; 98US-00904359P.
PR 24-JUN-1998; 98US-00904442P.
PR 24-JUN-1998; 98US-00904612P.
PR 24-JUN-1998; 98US-00905359P.
PR 24-JUN-1998; 98US-00905402P.
PR 25-JUN-1998; 98US-00906766P.
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Query Match		100.0%;	Score 3945;	DB 6;	Length 720;
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Qy	61	VVGTYTPCCNEECDSCLIHPCGCTIFENCKSCRNCSWGGLTDDFYVKGFCYCAECRAGW	120		
Db	61	VVGTYTPCCNEECDSCLIHPCGCTIFENCKSCRNCSWGGLTDDFYVKGFCYCAECRAGW	120		
Qy	121	YGGDCMRCGOVLAPKGOILLESYPLNAHCEWTHAKPGFVIQLRFVMLSLEFDYMCQYD	180		
Db	121	YGGDCMRCGOVLAPKGOILLESYPLNAHCEWTHAKPGFVIQLRFVMLSLEFDYMCQYD	180		
Qy	181	YVEVRDGDNRDGOIIRKVCNGNERPAPISQSSLSHLVLFHSDGSKNFDGFHAIYEEITACS	240		
Db	181	YVEVRDGDNRDGOIIRKVCNGNERPAPISQSSLSHLVLFHSDGSKNFDGFHAIYEEITACS	240		
Qy	241	SSPCFHDGTCVLKAGSYKACLAGYTGQRCENLLBERNCSDPGPVNGYQKITGGPGLI	300		
Db	241	SSPCFHDGTCVLKAGSYKACLAGYTGQRCENLLBERNCSDPGPVNGYQKITGGPGLI	300		
Qy	301	NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWSGKQPIKACREPKISDLVRRRL	360		
Db	301	NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWSGKQPIKACREPKISDLVRRRL	360		
Qy	361	PMQVQSRTEPLHQLYSAAFSKQLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYR	420		
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Qy	421	RLGSSRRTCURTGWGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL	480		
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Qy	481	HKGAWFLVCSGALVNRVTVAACHVTDLGKVTMIKTADLKVLFYRDDDRDEKTIQS	540		
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Qy	541	LQISAILHPNYDPIILDADIALKLDKARISTRVQPICLAASRDLSSTFQESHITVAG	600		
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Qy	601	WNVLADVRSFGKNDTLRSQVSVSDLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDI	660		
Db	601	WNVLADVRSFGKNDTLRSQVSVSDLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDI	660		
Qy	661	CTAETGGIAAVSPFGRASPRVHLMGLVSWSDYDKTCSHRLSTAFKVLFPFKDWIERNMK	720		
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RESULT 8
ABU84347
ID ABU84347 standard; protein; 720 AA.
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AC	ABU84347;
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DT	02-AUG-2003 (first entry)
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DE	Human secreted/transmembrane protein (PRO) #85.
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KW	Human; secreted and transmembrane protein; PRO; TNF-alpha;
KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
XX	tissue typing.
OS	Homo sapiens.
XX	
PN	US2003032112-A1.
XX	
PD	13-FEB-2003.
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PF	21-JUN-2002; 2002US-00176756.
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			Best Local Similarity		100.0%;
			Pred. No. 1.2e-204;		
			Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
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Db	1	MELGCTOLGTLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKRE	60		
QY	61	VVGYTIPCCRNEECDSLIHPGCTIPENCKSCRNGSWGTLDDFYVKGFCACRAGW	120		
Db	61	VVGYTIPCCRNEECDSLIHPGCTIPENCKSCRNGSWGTLDDFYVKGFCACRAGW	120		
QY	121	YGGDCMRCQVLRAPKQILLESYPLNAHCEWTTHAKPGFVIQLRFVMLSLFEDYMCQYD	180		
Db	121	YGGDCMRCQVLRAPKQILLESYPLNAHCEWTTHAKPGFVIQLRFVMLSLFEDYMCQYD	180		
QY	181	YVEVRDGNRDGQIIRKVCGNERPAPIQSIGSSLHLVLFHSDGSKNFDGFHAIYBEITACS	240		
Db	181	YVEVRDGNRDGQIIRKVCGNERPAPIQSIGSSLHLVLFHSDGSKNFDGFHAIYBEITACS	240		

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 DB 481 HKGAWFLVCSGALNVNRTVVAAHCVTDLGKVTMTADLKVLFKPYRDDRDEKTIOS 540
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 QY 661 CTAETGGIAAVSPFGGRASPEPRWHLMLGLVSWSDYDKTCSHRLSTAFKVLFPFKDWIERNMK 720
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RESULT 9

ABR66221
 ID ABR66221 standard; protein; 720 AA.

XX AC ABR66221;

XX DT 05-AUG-2003 (first entry)

XX DE Human secreted polypeptide PRO1344, SEQ ID NO:170.

XX KW Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnery; gene therapy.

XX OS Homo sapiens.

XX PN US2003027278-A1.

XX PD 06-FEB-2003.

XX PF 21-JUN-2002; 2002US-00176987.

XX PR 18-SEP-1997; 97US-0059263P.

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XX PR 17-OCT-1997; 97US-0062250P.

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QY	121	YGGDCMRCQVLRAPKQI	LLSSYPLNAHCETTHAKPGFVIQLRFVWLSLEFDMCOYD	180			
DB	121	YGGDCMRCQVLRAPKQI	LLSSYPLNAHCETTHAKPGFVIQLRFVWLSLEFDMCOYD	180			
QY	181	YVEVRDGNRDQGIKRV	CGNERPAPIQSIGSSLHVLFHS	DGSKNFDGFHAIYEEITACS	240		
DB	181	YVEVRDGNRDQGIKRV	CGNERPAPIQSIGSSLHVLFHS	DGSKNFDGFHAIYEEITACS	240		
QY	241	SSPCFHDGTCVLDKAGSYKCA	CLAGYTGQRCE	NLLFEERNCSDDPGPNVGYOKITGGPGLI	300		
DB	241	SSPCFHDGTCVLDKAGSYKCA	CLAGYTGQRCE	NLLFEERNCSDDPGPNVGYOKITGGPGLI	300		
QY	301	NGRHAKIGTVVVSFFC	NNNSYVLSGNEKRTCQ	ONGSWSGKQPICIKACREPKISDLVRRVL	360		
DB	301	NGRHAKIGTVVVSFFC	NNNSYVLSGNEKRTCQ	ONGSWSGKQPICIKACREPKISDLVRRVL	360		
QY	361	PMQVQSRETPHLQLYSAAFS	SKQLQSAPTKPPALPFGD	PMGYOHLHTQLQYECISPFYR	420		
DB	361	PMQVQSRETPHLQLYSAAFS	SKQLQSAPTKPPALPFGD	PMGYOHLHTQLQYECISPFYR	420		
QY	421	RLGSSRRTCLRTGKWSGRAP	SCIPICGKIENITAPKTQGLRW	PAQAIYRTSGVHDGSL	480		
DB	421	RLGSSRRTCLRTGKWSGRAP	SCIPICGKIENITAPKTQGLRW	PAQAIYRTSGVHDGSL	480		
QY	481	HKGAWFLVCSGALVNER	VVAACHVTDLGKVTMIKTADL	KVVLGKVFYRDDDRDEKTIQS	540		
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chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; Genetic analysis;
antiarthritic; vulnery; gene therapy.

Homo sapiens.

US2003036159-A1.

20-FEB-2003.

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PR	17-AUG-1998;	98US-0096757P.	PR	24-AUG-2000;	2000US-02023328.
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Db	1	MEGCGWTQGLTFLQILLISSLPREVTINEACPGAEMNIMCRECCCEYDQIECVCPGKRE	Db	1	YGGDCMRCQGVLRAPKGQILLESYPLNARCEWTHAKPGFVILRFVMLSLEFDYMCQYD
Qy	61	VVGYTIPCCRNEENECDSCLIHFGCTIFENCKSCRNGSWGTLDDFFVYKGFYCAECRAGW	Qy	121	YGGDCMRCQGVLRAPKGQILLESYPLNARCEWTHAKPGFVILRFVMLSLEFDYMCQYD
Db	61	VVGYTIPCCRNEENECDSCLIHFGCTIFENCKSCRNGSWGTLDDFFVYKGFYCAECRAGW	Db	121	YGGDCMRCQGVLRAPKGQILLESYPLNARCEWTHAKPGFVILRFVMLSLEFDYMCQYD
Qy	181	YVEVRDGNDRDGOIKKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFGPHAIYEITACS	Qy	181	YVEVRDGNDRDGOIKKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFGPHAIYEITACS

Query Match 100.0%; Score 3945; DB 6; Length 720;
 Best Local Similarity 100.0%; Pred. No. 1.2e-204;
 Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	181	YVEVRDGNDRQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNDFGHAIYEITACS	240	PR	07-MAY-1998;	98US-0084600P.
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Db	241	SSPCFHDGTCLVDKAGSYKACLAGVTGRCNLEERNCSDPGPGVNGYQKITGGPGLI	300	PR	02-JUN-1998;	98US-0087607P.
Qy	301	NGRHAKIGTVVSFFCNNSYVLSGNEKRTQQNGWSGKQPCIKACREPKISDLVRRVRL	360	PR	02-JUN-1998;	98US-0087609P.
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Qy	361	PNQVOSRETLHOLYSAPSKOKLOSAPTKKALPFGDLPMGYQHLLTQLOVEICISPFYR	420	PR	03-JUN-1998;	98US-0087827P.
Db	361	PNQVOSRETLHOLYSAPSKOKLOSAPTKKALPFGDLPMGYQHLLTQLOVEICISPFYR	420	PR	04-JUN-1998;	98US-0088021P.
Qy	421	RLGSSRRTRCLRTKWSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRRTSGVHDGSL	480	PR	04-JUN-1998;	98US-0088025P.
Db	421	RLGSSRRTRCLRTKWSGRAPSCIPICGKIENITAPKTQGLRMPQAAIYRRTSGVHDGSL	480	PR	04-JUN-1998;	98US-0088026P.
Qy	481	HKGAFPLVCSGALVNERTVVAACHVTDLGKVTMIKTADLKVVLGKPYRDDDRDKTIQS	540	PR	04-JUN-1998;	98US-0088028P.
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Qy	541	LOISAILHPNDPILLDADIALLKLDKARISTRVQICLAASRDLSFQESHITVAG	600	PR	04-JUN-1998;	98US-0088030P.
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Db	601	MNVLDVRSFGPKNDTLRSVVSVVDSLLCEQHEHDGIPVSVTDNMFCASWEPTAPSDI	660	PR	05-JUN-1998;	98US-0088167P.
Qy	661	CTAETGGIAAVSFPGRASPEPRHMLGLVSWSYDKTCSHRLSTAFKVLPPKDWIERNMK	720	PR	05-JUN-1998;	98US-0088202P.
Db	661	CTAETGGIAAVSFPGRASPEPRHMLGLVSWSYDKTCSHRLSTAFKVLPPKDWIERNMK	720	PR	05-JUN-1998;	98US-0088212P.
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XX	ABUS9111;					
DT	28-APR-2003	(first entry)				
DE	Novel human secreted or transmembrane protein PRO1344.					
XX	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;					
KW	cardiac insufficiency disorder; cancer; tumour; immune response;					
KW	adrenal cortical capillary endothelial growth; c-fos induction;					
KW	vascular endothelial growth factor inhibition; VEGF inhibition;					
KW	endothelial cell growth inhibitor; T-lymphocytes stimulation;					
KW	retinal neurons cell survival; rod photoreceptor cell survival;					
KW	retinal disorder; retinitis pigmentosa; kidney disease;					
KW	mammalian kidney mesangial cell proliferation; Berger disease;					
KW	dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;					
XX	chondrocyte redifferentiation; sports injury; arthritis.					
OS	Homo sapiens.					
XX	US2002132252-A1.					
PN	19-SEP-2002.					
PD	14-NOV-2001; 2001US-00990442.					
PP	16-JUN-1997; 97US-0049787P.					
XX	17-OCT-1997; 97US-0062250P.					
PR	05-NOV-1997; 97WO-US020069.					
PR	12-NOV-1997; 97US-0065186P.					
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PR	20-MAR-1998; 98US-0078910P.					
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PR	28-JUL-2000;					

11-AUG-2000; 2000MO-US022031.
 23-AUG-2000; 2000MO-US023522.
 24-AUG-2000; 2000MO-US023328.
 08-NOV-2000; 2000MO-US030952.
 01-DEC-2000; 2000MO-US032678.
 28-FEB-2001; 2001MO-US0008520.
 01-JUN-2001; 2001MO-US017800.
 20-JUN-2001; 2001MO-US019692.
 29-JUN-2001; 2001MO-US021066.
 09-JUL-2001; 2001MO-US021735.
 28-AUG-2001; 2001US-00941992.
 (GETH) GENENTECH INC.
 Auhkonazi AJ, Baker KP, Botstein D, Deenoyers L, Baton DL;
 Forrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 Grimaldi JC, Gurney AL, Kijavini TJ, Napier MA, Pan J, Paoni NF;
 Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 Zhang Z;
 WPI; 2003-247083/24.
 N-PSDB; ABX80270.
 Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
 are therapeutically useful for enhancing immune response and in cancer
 treatments.
 Claim 12; Fig 159; 648pp; English.
 The invention describes an isolated human PRO polypeptide. The PRO
 polypeptides are useful in detecting PRO polypeptides in a sample, in
 linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 in modulating at least one biological activity of a cell expressing a PRO
 polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 stimulate adrenal cortical capillary endothelial growth, and PRO336,
 PRO943, PRO828, PRO1068 or PRO335, PRO826, PRO819, PRO1126,
 PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 useful for treating conditions or disorders where angiogenesis would be
 beneficial, e.g. wound healing and antagonist of this polypeptide are
 useful for treating cancerous tumours. PRO812 inhibits vascular
 endothelial growth factor (VEGF) stimulated proliferation of endothelial
 cells and is thus useful for inhibiting endothelial cell growth in
 mammals which would be beneficial in inhibiting tumour growth. PRO826,
 PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
 stimulated T-lymphocytes and are therapeutically useful for enhancing
 immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
 retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 rod photoreceptor cells) and therefore are useful for treating retinal
 disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813
 and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 and therefore are useful for treating kidney disorders associated with
 decreased mesangial cell function such as Berger disease or other
 nephropathies associated with dermatitis, herpeticiformis or Crohn's
 disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 proliferation and/or redifferentiation of chondrocytes in culture and are
 thus useful for treating sports injuries, and arthritis. This is the
 amino acid sequence of a novel human PRO protein

121 YGDCMRCQVLRAPKQQLLESYFLNAHCEWTIIHAKPGFVIQLRFVMSLSEFDYMCQYD 180
 121 YGDCMRCQVLRAPKQQLLESYFLNAHCEWTIIHAKPGFVIQLRFVMSLSEFDYMCQYD 180
 181 YVEVRDGNDRGOIIRKVCGRNERPAPIOSIGSLHVLHSDGSKNFDGPHAYEEITACS 240
 181 YVEVRDGNDRGOIIRKVCGRNERPAPIOSIGSLHVLHSDGSKNFDGPHAYEEITACS 240
 241 SSPCFHDGTCLVDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGPGGLI 300
 241 SSPCFHDGTCLVDKAGSYKACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGPGGLI 300
 301 NGRHAKIGTVVSVFFCNNSVYLSGNEKRTCCQNGESGKQPCICIKACREPKISDLVRRVRL 360
 301 NGRHAKIGTVVSVFFCNNSVYLSGNEKRTCCQNGESGKQPCICIKACREPKISDLVRRVRL 360
 361 PMQVOSRETPHLHOLYSAAFSKQIASAPTKKPALPGDLPMGVOHLHTLOQECISPFYR 420
 361 PMQVOSRETPHLHOLYSAAFSKQIASAPTKKPALPGDLPMGVOHLHTLOQECISPFYR 420
 421 RLGSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480
 421 RLGSRRRTCLRTGKMSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSL 480
 481 HGWFLVCSGALVNERVTVVAAHCVTDLGKVTMIKTADLKVVLGKFPYRDDDRDEKTIQS 540
 481 HGWFLVCSGALVNERVTVVAAHCVTDLGKVTMIKTADLKVVLGKFPYRDDDRDEKTIQS 540
 541 LOISAILHPNYDPTILLADIAILKLLDKARISTRVQPICLAASRDLSSTFQESHITVAG 600
 541 LOISAILHPNYDPTILLADIAILKLLDKARISTRVQPICLAASRDLSSTFQESHITVAG 600
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 DT 26-JUN-2002 (first entry)
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 KW kidney's disease; Berger disease; nephropathy; dermatitis; herpeticiformis;
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Search completed: August 18, 2004, 16:23:42
 Job time : 63 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:16:43 ; Search time 50 Seconds
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4520.551 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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21	3945	100.0	720	10	US-09-989-734-231	Sequence 231, App
22	3945	100.0	720	10	US-09-997-653-231	Sequence 231, App
23	3945	100.0	720	10	US-09-993-867-231	Sequence 231, App
24	3945	100.0	720	10	US-09-997-428-231	Sequence 231, App
25	3945	100.0	720	10	US-09-997-666-231	Sequence 231, App
26	3945	100.0	720	10	US-09-990-438-231	Sequence 231, App
27	3945	100.0	720	10	US-09-990-562-231	Sequence 231, App
28	3945	100.0	720	10	US-09-990-711-231	Sequence 231, App
29	3945	100.0	720	10	US-09-989-726-231	Sequence 231, App
30	3945	100.0	720	10	US-09-998-156-231	Sequence 231, App
31	3945	100.0	720	10	US-09-990-437-231	Sequence 231, App
32	3945	100.0	720	10	US-09-991-157-231	Sequence 231, App
33	3945	100.0	720	10	US-09-997-514-231	Sequence 231, App
34	3945	100.0	720	10	US-09-997-573-231	Sequence 231, App
35	3945	100.0	720	10	US-09-991-172-231	Sequence 231, App
36	3945	100.0	720	10	US-09-990-726-231	Sequence 231, App
37	3945	100.0	720	10	US-09-997-559-231	Sequence 231, App
38	3945	100.0	720	10	US-09-997-601-231	Sequence 231, App
39	3945	100.0	720	10	US-09-990-443-231	Sequence 231, App
40	3945	100.0	720	10	US-09-991-854-231	Sequence 231, App
41	3945	100.0	720	10	US-09-997-628-231	Sequence 231, App
42	3945	100.0	720	10	US-09-997-683-231	Sequence 231, App
43	3945	100.0	720	10	US-09-989-729A-231	Sequence 231, App
44	3945	100.0	720	10	US-09-997-349-231	Sequence 231, App
45	3945	100.0	720	10	US-09-997-440-231	Sequence 231, App
46	3945	100.0	720	10	US-09-990-440-231	Sequence 231, App
47	3945	100.0	720	10	US-09-993-469-231	Sequence 231, App
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49	3945	100.0	720	10	US-09-993-748-231	Sequence 231, App
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51	3945	100.0	720	10	US-09-990-427-231	Sequence 231, App
52	3945	100.0	720	10	US-09-989-328-231	Sequence 231, App
53	3945	100.0	720	10	US-09-993-583-231	Sequence 231, App
54	3945	100.0	720	10	US-09-941-992-231	Sequence 231, App
55	3945	100.0	720	10	US-09-992-521-231	Sequence 231, App
56	3945	100.0	720	10	US-09-997-333-231	Sequence 231, App
57	3945	100.0	720	10	US-09-997-384-231	Sequence 231, App
58	3945	100.0	720	10	US-09-998-041-231	Sequence 231, App
59	3945	100.0	720	10	US-09-997-585-231	Sequence 231, App
60	3945	100.0	720	10	US-09-997-614-231	Sequence 231, App
61	3945	100.0	720	10	US-09-989-862-231	Sequence 231, App
62	3945	100.0	720	10	US-09-997-529-231	Sequence 231, App
63	3945	100.0	720	10	US-09-989-725-231	Sequence 231, App
64	3945	100.0	720	11	US-09-989-733-231	Sequence 231, App
65	3945	100.0	720	11	US-09-992-643-231	Sequence 231, App
66	3945	100.0	720	12	US-10-206-915-170	Sequence 170, App
67	3945	100.0	720	12	US-10-199-670-170	Sequence 170, App
68	3945	100.0	720	12	US-10-201-858-170	Sequence 170, App
69	3945	100.0	720	12	US-10-205-890-170	Sequence 170, App
70	3945	100.0	720	12	US-10-208-024-170	Sequence 170, App
71	3945	100.0	720	12	US-10-201-853-170	Sequence 170, App
72	3945	100.0	720	12	US-10-063-745-38	Sequence 38, Appl
73	3945	100.0	720	12	US-09-989-724-231	Sequence 231, App
74	3945	100.0	720	12	US-09-989-728-231	Sequence 231, App
75	3945	100.0	720	12	US-09-990-441-231	Sequence 231, App
76	3945	100.0	720	12	US-10-063-512-38	Sequence 38, Appl
77	3945	100.0	720	12	US-10-063-513-38	Sequence 38, Appl
78	3945	100.0	720	12	US-10-063-515-38	Sequence 38, Appl
79	3945	100.0	720	12	US-10-063-549-38	Sequence 38, Appl
80	3945	100.0	720	12	US-10-063-569-38	Sequence 38, Appl
81	3945	100.0	720	12	US-10-063-551-38	Sequence 38, Appl
82	3945	100.0	720	12	US-10-174-581-170	Sequence 170, App
83	3945	100.0	720	12	US-10-176-483-170	Sequence 170, App
84	3945	100.0	720	12	US-10-176-749-170	Sequence 170, App
85	3945	100.0	720	12	US-10-176-914-170	Sequence 170, App
86	3945	100.0	720	12	US-10-176-915-170	Sequence 170, App
87	3945	100.0	720	12	US-09-997-857-231	Sequence 231, App
88	3945	100.0	720	12	US-10-063-555-38	Sequence 38, Appl

89	3945	100.0	720	12	US-10-063-563-38	Sequence 38, App1	162	3945	100.0	720	14	US-10-184-658-170	Sequence 170, App
90	3945	100.0	720	12	US-10-063-594-38	Sequence 38, App1	163	3945	100.0	720	14	US-10-176-991-170	Sequence 170, App
91	3945	100.0	720	12	US-10-063-553-38	Sequence 38, App1	164	3945	100.0	720	14	US-10-173-695-170	Sequence 170, App
92	3945	100.0	720	12	US-10-063-554-38	Sequence 38, App1	165	3945	100.0	720	14	US-10-173-697-170	Sequence 170, App
93	3945	100.0	720	12	US-10-176-484-170	Sequence 170, App	166	3945	100.0	720	14	US-10-173-705-170	Sequence 170, App
94	3945	100.0	720	12	US-10-180-550-170	Sequence 170, App	167	3945	100.0	720	14	US-10-174-576-170	Sequence 170, App
95	3945	100.0	720	12	US-10-183-014-170	Sequence 170, App	168	3945	100.0	720	14	US-10-174-585-170	Sequence 170, App
96	3945	100.0	720	12	US-10-187-738-170	Sequence 170, App	169	3945	100.0	720	14	US-10-174-586-170	Sequence 170, App
97	3945	100.0	720	12	US-10-187-740-170	Sequence 170, App	170	3945	100.0	720	14	US-10-175-747-170	Sequence 170, App
98	3945	100.0	720	12	US-10-187-683-170	Sequence 170, App	171	3945	100.0	720	14	US-10-176-481-170	Sequence 170, App
99	3945	100.0	720	12	US-10-194-363-170	Sequence 170, App	172	3945	100.0	720	14	US-10-176-485-170	Sequence 170, App
100	3945	100.0	720	12	US-10-194-460-170	Sequence 170, App	173	3945	100.0	720	14	US-10-176-487-170	Sequence 170, App
101	3945	100.0	720	12	US-10-194-463-170	Sequence 170, App	174	3945	100.0	720	14	US-10-176-493-170	Sequence 170, App
102	3945	100.0	720	12	US-10-194-484-170	Sequence 170, App	175	3945	100.0	720	14	US-10-176-756-170	Sequence 170, App
103	3945	100.0	720	12	US-10-195-884-170	Sequence 170, App	176	3945	100.0	720	14	US-10-176-911-170	Sequence 170, App
104	3945	100.0	720	12	US-10-195-896-170	Sequence 170, App	177	3945	100.0	720	14	US-10-176-919-170	Sequence 170, App
105	3945	100.0	720	12	US-10-196-744-170	Sequence 170, App	178	3945	100.0	720	14	US-10-176-925-170	Sequence 170, App
106	3945	100.0	720	12	US-10-196-755-170	Sequence 170, App	179	3945	100.0	720	14	US-10-176-978-170	Sequence 170, App
107	3945	100.0	720	12	US-10-196-757-170	Sequence 170, App	180	3945	100.0	720	14	US-10-179-510-170	Sequence 170, App
108	3945	100.0	720	12	US-10-197-704-170	Sequence 170, App	181	3945	100.0	720	14	US-10-180-543-170	Sequence 170, App
109	3945	100.0	720	12	US-10-197-710-170	Sequence 170, App	182	3945	100.0	720	14	US-10-180-548-170	Sequence 170, App
110	3945	100.0	720	12	US-10-198-758-170	Sequence 170, App	183	3945	100.0	720	14	US-10-180-545-170	Sequence 170, App
111	3945	100.0	720	12	US-10-198-766-170	Sequence 170, App	184	3945	100.0	720	14	US-10-180-547-170	Sequence 170, App
112	3945	100.0	720	12	US-10-199-304-170	Sequence 170, App	185	3945	100.0	720	14	US-10-180-549-170	Sequence 170, App
113	3945	100.0	720	12	US-10-199-309-170	Sequence 170, App	186	3945	100.0	720	14	US-10-180-555-170	Sequence 170, App
114	3945	100.0	720	12	US-10-199-313-170	Sequence 170, App	187	3945	100.0	720	14	US-10-180-559-170	Sequence 170, App
115	3945	100.0	720	12	US-10-199-456-170	Sequence 170, App	188	3945	100.0	720	14	US-10-181-000-170	Sequence 170, App
116	3945	100.0	720	12	US-10-201-329-170	Sequence 170, App	189	3945	100.0	720	14	US-10-183-010-170	Sequence 170, App
117	3945	100.0	720	12	US-10-202-412-170	Sequence 170, App	190	3945	100.0	720	14	US-10-183-012-170	Sequence 170, App
118	3945	100.0	720	12	US-10-206-919-170	Sequence 170, App	191	3945	100.0	720	14	US-10-184-614-170	Sequence 170, App
119	3945	100.0	720	12	US-10-206-922-170	Sequence 170, App	192	3945	100.0	720	14	US-10-184-623-170	Sequence 170, App
120	3945	100.0	720	12	US-10-206-924-170	Sequence 170, App	193	3945	100.0	720	14	US-10-184-635-170	Sequence 170, App
121	3945	100.0	720	12	US-10-206-928-170	Sequence 170, App	194	3945	100.0	720	14	US-10-184-637-170	Sequence 170, App
122	3945	100.0	720	12	US-10-207-914-170	Sequence 170, App	195	3945	100.0	720	14	US-10-184-646-170	Sequence 170, App
123	3945	100.0	720	12	US-10-207-921-170	Sequence 170, App	196	3945	100.0	720	14	US-10-184-647-170	Sequence 170, App
124	3945	100.0	720	12	US-10-207-922-170	Sequence 170, App	197	3945	100.0	720	14	US-10-184-652-170	Sequence 170, App
125	3945	100.0	720	12	US-10-208-027-170	Sequence 170, App	198	3945	100.0	720	14	US-10-187-594-170	Sequence 170, App
126	3945	100.0	720	12	US-09-997-641-231	Sequence 231, App	199	3945	100.0	720	14	US-10-187-596-170	Sequence 170, App
127	3945	100.0	720	12	US-09-991-150-231	Sequence 231, App	200	3945	100.0	720	14	US-10-187-745-170	Sequence 170, App
128	3945	100.0	720	12	US-10-174-570-170	Sequence 170, App	201	3945	100.0	720	14	US-10-187-785-170	Sequence 170, App
129	3945	100.0	720	12	US-10-183-005-170	Sequence 170, App	202	3945	100.0	720	14	US-10-187-886-170	Sequence 170, App
130	3945	100.0	720	13	US-10-006-867-38	Sequence 38, App1	203	3945	100.0	720	14	US-10-199-464-170	Sequence 170, App
131	3945	100.0	720	13	US-10-052-866-170	Sequence 170, App	204	3945	100.0	720	14	US-10-196-756-170	Sequence 170, App
132	3945	100.0	720	13	US-10-063-547-38	Sequence 38, App1	205	3945	100.0	720	14	US-10-176-751-170	Sequence 170, App
133	3945	100.0	720	13	US-10-174-590-170	Sequence 170, App	206	3945	100.0	720	14	US-10-176-760-170	Sequence 170, App
134	3945	100.0	720	14	US-10-176-758-170	Sequence 170, App	207	3945	100.0	720	14	US-10-176-990-170	Sequence 170, App
135	3945	100.0	720	14	US-10-175-737-170	Sequence 170, App	208	3945	100.0	720	14	US-10-180-541-170	Sequence 170, App
136	3945	100.0	720	14	US-10-063-616-38	Sequence 38, App1	209	3945	100.0	720	14	US-10-180-543-170	Sequence 170, App
137	3945	100.0	720	14	US-10-173-706-170	Sequence 170, App	210	3945	100.0	720	14	US-10-180-548-170	Sequence 170, App
138	3945	100.0	720	14	US-10-175-738-170	Sequence 170, App	211	3945	100.0	720	14	US-10-180-551-170	Sequence 170, App
139	3945	100.0	720	14	US-10-175-752-170	Sequence 170, App	212	3945	100.0	720	14	US-10-180-998-170	Sequence 170, App
140	3945	100.0	720	14	US-10-176-482-170	Sequence 170, App	213	3945	100.0	720	14	US-10-180-999-170	Sequence 170, App
141	3945	100.0	720	14	US-10-176-913-170	Sequence 170, App	214	3945	100.0	720	14	US-10-183-013-170	Sequence 170, App
142	3945	100.0	720	14	US-10-176-917-170	Sequence 170, App	215	3945	100.0	720	14	US-10-184-612-170	Sequence 170, App
143	3945	100.0	720	14	US-10-180-552-170	Sequence 170, App	216	3945	100.0	720	14	US-10-184-616-170	Sequence 170, App
144	3945	100.0	720	14	US-10-180-557-170	Sequence 170, App	217	3945	100.0	720	14	US-10-184-617-170	Sequence 170, App
145	3945	100.0	720	14	US-10-063-502-38	Sequence 38, App1	218	3945	100.0	720	14	US-10-184-622-170	Sequence 170, App
146	3945	100.0	720	14	US-10-173-700-170	Sequence 170, App	219	3945	100.0	720	14	US-10-184-628-170	Sequence 170, App
147	3945	100.0	720	14	US-10-174-572-170	Sequence 170, App	220	3945	100.0	720	14	US-10-184-629-170	Sequence 170, App
148	3945	100.0	720	14	US-10-174-579-170	Sequence 170, App	221	3945	100.0	720	14	US-10-184-630-170	Sequence 170, App
149	3945	100.0	720	14	US-10-174-582-170	Sequence 170, App	222	3945	100.0	720	14	US-10-184-631-170	Sequence 170, App
150	3945	100.0	720	14	US-10-174-588-170	Sequence 170, App	223	3945	100.0	720	14	US-10-184-632-170	Sequence 170, App
151	3945	100.0	720	14	US-10-175-739-170	Sequence 170, App	224	3945	100.0	720	14	US-10-184-636-170	Sequence 170, App
152	3945	100.0	720	14	US-10-175-740-170	Sequence 170, App	225	3945	100.0	720	14	US-10-184-640-170	Sequence 170, App
153	3945	100.0	720	14	US-10-175-743-170	Sequence 170, App	226	3945	100.0	720	14	US-10-184-650-170	Sequence 170, App
154	3945	100.0	720	14	US-10-176-488-170	Sequence 170, App	227	3945	100.0	720	14	US-10-184-651-170	Sequence 170, App
155	3945	100.0	720	14	US-10-176-492-170	Sequence 170, App	228	3945	100.0	720	14	US-10-187-588-170	Sequence 170, App
156	3945	100.0	720	14	US-10-176-747-170	Sequence 170, App	229	3945	100.0	720	14	US-10-187-597-170	Sequence 170, App
157	3945	100.0	720	14	US-10-176-750-170	Sequence 170, App	230	3945	100.0	720	14	US-10-187-598-170	Sequence 170, App
158	3945	100.0	720	14	US-10-176-985-170	Sequence 170, App	231	3945	100.0	720	14	US-10-187-600-170	Sequence 170, App
159	3945	100.0	720	14	US-10-176-987-170	Sequence 170, App	232	3945	100.0	720	14	US-10-187-601-170	Sequence 170, App
160	3945	100.0	720	14	US-10-176-992-170	Sequence 170, App	233	3945	100.0	720	14	US-10-187-602-170	Sequence 170, App
161	3945	100.0	720	14	US-10-176-993-170	Sequence 170, App	234	3945	100.0	720	14	US-10-187-603-170	Sequence 170, App

235	3945	100.0	720	14	US-10-187-741-170	Sequence 170, App	308	3945	100.0	720	14	US-10-194-425-170	Sequence 170, App
236	3945	100.0	720	14	US-10-187-743-170	Sequence 170, App	309	3945	100.0	720	14	US-10-194-485-170	Sequence 170, App
237	3945	100.0	720	14	US-10-187-746-170	Sequence 170, App	310	3945	100.0	720	14	US-10-195-885-170	Sequence 170, App
238	3945	100.0	720	14	US-10-187-747-170	Sequence 170, App	311	3945	100.0	720	14	US-10-195-899-170	Sequence 170, App
239	3945	100.0	720	14	US-10-187-751-170	Sequence 170, App	312	3945	100.0	720	14	US-10-196-748-170	Sequence 170, App
240	3945	100.0	720	14	US-10-187-753-170	Sequence 170, App	313	3945	100.0	720	14	US-10-196-750-170	Sequence 170, App
241	3945	100.0	720	14	US-10-187-754-170	Sequence 170, App	314	3945	100.0	720	14	US-10-197-699-170	Sequence 170, App
242	3945	100.0	720	14	US-10-187-757-170	Sequence 170, App	315	3945	100.0	720	14	US-10-197-700-170	Sequence 170, App
243	3945	100.0	720	14	US-10-187-884-170	Sequence 170, App	316	3945	100.0	720	14	US-10-197-705-170	Sequence 170, App
244	3945	100.0	720	14	US-10-188-767-170	Sequence 170, App	317	3945	100.0	720	14	US-10-197-708-170	Sequence 170, App
245	3945	100.0	720	14	US-10-188-769-170	Sequence 170, App	318	3945	100.0	720	14	US-10-198-764-170	Sequence 170, App
246	3945	100.0	720	14	US-10-188-770-170	Sequence 170, App	319	3945	100.0	720	14	US-10-198-765-170	Sequence 170, App
247	3945	100.0	720	14	US-10-188-773-170	Sequence 170, App	320	3945	100.0	720	14	US-10-198-768-170	Sequence 170, App
248	3945	100.0	720	14	US-10-188-781-170	Sequence 170, App	321	3945	100.0	720	14	US-10-198-769-170	Sequence 170, App
249	3945	100.0	720	14	US-10-194-361-170	Sequence 170, App	322	3945	100.0	720	14	US-10-199-305-170	Sequence 170, App
250	3945	100.0	720	14	US-10-194-423-170	Sequence 170, App	323	3945	100.0	720	14	US-10-199-306-170	Sequence 170, App
251	3945	100.0	720	14	US-10-195-897-170	Sequence 170, App	324	3945	100.0	720	14	US-10-199-310-170	Sequence 170, App
252	3945	100.0	720	14	US-10-195-901-170	Sequence 170, App	325	3945	100.0	720	14	US-10-199-311-170	Sequence 170, App
253	3945	100.0	720	14	US-10-195-902-170	Sequence 170, App	326	3945	100.0	720	14	US-10-199-314-170	Sequence 170, App
254	3945	100.0	720	14	US-10-196-743-170	Sequence 170, App	327	3945	100.0	720	14	US-10-199-317-170	Sequence 170, App
255	3945	100.0	720	14	US-10-196-760-170	Sequence 170, App	328	3945	100.0	720	14	US-10-199-665-170	Sequence 170, App
256	3945	100.0	720	14	US-10-196-768-170	Sequence 170, App	329	3945	100.0	720	14	US-10-199-666-170	Sequence 170, App
257	3945	100.0	720	14	US-10-176-479-170	Sequence 170, App	330	3945	100.0	720	14	US-10-199-669-170	Sequence 170, App
258	3945	100.0	720	14	US-10-176-748-170	Sequence 170, App	331	3945	100.0	720	14	US-10-201-534-170	Sequence 170, App
259	3945	100.0	720	14	US-10-176-916-170	Sequence 170, App	332	3945	100.0	720	14	US-10-201-534-170	Sequence 170, App
260	3945	100.0	720	14	US-10-179-507-170	Sequence 170, App	333	3945	100.0	720	14	US-10-201-855-170	Sequence 170, App
261	3945	100.0	720	14	US-10-179-516-170	Sequence 170, App	334	3945	100.0	720	14	US-10-201-855-170	Sequence 170, App
262	3945	100.0	720	14	US-10-179-519-170	Sequence 170, App	335	3945	100.0	720	14	US-10-202-469-170	Sequence 170, App
263	3945	100.0	720	14	US-10-179-545-170	Sequence 170, App	336	3945	100.0	720	14	US-10-202-469-170	Sequence 170, App
264	3945	100.0	720	14	US-10-180-545-170	Sequence 170, App	337	3945	100.0	720	14	US-10-202-476-170	Sequence 170, App
265	3945	100.0	720	14	US-10-180-545-170	Sequence 170, App	338	3945	100.0	720	14	US-10-202-476-170	Sequence 170, App
266	3945	100.0	720	14	US-10-183-006-170	Sequence 170, App	339	3945	100.0	720	14	US-10-202-935-170	Sequence 170, App
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ALIGNMENTS

US-09-989-722-231
Sequence 231, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
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APPLICANT: Baker, Kevin P.
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C63
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: US/09/989,722
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
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RESULT 2
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; Sequence 231, Application US/09989723

Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 9; Length 720;
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Qy 61 VVGVTIPCCRNNEECDSLIHPCTIFENCKSCRNCSWGGLDDFFVYKGFYCAECRAGW 120
Db 61 VVGVTIPCCRNNEECDSLIHPCTIFENCKSCRNCSWGGLDDFFVYKGFYCAECRAGW 120

Qy 121 YGGDCMCGQVLRAPKPGQILLESPLNAHCERTTHAKPGFVIQLRFVWLSPEDPYMCQYD 180
Db 121 YGGDCMCGQVLRAPKPGQILLESPLNAHCERTTHAKPGFVIQLRFVWLSPEDPYMCQYD 180

Qy 181 YVEVRDGNDRDQGIKRVCGNERPAPIQSGSSLHVLFHSKSNFDPGFHAIYEITACS 240
Db 181 YVEVRDGNDRDQGIKRVCGNERPAPIQSGSSLHVLFHSKSNFDPGFHAIYEITACS 240

; 241 SSPCFHDGTCVLDKAGSYKACACLAGYTGORCENLLERNCSDFGGPVNGYQKITGGPGLI 300
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; 601 WNVLADVRSPGKNDTLRSQVSVVDSILCEBQEDHGIPIVSVTDNMFCASWEPAPSIDI 660
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; 661 CTAETGCGIAAVSPGGRASPEPRWHLMLGLVSWSDYDKTCSHRLSTAFKTKVLPFKDWIERNMK 720
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RESULT 3
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; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C56
; CURRENT APPLICATION NUMBER: US/09/989,279
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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[illegible]

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1 PRIOR FILING DATE: 1998-07-02
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1 PRIOR FILING DATE: 1998-07-07
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1 PRIOR FILING DATE: 1998-07-09

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Qy	181	YVEVRDGDNRDQIILKVCNGNERPAPISQSSLSHLVLFHSDGSKNPGFPHAIYEEITACS	240		
Db	181	YVEVRDGDNRDQIILKVCNGNERPAPISQSSLSHLVLFHSDGSKNPGFPHAIYEEITACS	240		
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC65
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1 PRIOR FILING DATE: 1998-07-07
1 PRIOR APPLICATION NUMBER: 60/092182
1 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 9; Length 720;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 720; Conservative 0;

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Db 1 MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCYDQIECVCPGKRE 60
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Qy 181 YVEVRDGNDRDQIIRKVCNRPAPIOSIGSSHLVFLHSDGSKNFDGFAHYEETACS 240
Db 181 YVEVRDGNDRDQIIRKVCNRPAPIOSIGSSHLVFLHSDGSKNFDGFAHYEETACS 240

Db 181 YVEVRDGNDRGQIIRKVCNERPAPIQSTIGSLHLVLFHSDGSKNFDGFHAIYVEBITACS 240
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Db 481 HKGAWFLVCSGALVWERTVVAACHVCTDLGKVTMIKTADLKVLGKPYRDDDRDEKTIQS 540
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RESULT 5
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; Sequence 231, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Forrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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QY 181 YVEVRDGNRDGQIIKRYCGNERPAPIOSIGSSHLVLFHSDGSKNDFGHAIYEBITACS 240
DB 181 YVEVRDGNRDGQIIKRYCGNERPAPIOSIGSSHLVLFHSDGSKNDFGHAIYEBITACS 240
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DB 241 SSPCFHDGTCVLDKAGSYKACLAGYTQRCENLLEERNCSDPGPGVNGYQKITGGPGLI 300
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US-09-989-732-231
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertschen, Mary E.
APPLICANT: Goddard, Audrey
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APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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/ PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC8
; CURRENT APPLICATION NUMBER: US/09/990,442
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;; PRIOR FILING DATE: 1998-07-09

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tuma, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: Acids Encoding the Same
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; CURRENT FILING DATE: 2001-11-14
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Query Match      100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MELGCTQLGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRECEYDQIECVCPKRE 60
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QY 61 VVGYYTIPCCRNEECDCSLIHPGCTI FENCSCRNCSGGTLLDDPYVGFYCAECRAGW 120
   |||||
Db 61 VVGYYTIPCCRNEECDCSLIHPGCTI FENCSCRNCSGGTLLDDPYVGFYCAECRAGW 120
   |||||

QY 121 YGDCMRCQVLRAPKQIILLESYPLNAHCEWTIHAKEGFIQLRFVWMLSLFEDYMCQVD 180
   |||||
Db 121 YGDCMRCQVLRAPKQIILLESYPLNAHCEWTIHAKEGFIQLRFVWMLSLFEDYMCQVD 180
   |||||

QY 181 YVEVRDGNRDGQIKRVCNERPAPIQSIGSLHLVLFHSDGSKNPDGPHAIYEETACS 240
   |||||
Db 181 YVEVRDGNRDGQIKRVCNERPAPIQSIGSLHLVLFHSDGSKNPDGPHAIYEETACS 240
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QY 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLERNCSPPGGVNGYQKITGGPGLI 300
   |||||
Db 241 SSPCFHDGTCVLDKAGSYKACLAGYTGORCENLLERNCSPPGGVNGYQKITGGPGLI 300
   |||||

QY 301 NGRHAKIGTVWSFFCNSVYLSGNEKRTCOQNGWSGKQPICIKACREPKISDLVRRVL 360
   |||||
Db 301 NGRHAKIGTVWSFFCNSVYLSGNEKRTCOQNGWSGKQPICIKACREPKISDLVRRVL 360
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QY 361 PMQVQSRETPHLQLYSAAFSKQKLSAPTKKALPGDLPNGYQHLHTLOIECISPFYR 420
   |||||
Db 361 PMQVQSRETPHLQLYSAAFSKQKLSAPTKKALPGDLPNGYQHLHTLOIECISPFYR 420
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QY 421 RLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWEPQAAIYRRTSGVHDGSL 480
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Db 421 RLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWEPQAAIYRRTSGVHDGSL 480
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QY 481 HKGAWFLVCSGALVNBRTVVAAHCVTDLGKVTMIKTADLVVGLKGFYRDDDEKTIQS 540
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Db 481 HKGAWFLVCSGALVNBRTVVAAHCVTDLGKVTMIKTADLVVGLKGFYRDDDEKTIQS 540
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QY 541 LQISAIILHPNYDPIILLDADIALKLLDKARISTRVOPICLAASRDLSSTFQESHITVAG 600
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QY 601 WNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHDHGIPVSVTDNMFCASWEPTAPSDI 660
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QY 661 CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK 720
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RESULT 10
US-09-993-604-231
Sequence 231, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Gerber, Hanspeter
APPLICANT: Grøttsen, Mary E.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC25
CURRENT APPLICATION NUMBER: US/09/993,604
CURRENT FILING DATE: 2001-11-14
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/ PRIOR APPLICATION NUMBER: 60/092182
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Qy 61 VVGVTIPCCRNENECDSCLTHPCCTIFENCKSCRNCSWGGLTDDFYVKGFCYCAECAGW 120
Db 61 VVGVTIPCCRNENECDSCLTHPCCTIFENCKSCRNCSWGGLTDDFYVKGFCYCAECAGW 120

Qy 121 YGGDCMRGQVLRAPKPGQILLESYPLNACHCWTTHAKPGFVIQRLRVNLSLEFDYMCQYD 180
Db 121 YGGDCMRGQVLRAPKPGQILLESYPLNACHCWTTHAKPGFVIQRLRVNLSLEFDYMCQYD 180

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Qy 181 YVEVRDGDNRDGOIIRKVCNERPAPIQSIGSLHVLFHSDGSKNFDGFHAIYEEITACS 240
Db 181 YVEVRDGDNRDGOIIRKVCNERPAPIQSIGSLHVLFHSDGSKNFDGFHAIYEEITACS 240

Qy 241 SSPCFHDGTCVLDKAGSYKACLAGYTGRCENLLEERNCSDPGGVNGVQKITGGPGLI 300
Db 241 SSPCFHDGTCVLDKAGSYKACLAGYTGRCENLLEERNCSDPGGVNGVQKITGGPGLI 300

Qy 301 NGRHAKIGTVVSPFCNNNSYVLSGNEKRTCOQNGESGKQPCIKACREPKISDLVRRVRL 360
Db 301 NGRHAKIGTVVSPFCNNNSYVLSGNEKRTCOQNGESGKQPCIKACREPKISDLVRRVRL 360

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Db 361 PMOVQSRPTPLHOLYSAAFSKQKQSAPTYKPPALPGDLPMGYOHUHLTQLOECISPPFYR 420

Qy 421 RLGSSRRTCLRTGKWSRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL 480
Db 421 RLGSSRRTCLRTGKWSRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSL 480

Qy 481 HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKPYRDDDRDEKTIQS 540
Db 481 HKGAWFLVCSGALVNERTVVAAHCVTDLGKVTMIKTADLKVVLGKPYRDDDRDEKTIQS 540

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Qy 661 CTAETGGAIAVSPFGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK 720
Db 661 CTAETGGAIAVSPFGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK 720

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Sequence 231, Application US/09990456
Patent No. US20020137890A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787

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/	PRIOR APPLICATION NUMBER:	60/092182
/	PRIOR FILING DATE:	1998-07-09
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Best Local Similarity 100.0%; Pred. No. 0;		
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DB	1 MELGCMTQLGLTTFLQLLIISSLPREYTIVINEACPGAENIMCRECCYDQIECVCPGRKE	60
QY	61 VVGTYTPCCRNEEBCDSLHPGCITIFENCKSCRNSWGSGTLDDFVVKGFYCAECRAGW	120
DB	61 VVGTYTPCCRNEEBCDSLHPGCITIFENCXSCRNSWGSGTLDDFVVKGFYCAECRAGW	120
QY	121 YGGDCMRCGOVLAPKQGQIILLESVPLNAHCEWTTHAKGPVIOLRFVMLSLEFDYMCOYD	180
DB	121 YGGDCMRCGOVLAPKQGQIILLESVPLNAHCEWTTHAKPGPFIQRUFVMLSLEFDYMCOYD	180
QY	181 YVEVRDGNDRDGQIIKERVCNGNERPAPIQSIGSSLHLVLFHSDGSKNFGFHAIYEETACS	240
DB	181 YVEVRDGNDRGQIIKERVCNGNERPAPIQSIGSSLHLVLFHSDGSKNFGFHAIYEETACS	240
QY	241 SSPCFHDGTCTLVDKAGSYKCACLGYTGRCORENULBERNCSDPCGPNVGYOKITGGPGLI	300
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QY	361 PMOVQSRETPLHQLYSAAFSKQLOSAPTKKPALPFGBDLPMGYQHHTOLOVECISPFPYR	420
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QY	481 HKGAWLFCVCSGALVNERTVVAACHVTLDLGKVMTIKTDADLKVLGKFYRDDDRDEKTIQS	540
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QY	541 LOISAAILPHNYDPILLDAIDIAIKLDKARISTRVQIPICLAASRDISTSPQEHSITTAVG	600
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QY	661 CTABTAGIAAASFPGRASPEPRWHLMGLVSNYSYDKTCSHRILTSTAFTKVLPPFKDWIERNNK	720
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 14

US-09-989-293A-231

Sequence 231, Application US/09989293A

Patent No. US20020177164A1

GENERAL INFORMATION:

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APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gertschen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

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APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PLC66

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; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC61
; CURRENT APPLICATION NUMBER: US/09/989,735

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1 PRIOR FILING DATE: 1998-07-02
1 PRIOR APPLICATION NUMBER: 60/091633
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1 PRIOR APPLICATION NUMBER: 60/091978
1 PRIOR FILING DATE: 1998-07-07
1 PRIOR APPLICATION NUMBER: 60/091982
1 PRIOR FILING DATE: 1998-07-07
1 PRIOR APPLICATION NUMBER: 60/092182
1 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 3945; DB 9; Length 720;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 720; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MELGCTQLGLTFLQLLLSL	PREYTVINEACPGAENIMCRECCEYDQIECVCPGKRE	60
Db	1	MELGCTQLGLTFLQLLLSL	PREYTVINEACPGAENIMCRECCEYDQIECVCPGKRE	60
Qy	61	VVGTYTPCCRNEECDSLIHPCCTIFENCKSCRN	SGWGTLLDDPFVKGFCYCAECRAGW	120
Db	61	VVGTYTPCCRNEECDSLIHPCCTIFENCKSCRN	SGWGTLLDDPFVKGFCYCAECRAGW	120
Qy	121	YGGDCRRCQVLRAPKQIILLESYPLNHCWTHAKPG	EVIOLRVWMLSLSEEDYMCQYD	180
Db	121	YGGDCRRCQVLRAPKQIILLESYPLNHCWTHAKPG	EVIOLRVWMLSLSEEDYMCQYD	180
Qy	181	YVEVRDGNRDGOIIRKVCNERNPAPIQSGSLHLVL	FHSDGSKNPDGFHAIYEEITACS	240
Db	181	YVEVRDGNRDGOIIRKVCNERNPAPIQSGSLHLVL	FHSDGSKNPDGFHAIYEEITACS	240
Qy	241	SSPCFHDGTCVLDKAGSYKACLAGYTGRCENLLEERN	CSDPGPVNGYQKITGGPGLI	300
Db	241	SSPCFHDGTCVLDKAGSYKACLAGYTGRCENLLEERN	CSDPGPVNGYQKITGGPGLI	300
Qy	301	NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWS	GKQPICIKACREPKISDLVRRRVL	360
Db	301	NGRHAKIGTVVSPFCNNSYVLSGNEKRTCOONGEWS	GKQPICIKACREPKISDLVRRRVL	360
Qy	361	PMOVQSRTEPLHOLYSAAFQSKQLQSAPT	KKPALPFGDLPMGYQHLHTQLQYECISPFYR	420
Db	361	PMOVQSRTEPLHOLYSAAFQSKQLQSAPT	KKPALPFGDLPMGYQHLHTQLQYECISPFYR	420
Qy	421	RLGSSRRTECLRTGKWSGRAPSCIPICGKIENITAPKT	QGLRWPWQAAIYRRTSGVHDGSL	480
Db	421	RLGSSRRTECLRTGKWSGRAPSCIPICGKIENITAPKT	QGLRWPWQAAIYRRTSGVHDGSL	480
Qy	481	HKGAWFLVCSGALVNERVTVAAHCVTDLGKVTMTI	KTADLKVLGKPYRDDDRDEKTIQS	540
Db	481	HKGAWFLVCSGALVNERVTVAAHCVTDLGKVTMTI	KTADLKVLGKPYRDDDRDEKTIQS	540
Qy	541	LQISAILLHPNDPILLADADIALKLDKARISTRVQPI	CLAASRDISTSFQESHITVAG	600
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Qy	601	WNVLADVRSPGFNDTLRSVGVSVDLLCEEQHEHGHGIP	VSVTDNMFCASWEPTAPSDI	660
Db	601	WNVLADVRSPGFNDTLRSVGVSVDLLCEEQHEHGHGIP	VSVTDNMFCASWEPTAPSDI	660
Qy	661	CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSYDKTCS	HRILSTAFKVLPPKDWIERNMK	720

Db 661 CTAETGGIAAVSPGRASPEPRWHLMLGLVSWSYDKTCSHRILSTAFKVLPPKDWIERNMK 720
Search completed: August 18, 2004, 16:22:31
Job time : 54 secs

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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:17:43 ; Search time 13 Seconds
(without alignments)
2883.886 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MELGCWTQLGLTFLQLLLIS.....LSTAFKTVLPFKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	672	17.0	1019	1	LFC TACTR
2	665	16.9	1019	1	LFC CARPO
3	478	12.1	699	1	CRAR HUMAN
4	475	12.0	704	1	CRAR MOUSE
5	403.5	10.2	705	1	CIR HUMAN
6	400.5	10.2	686	1	MAS2 HUMAN
7	378.5	9.6	695	1	CASP MESAU
8	334	8.5	688	1	CIS HUMAN
9	331.5	8.4	1019	1	ENTK HUMAN
10	330.5	8.4	1034	1	ENTK PIG
11	329.5	8.4	3565	1	CSM1 HUMAN
12	329	8.3	3564	1	CSM1 MOUSE
13	328	8.3	855	1	ST14 HUMAN
14	320	8.1	461	1	PRTC MOUSE
15	318	8.1	3487	1	CSM2 HUMAN
16	317.5	8.0	1035	1	ENTK BOVIN
17	315	8.0	444	1	FA7 RABIT
18	314.5	8.0	475	1	FA10 CHICK
19	314	8.0	855	1	ST14 MOUSE
20	310.5	7.9	461	1	PRTC HUMAN
21	309.5	7.8	811	1	TMS6 MOUSE
22	304	7.7	1069	1	ENTK MOUSE
23	302.5	7.7	446	1	FA7 MOUSE
24	297	7.5	459	1	PRTC PIG
25	296	7.5	458	1	PRTC RABIT
26	293.5	7.4	407	1	FA7 BOVIN
27	292	7.4	461	1	PRTC RAT
28	291	7.4	376	1	FA10 TROCA
29	287.5	7.3	811	1	TMS6 HUMAN
30	285.5	7.2	452	1	FA9 CANFA
31	283	7.2	376	1	FA10 HOPST
32	282	7.1	456	1	PRTC BOVIN
33	281	7.1	492	1	FA10 BOVIN

34	280.5	7.1	264	1	CTRL HUMAN
35	280	7.1	562	1	TPA HUMAN
36	278.5	7.1	466	1	FA7 HUMAN
37	278	7.0	488	1	FA10 HUMAN
38	278	7.0	1113	1	COR1 MOUSE
39	277	7.0	559	1	TPA RAT
40	276.5	7.0	655	1	HGFA HUMAN
41	274.5	7.0	625	1	THRB BOVIN
42	274.5	7.0	3670	1	CSM3 HUMAN
43	273.5	6.9	566	1	TPA BOVIN
44	273	6.9	2796	1	CSM3 MOUSE
45	271.5	6.9	244	1	KLK6 HUMAN
46	271	6.9	559	1	TPA MOUSE
47	270	6.8	477	1	URT1 DESRO
48	270	6.8	490	1	FA10 RABIT
49	264.5	6.7	431	1	URTB DESRO
50	264.5	6.7	618	1	THRB MOUSE
51	264	6.7	653	1	HGFA MOUSE
52	262.5	6.7	461	1	FA9 HUMAN
53	262.5	6.7	461	1	FA9 PANTR
54	262.5	6.7	1042	1	COR1 HUMAN
55	262	6.6	477	1	URT2 DESRO
56	261.5	6.6	442	1	UROK PIG
57	261	6.6	431	1	UROK HUMAN
58	261	6.6	433	1	UROK BOVIN
59	259	6.6	245	1	CTRB GADMO
60	259	6.6	416	1	FA9 BOVIN
61	258.5	6.6	786	1	STUB DROME
62	258	6.5	433	1	UROK PAPCY
63	254	6.4	617	1	THRB RAT
64	250.5	6.3	347	1	HPT RABIT
65	250	6.3	306	1	BSS4 MOUSE
66	249.5	6.3	875	1	NETR HUMAN
67	248.5	6.3	459	1	FA9 MOUSE
68	248	6.3	263	1	CTRB HUMAN
69	248	6.3	638	1	KAL HUMAN
70	248	6.3	764	1	CFAB PANTR
71	247.5	6.3	991	1	BMPI MOUSE
72	247	6.3	275	1	TRYT CANFA
73	247	6.3	764	1	CFAB HUMAN
74	247	6.3	986	1	BMPI HUMAN
75	246.5	6.2	347	1	HPT ATSGE
76	246.5	6.2	622	1	THRB HUMAN
77	246	6.2	812	1	PLMN BOVIN
78	245	6.2	639	1	BMPI STRPU
79	244	6.2	638	1	KAL MOUSE
80	243	6.2	273	1	TRYT SHEEP
81	241	6.1	346	1	HPT MESAU
82	239.5	6.1	406	1	HPT HUMAN
83	239	6.1	245	1	CTRA BOVIN
84	239	6.1	436	1	HEPS MOUSE
85	238	6.0	237	1	TRYP ASTFL
86	238	6.0	263	1	CTR2 CANFA
87	238	6.0	275	1	TRYT PIG
88	238	6.0	375	1	PCE TACTR
89	237.5	6.0	810	1	PLMN ERIEU
90	237	6.0	263	1	CTRB RAT
91	236.5	6.0	274	1	MCT6 RAT
92	236.5	6.0	707	1	BMPI XENLA
93	236	6.0	812	1	PLMN MOUSE
94	235	6.0	270	1	TRYT MERIN
95	235	6.0	1420	1	APOA MACMU
96	234.5	5.9	453	1	TMS3 MOUSE
97	233.5	5.9	263	1	CTRA GADMO
98	232	5.9	416	1	HEPS RAT
99	232	5.9	638	1	KAL RAT
100	231.5	5.9	269	1	EL2 BOVIN
101	229.5	5.8	329	1	HPT CANFA
102	228.5	5.8	2531	1	NTCI MOUSE
103	227.5	5.8	242	1	TRY1 SALSA
104	227.5	5.8	251	1	KLKE HUMAN
105	227	5.8	324	1	TEST MOUSE
106	226.5	5.7	238	1	TRY3 SALSA

P40313	homo sapien
P00750	homo sapien
P08709	homo sapien
P00742	homo sapien
Q92319	mus musculus
P19637	rattus norv
Q04756	homo sapien
P00735	bos taurus
Q28407	homo sapien
Q28198	bos taurus
Q80479	mus musculus
Q92876	homo sapien
P11214	mus musculus
P98119	desmodus ro
Q19045	oryctolagus
P98121	desmodus ro
P19221	mus musculus
Q9098	mus musculus
P00740	homo sapien
Q95nd7	pan troglod
Q9y5q5	homo sapien
P15638	desmodus ro
P04185	sus scrofa
P00749	homo sapien
Q05589	bos taurus
P80646	gadus morhu
P00741	bos taurus
Q05319	drosofila
P16227	papio cynoc
P18292	rattus norv
P19007	oryctolagus
Q9er10	mus musculus
P56730	homo sapien
P16294	mus musculus
P17538	homo sapien
P03952	homo sapien
Q86440	pan troglod
P98083	mus musculus
P15944	canis fami
P00751	homo sapien
P13457	homo sapien
P50417	ateles geof
P00734	homo sapien
P06868	bos taurus
P98069	strongyloce
P26262	mus musculus
Q9xnm2	ovis aries
Q35086	mesocricetu
P00738	homo sapien
P00766	bos taurus
Q35453	mus musculus
P00765	astacus flu
P50343	rattus norv
P98070	xenopus lae
P20918	mus musculus
P50342	meriones un
P14417	macaca mula
Q8K10	mus musculus
P47796	gadus morhu
Q05511	rattus norv
P14272	rattus norv
Q29461	bos taurus
P19006	canis fami
Q01705	mus musculus
P35031	salmo salar
Q9p0g3	homo sapien
Q9jh17	mus musculus
P35033	salmo salar

107	226.5	5.7	761	1	NETR_MOUSE	O08762 mus musculus	180	205.5	5.2	347	1	HPT_RAT	P06866 rattus norv
108	226.5	5.7	1429	1	UTRG_HUMAN	O75882 mus sapien	181	205.5	5.2	492	1	TMS2_HUMAN	O15393 homo sapien
109	226	5.7	394	1	UTRG_DESRO	O49150 desmodus ro	182	205	5.2	256	1	HYBP_HYPLI	P35588 hypodermia 1
110	226	5.7	437	1	TMS4_HUMAN	O9nr84 homo sapien	183	204.5	5.2	246	1	TRY2_RAT	P35073 rattus norv
111	226	5.7	625	1	FAL1_HUMAN	O39511 homo sapien	184	204.5	5.2	256	1	TRYC_MANSE	P35047 manduca sex
112	225.5	5.7	347	1	HPT_PIG	O89987 sus scrofa	185	204.5	5.2	2470	1	NTC2_MOUSE	O35516 mus musculus
113	225.5	5.7	457	1	TMS5_HUMAN	O9r383 homo sapien	186	204	5.2	260	1	KLK8_HUMAN	O60259 homo sapien
114	225	5.7	615	1	FAL2_HUMAN	P00748 homo sapien	187	203.5	5.2	247	1	TRY2_HUMAN	P07478 homo sapien
115	224.5	5.7	271	1	EL2_RAT	P00774 rattus norv	188	203.5	5.2	263	1	CFAD_RAT	P32038 rattus norv
116	224.5	5.7	274	1	TRY1_ANOGA	P35035 anopheles g	189	203.5	5.2	285	1	FA9_CAVPO	P16295 cavia porce
117	224.5	5.7	347	1	HPT_MOUSE	O61646 mus musculus	190	202	5.1	241	1	TRY1_GADMO	P16049 gadus morhu
118	224.5	5.7	1022	1	TLD_BRARE	O57460 brachydania	191	202	5.1	246	1	KLK_PIG	P00752 sus scrofa
119	224	5.7	245	1	CTRB_BOVIN	P00767 bos taurus	192	202	5.1	2321	1	NTC3_HUMAN	O9um47 homo sapien
120	224	5.7	490	1	TMS2_MOUSE	O9j1q8 mus musculus	193	201.5	5.1	246	1	TRY2_MOUSE	P07146 mus musculus
121	223.5	5.7	348	1	HPTR_HUMAN	P00739 homo sapien	194	201.5	5.1	256	1	KLK8_HUMAN	O9nr25 homo sapien
122	223.5	5.7	1242	1	JAG1_BRARE	O90y57 brachydania	195	200.5	5.1	231	1	TRYP_PIG	P00761 sus scrofa
123	223	5.7	454	1	TMS3_HUMAN	P57727 homo sapien	196	200.5	5.1	752	1	CO2_HUMAN	P06681 homo sapien
124	222.5	5.6	417	1	HEPS_HUMAN	P05981 homo sapien	197	200.5	5.1	810	1	PLMN_MACMU	P12545 macaca mula
125	222.5	5.6	434	1	UROK_CHICK	P15120 gallus gall	198	200	5.1	385	1	TMS0_HUMAN	O9ui38 homo sapien
126	222.5	5.6	455	1	TMS5_MOUSE	O9er04 mus musculus	199	199.5	5.1	247	1	TRY3_RAT	P08426 rattus norv
127	222.5	5.6	790	1	PLMN_PIG	P06867 sus scrofa	200	199.5	5.1	257	1	KLK1_MACFA	O72736 macaca fasc
128	222	5.6	269	1	EL2_PIG	P08419 sus scrofa	201	199.5	5.1	275	1	TRY3_ANOGA	P35037 anopheles g
129	222	5.6	275	1	TRBA_HUMAN	P20231 homo sapien	202	199.5	5.1	2556	1	NTC1_HUMAN	P46531 homo sapien
130	222	5.6	275	1	TRYA_HUMAN	P15157 homo sapien	203	198.5	5.0	243	1	TRY1_BOVIN	P00760 bos taurus
131	222	5.6	422	1	DE51_HUMAN	O9ul52 homo sapien	204	198.5	5.0	311	1	TRYG_MOUSE	O9qul7 mus musculus
132	221.5	5.6	2531	1	NTC1_RAT	O07008 rattus norv	205	198	5.0	235	1	TRYD_HUMAN	O9bz13 homo sapien
133	221	5.6	231	1	TRY2_SALSA	P35032 salmo salar	206	198	5.0	259	1	DEP3_DERPA	P49275 dermatophag
134	221	5.6	268	1	CLCR_RAT	P55091 rattus norv	207	198	5.0	760	1	CO2_MOUSE	P21180 mus musculus
135	221	5.6	273	1	MCT7_RAT	P27435 rattus norv	208	198	5.0	1024	1	SZ6L_HUMAN	O9bhl1 homo sapien
136	220.5	5.6	1057	1	TLD_DROME	P25723 drosophila	209	197.5	5.0	226	1	COGS_UCAPU	P00771 uca pugilat
137	220	5.6	275	1	TRB1_HUMAN	O15661 homo sapien	210	197.5	5.0	248	1	KLK8_HUMAN	O9ukr0 homo sapien
138	219.5	5.6	244	1	TRY2_XENLA	P70059 xenopus lae	211	197	5.0	338	1	PLMN_HORSE	P80010 equus cabal
139	219.5	5.6	271	1	EL2_MOUSE	P05208 mus musculus	212	196.5	5.0	269	1	ELB2_HUMAN	P48018 homo sapien
140	219.5	5.6	347	1	HPT_MUSCR	O60574 mus musculus	213	196.5	5.0	570	1	FEP3_STRPU	P49213 strongyloce
141	219.5	5.6	761	1	CFAB_MOUSE	P04186 mus musculus	214	196.5	5.0	2524	1	EL3B_HUMAN	P21783 xenopus lae
142	219	5.6	343	1	PS88_HUMAN	O16651 homo sapien	215	196	5.0	270	1	GRAM_HUMAN	P51124 homo sapien
143	218.5	5.5	435	1	TMS4_MOUSE	O8vca5 mus musculus	216	195.5	5.0	257	1	FA9_PIG	P16293 sus scrofa
144	217	5.5	239	1	KLK2_CAVPO	P12323 cavia porce	217	195.5	5.0	271	1	CO2_PANTR	O98q74 pan troglod
145	217	5.5	268	1	CLCR_HUMAN	O99895 homo sapien	218	195.5	5.0	752	1	NTC2_HUMAN	O47421 mus musculus
146	217	5.5	273	1	MCT7_MOUSE	O28444 mus musculus	219	195.5	5.0	2471	1	KLK6_MOUSE	P15947 mus musculus
147	217	5.5	603	1	FAL2_CAVPO	O04962 cavia porce	220	195	4.9	261	1	UROK_RAT	P29598 rattus norv
148	217	5.5	2703	1	NOTC_DROME	P07207 drosophila	221	195	4.9	432	1	TRY1_RAT	P00762 rattus norv
149	216.5	5.5	2616	1	NDL_DROME	P98159 drosophila	222	194.5	4.9	246	1	PLMN_SHEEP	P81286 ovis aries
150	216	5.5	1218	1	JAG1_MOUSE	O9exx0 mus musculus	223	194.5	4.9	343	1	CFAD_PIG	P51779 sus scrofa
151	215.5	5.5	248	1	TRY3_CANFA	O06872 canis famli	224	194	4.9	259	1	TRY7_ANOGA	P35041 anopheles g
152	215.5	5.5	247	1	TRY3_CHICK	O90629 gallus gall	225	194	4.9	267	1	NTC2_RAT	O9qW30 rattus norv
153	215.5	5.5	317	1	BS84_HUMAN	O9gzn4 homo sapien	226	193.5	4.9	2471	1	CAC3_BOVIN	P05805 bos taurus
154	215	5.4	241	1	PLMN_GADMO	O91041 gadus morhu	227	193	4.9	256	1	TRYP_CHOFOU	P35042 choristoneu
155	215	5.4	810	1	TRYX_HUMAN	P00747 homo sapien	228	192.5	4.9	247	1	TRY1_HUMAN	P07477 homo sapien
156	214.5	5.4	247	1	TRY2_BOVIN	O29463 bos taurus	229	191.5	4.9	247	1	LEM3_HUMAN	P16109 homo sapien
157	214.5	5.4	593	1	FAL2_BOVIN	P98140 bos taurus	230	191.5	4.9	830	1	KLK4_HUMAN	O9y5k2 homo sapien
158	214.5	5.4	1428	1	ATRN_MOUSE	O9w460 mus musculus	231	191	4.8	254	1	LEM3_MOUSE	O01102 mus musculus
159	214	5.4	342	1	PS88_RAT	O9ee87 rattus norv	232	190.5	4.8	768	1	LEM3_MOUSE	O01079 strongyloce
160	212.5	5.4	250	1	KLK8_HUMAN	O9ubx7 homo sapien	233	190.5	4.8	1064	1	FEP1_STRPU	P32822 rattus norv
161	212	5.4	260	1	NRPN_MOUSE	O61955 mus musculus	234	189	4.8	246	1	TRYB_RAT	P12788 rattus norv
162	211.5	5.4	418	1	HATT_HUMAN	O60235 homo sapien	235	189	4.8	247	1	TRY4_RAT	P49862 homo sapien
163	211	5.3	276	1	MCT6_MOUSE	P21845 mus musculus	236	189	4.8	253	1	KLK7_HUMAN	P42201 bos taurus
164	211	5.3	1218	1	JAG1_HUMAN	P78504 homo sapien	237	189	4.8	646	1	LEM3_BOVIN	P2696 rattus norv
165	210.5	5.3	342	1	TRYP_SIMVI	P35048 simulium vi	238	188.5	4.8	282	1	FA9_RAT	O9bqR3 homo sapien
166	210.5	5.3	342	1	PS88_MOUSE	O9ed11 mus musculus	239	188.5	4.8	290	1	PR27_HUMAN	O9bqR3 rattus norv
167	210.5	5.3	1219	1	JAG1_RAT	O63722 rattus norv	240	188.5	4.8	714	1	DLL1_RAT	P97677 rattus norv
168	210	5.3	2437	1	NTC1_BRARE	P46530 brachydania	241	188	4.8	253	1	CFAD_HUMAN	P00746 homo sapien
169	209.5	5.3	347	1	HPT_MUSSA	O63558 mus saxicol	242	188	4.8	263	1	KLK8_PRANA	P32824 praomys nat
170	209	5.3	433	1	UROK_MOUSE	P06869 mus musculus	243	188	4.8	333	1	PLMN_CANFA	P80009 canis famli
171	207.5	5.3	256	1	TRYB_MANSE	P35046 manduca sex	244	187.5	4.8	304	1	TRY3_HUMAN	P35030 homo sapien
172	207.5	5.3	238	1	EL2A_HUMAN	P08217 homo sapien	245	187	4.7	246	1	TRYA_RAT	P32821 rattus norv
173	207	5.2	238	1	TRY5_AEDAE	P29787 aedes aegypt	246	187	4.7	271	1	CTRI_PENYA	O00871 penaeus van
174	207	5.2	260	1	NRPN_RAT	O88780 rattus norv	247	185.5	4.7	261	1	DER3_DERPT	P39675 dermatophag
175	206.5	5.2	256	1	TRYA_MANSE	P35045 manduca sex	248	185	4.7	711	1	HGFL_HUMAN	P26927 homo sapien
176	206.5	5.2	321	1	TRYG_HUMAN	O9nr12 homo sapien	249	185.5	4.7	928	1	NRP1_XENLA	P28824 xenopus lae
177	206	5.2	430	1	SNAP_DROME	P05049 drosophila	250	185	4.7	256	1	KLK4_MOUSE	P00757 mus musculus
178	206	5.2	4548	1	APOA_HUMAN	P08519 homo sapien	251	185	4.7	258	1	KLK1_PAPHA	O28773 papio hamad
179	205.5	5.2	269	1	TRYM_CANFA	P19236 canis famli	252	184.5	4.7	1213	1	JAG3_BRARE	O90y54 brachydania

253	184	4.7	314	1	TEST HUMAN	Q9y6m0 homo sapien	326	172	4.4	242	1	FIBC_LUMRU	P83298 lumbricus r
254	183	4.6	161	1	PRTC_MACWU	Q28506 macaca mula	327	172	4.4	254	1	TRYP_SARBU	P51588 sarcophaga
255	183	4.6	261	1	KLK1_RAT	P00758 rattus norv	328	172	4.4	260	1	ESTA_CANFA	P09582 canis famil
256	183	4.6	392	1	EAST_DROME	P13582 drosophila	329	172	4.4	261	1	KLK8_MOUSE	P07628 mus musculus
257	182.5	4.6	248	1	TRV1_CHICK	Q90627 gallus gall	330	172	4.4	262	1	TRV1_DROME	P42728 drosophila
258	182.5	4.6	468	1	PCO1_RAT	Q08628 rattus norv	331	172	4.4	415	1	ACRO_PIG	P08001 sus scrofa
259	182.5	4.6	484	1	LEM2_PIG	P98110 sus scrofa	332	172	4.4	147	1	JAG2_MOUSE	Q9qy65 mus musculus
260	182.5	4.6	722	1	DLK1_MOUSE	Q61483 mus musculus	333	171.5	4.3	262	1	KLK1_HUMAN	P06870 homo sapien
261	182	4.6	261	1	KLK5_MOUSE	P15945 mus musculus	334	171	4.3	260	1	GRAA_MOUSE	P11032 mus musculus
262	182	4.6	262	1	TRV1_DROER	P54628 drosophila	335	171	4.3	266	1	ELI_RAT	P00773 rattus norv
263	182	4.6	1238	1	JAG2_HUMAN	Q9y219 homo sapien	336	171	4.3	273	1	TRV6_ANOGA	P35040 anopheles g
264	181.5	4.6	247	1	GRAB_MOUSE	Q04187 mus musculus	337	171	4.3	277	1	KLK2_HUMAN	Q9ukr3 homo sapien
265	181.5	4.6	258	1	GRAM_RAT	Q03238 rattus norv	338	171	4.3	611	1	LEM2_CANFA	P13730 canis famil
266	181.5	4.6	437	1	ACRO_RAT	P29293 rattus norv	339	170	4.3	2339	1	CRB_DROME	P10040 drosophila
267	181	4.6	261	1	KLK3_MOUSE	P00756 mus musculus	340	170	4.3	245	1	MCT1_SHEEP	P80931 ovis aries
268	181	4.6	1271	1	YC81_CASEL	Q19981 caenorhabdi	341	170	4.3	248	1	TRVE_DROME	Q06606 rattus norv
269	180.5	4.6	248	1	TRV2_CHICK	Q06628 gallus gall	342	170	4.3	256	1	TRVE_DROME	P35005 drosophila
270	180.5	4.6	261	1	EUM3_EURMA	O97370 euroglyphus	343	169.5	4.3	251	1	MCT3_SHEEP	Q46683 ovis aries
271	180.5	4.6	275	1	FA9_RABIT	P16292 oryctolagus	344	169.5	4.3	261	1	KLK3_MACMU	P33619 macaca mula
272	180.5	4.6	436	1	ACRO_MOUSE	P23578 mus musculus	345	169	4.3	214	1	ACH2_LONAC	P23505 lonomia ach
273	180	4.6	157	1	PRTC_HORSE	Q28380 equus cabal	346	169	4.3	246	1	MCT1_MERUN	P50340 meriones un
274	180	4.6	261	1	KLKB_MOUSE	P15946 mus musculus	347	169	4.3	259	1	KLK3_RAT	P36376 rattus norv
275	180	4.6	275	1	TRV4_ANOGA	P35038 anopheles g	348	168.5	4.3	248	1	GRLL_RAT	Q06605 rattus norv
276	179.5	4.6	243	1	TRV1_XENLA	P39799 xenopus lae	349	168	4.3	262	1	TRVU_DROME	P42279 drosophila
277	179.5	4.6	250	1	KLK9_HUMAN	Q9ukq3 homo sapien	350	168	4.3	923	1	NRP1_HUMAN	O14786 homo sapien
278	179.5	4.6	258	1	TRVU_DROER	P54629 drosophila	351	167.5	4.2	261	1	KLK3_HUMAN	P07288 homo sapien
279	179.5	4.6	259	1	CFAD_MOUSE	P03953 mus musculus	352	167.5	4.2	383	1	DLK_HUMAN	P80370 homo sapien
280	179.5	4.6	274	1	FA9_SHEEP	P16291 ovis aries	353	167	4.2	247	1	MCT8_MOUSE	P43430 mus musculus
281	179	4.5	253	1	TRV5_DROER	P54625 drosophila	354	166.5	4.2	723	1	DLK1_HUMAN	O00548 homo sapien
282	179	4.5	266	1	EL1_PIG	P00772 sus scrofa	355	166.5	4.2	769	1	LEM3_SHEEP	P98109 ovis aries
283	179	4.5	280	1	TRV2_DROME	P42280 drosophila	356	166	4.2	157	1	PRTC_FELCA	Q28412 felis silve
284	179	4.5	549	1	LEM2_RAT	P98105 rattus norv	357	166	4.2	597	1	BP10_PARLI	P42674 paracentrot
285	179	4.5	612	1	LEM2_MOUSE	Q06690 mus musculus	358	165.5	4.2	616	1	SEF6_STRPU	P98068 strongyloce
286	178.5	4.5	255	1	TRV4_LUCU	P35044 lucilia cup	359	164.5	4.2	279	1	DEPA_DRFPA	P49276 dermatophag
287	178.5	4.5	468	1	PCO1_MOUSE	Q61398 mus musculus	360	164.5	4.2	1231	1	CFAH_HUMAN	P08603 homo sapien
288	178.5	4.5	922	1	NRP1_RAT	Q9qy19 rattus norv	361	164	4.2	2871	1	FBN1_MOUSE	O61554 mus musculus
289	178.5	4.5	923	1	NRP1_MOUSE	P97333 mus musculus	362	163	4.1	252	1	TRV1_DROME	P52905 drosophila
290	178	4.5	157	1	PRTC_CANFA	Q28278 canis famil	363	163.5	4.1	859	1	ST7_HUMAN	Q9y561 homo sapien
291	178	4.5	253	1	TRVU_DROER	P54626 drosophila	364	162.5	4.1	253	1	TRV6_DROME	P98065 oryctolagus
292	178	4.5	528	1	GD_DROME	O62589 drosophila	365	162	4.1	253	1	TRV6_DROME	P35004 drosophila
293	177.5	4.5	248	1	NKPL1_RAT	P18291 rattus norv	366	162	4.1	261	1	KLK2_MOUSE	P36369 mus musculus
294	177.5	4.5	1964	1	NTC4_MOUSE	P31695 mus musculus	367	161.5	4.1	226	1	DDN1_BOVIN	P80219 bos taurus
295	177	4.5	271	1	CTR2_PENVA	P36178 penaeus van	368	161.5	4.1	248	1	GRAE_MOUSE	P08884 mus musculus
296	177	4.5	473	1	FP2_MYTA	Q25464 mytilus gal	369	161.5	4.1	250	1	TRYP_PLEPL	P35034 pleuronecte
297	176.5	4.5	925	1	NRP2_RAT	Q35276 rattus norv	370	161.5	4.1	1025	1	CATG_MOUSE	P28293 mus musculus
298	176.5	4.5	931	1	NRP2_MOUSE	Q35375 mus musculus	371	161.5	4.1	293	1	KLK5_HUMAN	P19070 mus musculus
299	176.5	4.5	2003	1	NTC4_HUMAN	Q99466 homo sapien	372	161	4.1	661	1	F13B_HUMAN	Q9y337 homo sapien
300	176	4.5	261	1	KLK7_RAT	P36373 rattus norv	373	160.5	4.1	262	1	GRAA_HUMAN	P05160 homo sapien
301	176	4.5	261	1	KLK9_MOUSE	P15949 mus musculus	374	160	4.1	630	1	LEM2_HORSE	P12544 homo sapien
302	176	4.5	264	1	VDP_BOMMO	Q07943 bombyx mori	375	160	4.1	2871	1	FBN1_HUMAN	Q95191 equus cabal
303	176	4.5	270	1	ELJ3_HUMAN	P09093 homo sapien	376	160	4.1	248	1	GRAD_MOUSE	P35555 homo sapien
304	176	4.5	2318	1	NTC3_MOUSE	Q61982 mus musculus	377	159.5	4.0	248	1	KLK4_RAT	P11033 mus musculus
305	176	4.5	2319	1	NTC3_RAT	Q9r172 rattus norv	378	159	4.0	244	1	KLK6_MOUSE	P36375 rattus norv
306	175.5	4.4	274	1	TRV5_ANOGA	P35039 anopheles g	379	159	4.0	261	1	KLK7_MOUSE	P04071 mus musculus
307	175	4.4	421	1	ACRO_HUMAN	P10323 homo sapien	380	159	4.0	2907	1	FBN2_MOUSE	O61555 mus musculus
308	175	4.4	931	1	NRP2_HUMAN	O60462 homo sapien	381	159	4.0	2911	1	FBN2_HUMAN	P35556 homo sapien
309	174.5	4.4	246	1	TRV1_CANFA	Q06871 canis famil	382	158.5	4.0	247	1	MCT3_RAT	P50339 rattus norv
310	174	4.4	258	1	EL1_HUMAN	P5948 mus musculus	383	158.5	4.0	256	1	HYPA_HYPLI	Q09163 mus musculus
311	174	4.4	259	1	KLK6_MOUSE	P00755 mus musculus	384	158.5	4.0	833	1	DLK_MOUSE	P10041 drosophila
312	174	4.4	261	1	KLK1_MOUSE	Q28153 bos taurus	385	158	4.0	256	1	TRVE_DROER	P54627 drosophila
313	174	4.4	266	1	EL1_BOVIN	P35039 caenorhabdi	386	158	4.0	522	1	TOH2_CAEEL	P98067 caenorhabdi
314	173.5	4.4	1295	1	GLP1_CAEEL	P13508 caenorhabdi	387	158	4.0	522	1	VSPI_VIPLE	Q9pt41 vipera lebe
315	173.5	4.4	260	1	COGS_HYPLI	P08897 hypoderma l	388	157.5	4.0	259	1	TRV2_DROER	P54630 drosophila
316	173.5	4.4	914	1	NRP1_CHICK	P79795 gallus gall	389	157	4.0	281	1	LEM2_HUMAN	P16581 homo sapien
317	173	4.4	229	1	TRYP_SQUAC	P00764 squallus aca	390	157	4.0	610	1	LEM2_HUMAN	Q9ji71 mus musculus
318	173	4.4	248	1	MCT8_RAT	P97594 rattus norv	391	157	4.0	686	1	DLK4_MOUSE	O08859 mus musculus
319	173	4.4	768	1	LEM3_RAT	P98106 rattus norv	392	156.5	4.0	275	1	TSG6_MOUSE	P14585 caenorhabdi
320	172.5	4.4	248	1	GRAC_MOUSE	P08882 mus musculus	393	156.5	4.0	3718	1	LMAS_CAEEL	P14585 caenorhabdi
321	172.5	4.4	277	1	TRV2_ANOGA	P48038 oryctolagus g	394	156.5	4.0	253	1	TRVU_DROME	O61001 mus musculus
322	172.5	4.4	431	1	ACRO_RABIT	P35036 anopheles g	395	156	4.0	259	1	KLK2_RAT	P42276 drosophila
323	172.5	4.4	449	1	PCO1_HUMAN	Q51113 homo sapien	396	156	4.0	259	1	KLK2_RAT	P00759 rattus norv
324	172.5	4.4	1202	1	JAG2_RAT	P97607 rattus norv	397	156	4.0	261	1	KLK2_HUMAN	P20151 homo sapien
325	172	4.4	157	1	PRTC_CAPHI	Q28315 capra hircu	398	155.5	3.9	213	1	ACHI_LONAC	P23604 lonomia ach

399	155.5	3.9	485	1	LEM2_BOVIN	P98107 bos taurus	472	140	3.5	260	1	VSP4_AGRAC	Q918w9 agkistrodon
400	155	3.9	1033	1	TRV3_DROME	P42277 drosophila	473	140	3.5	396	1	PRTZ_BOVIN	P00744 bos taurus
401	155	3.9	253	1	CR2_HUMAN	P20023 homo sapien	474	140	3.5	4590	1	FATH_HUMAN	Q14517 homo sapien
402	155	3.9	1376	1	CRB8_HUMAN	P28279 homo sapien	475	139.5	3.5	256	1	TRP3_PSEAM	Q93267 pseudopleur
403	154.5	3.9	252	1	C4BB_HUMAN	P28851 homo sapien	476	139.5	3.5	258	1	CTR2_ANOGA	Q17025 anopheles g
404	154	3.9	248	1	TRIP_FUSOX	P35049 fusarium ox	477	139.5	3.5	457	1	DAF2_MOUSE	Q51476 mus musculus
405	154	3.9	685	1	CFAH_BOVIN	P28085 bos taurus	478	139.5	3.5	514	1	UVS2_XENLA	P78539 xenopus lae
406	154	3.9	2039	1	CR1_HUMAN	P17927 homo sapien	479	139	3.5	464	1	SRPX_HUMAN	P23946 homo sapien
407	154	3.9	2871	1	FBNI_PIG	Q95v36 sus scrofa	480	138.5	3.5	247	1	FBNI_MOUSE	Q08879 mus musculus
408	153.5	3.9	260	1	MCT1_RAT	P09650 rattus norv	481	138.5	3.5	705	1	HIG_DROME	Q09101 drosophila
409	153.5	3.9	551	1	LEM2_RABIT	P27113 oryctolagus	482	138	3.5	958	1	TRV3_DROME	P24664 saccharopol
410	153.5	3.9	1786	1	LEM1_MOUSE	P02469 mus musculus	483	137	3.5	227	1	TRV3_DROME	Q03515 rattus norv
411	153	3.9	151	1	CFAB_PIG	P03710 sus scrofa	484	137	3.5	258	1	C4BB_RAT	P20836 rattus norv
412	153	3.9	254	1	TRV3_AEDAE	P29786 aedes aegypt	485	137	3.5	372	1	LEM1_RAT	P52195 papio hamad
413	153	3.9	2871	1	FBNI_BOVIN	P98133 bos taurus	486	136.5	3.5	247	1	MCT1_PAPHA	P00770 rattus norv
414	152.5	3.9	248	1	GRAF_MOUSE	P08883 mus musculus	487	136.5	3.5	247	1	MCT2_RAT	Q9nyj7 homo sapien
415	152.5	3.9	264	1	GRAB_HUMAN	P49863 homo sapien	488	136.5	3.5	618	1	DLI3_HUMAN	P02749 homo sapien
416	152.5	3.9	400	1	PRTZ_HUMAN	P22891 homo sapien	489	136	3.4	345	1	APCH_HUMAN	Q01016 herpesvirus
417	152	3.9	247	1	GRAB_HUMAN	P10144 h granzyme	490	136	3.4	360	1	CCPH_HSVSA	P02468 mus musculus
418	151.5	3.8	261	1	KLK8_RAT	P36374 rattus norv	491	136	3.4	1607	1	LMG1_MOUSE	P08607 mus musculus
419	151.5	3.8	716	1	HGFL_MOUSE	P26928 mus musculus	492	135.5	3.4	469	1	C4BP_MOUSE	O42182 brachydanio
420	151	3.8	249	1	MCT1_CANFA	P21842 canis famli	493	135	3.4	681	1	FBLI_BRARE	P34576 caenorhabdi
421	151	3.8	261	1	KLK6_MOUSE	P36368 mus musculus	494	135	3.4	3767	1	MUA3_CABEL	Q94813 homo sapien
422	150.5	3.8	277	1	TS66_HUMAN	P98066 homo sapien	495	134.5	3.4	1529	1	SLT2_HUMAN	Q28768 papio hamad
423	150.5	3.8	685	1	DLI4_HUMAN	Q9nr61 homo sapien	496	134	3.4	232	1	VSPA_BOTJA	P81661 bothrops ja
424	150	3.8	263	1	VCP_VACCV	P10998 vaccinia vi	497	134	3.4	3034	1	CUR1_MOUSE	Q35161 mus musculus
425	150	3.8	267	1	ELNE_HUMAN	P08246 homo sapien	498	133.5	3.4	381	1	DAF_HUMAN	P08174 homo sapien
426	150	3.8	276	1	KLKA_HUMAN	O43240 homo sapien	499	133	3.4	257	1	VSPC_TRIGA	O13062 trimeresuru
427	150	3.8	703	1	FBLI_HUMAN	P23142 homo sapien	500	133	3.4	810	1	NEL1_RAT	Q62919 rattus norv
428	150	3.8	3712	1	LMA_DROME	Q00174 drosophila	501	132.5	3.4	247	1	MCT1_WACFA	P56435 macaca fasc
429	149.5	3.8	236	1	VSPA_DABRU	P18964 daboia russ	502	132.5	3.4	260	1	VSP1_AGRAC	Q918x2 agkistrodon
430	149.5	3.8	259	1	TRYP_STRGR	P00775 streptomyce	503	132	3.3	246	1	MCTX_MOUSE	Q00356 mus musculus
431	149.5	3.8	260	1	VSPB_TRIGA	O13061 trimeresuru	504	132	3.3	345	1	AFOP_PANTR	Q951b0 pan troglod
432	149	3.8	216	1	CTR2_VESOR	P00768 vespa orien	505	132	3.3	372	1	LEM1_MACNU	Q95198 macaca mula
433	149	3.8	1408	1	SERR_DROME	P18168 drosophila	506	132	3.3	372	1	LEM1_PAPHA	Q28768 papio hamad
434	148.5	3.8	271	1	S24D_ANOGA	Q17004 anopheles g	507	132	3.3	558	1	C4BP_RAT	Q63514 rattus norv
435	148	3.8	218	1	CTR2_VESCR	P00769 vespa crabr	508	132	3.3	830	1	SREC_HUMAN	Q14162 homo sapien
436	148	3.8	464	1	SRFX_RAT	Q63769 rattus norv	509	132	3.3	2109	1	PGCA_CHICK	P07898 gallus gall
437	148	3.8	668	1	F13B_MOUSE	Q07968 mus musculus	510	131.5	3.3	263	1	GRAB_MOUSE	Q35205 mus musculus
438	148	3.8	1504	1	SLIT_DROME	P24014 drosophila	511	131.5	3.3	810	1	NEL1_HUMAN	Q28832 homo sapien
439	147.5	3.7	244	1	MCT2_MOUSE	P15119 mus musculus	512	131.5	3.3	1268	1	PCGN_MOUSE	P55066 mus musculus
440	147.5	3.7	1786	1	LMB1_HUMAN	P07942 homo sapien	513	130.5	3.3	507	1	DAF_CAVPO	Q60401 cavia porce
441	147.5	3.7	3695	1	LMA5_HUMAN	O15230 homo sapien	514	130.5	3.3	1257	1	PCGN_RAT	P55067 rattus norv
442	147.5	3.7	4391	1	PGBM_HUMAN	P98160 homo sapien	515	130.5	3.3	3672	1	LM2_CABEL	Q21313 caenorhabdi
443	147	3.7	259	1	KLK9_RAT	P07647 rattus norv	516	130	3.3	258	1	VSP3_TRIGA	O13063 trimeresuru
444	147	3.7	262	1	VSP1_AGRCA	Q91053 agkistrodon	517	130	3.3	390	1	DAF1_MOUSE	Q61475 mus musculus
445	147	3.7	1535	1	LM11_CABEL	O18823 caenorhabdi	518	130	3.3	592	1	DLI3_MOUSE	O88516 mus musculus
446	147	3.7	3084	1	LM1_MOUSE	P19137 mus musculus	519	129.5	3.3	246	1	MCT9_MOUSE	O35164 mus musculus
447	146.5	3.7	236	1	VSPC_DABRU	P18965 daboia russ	520	129.5	3.3	652	1	CD93_HUMAN	Q9npv3 homo sapien
448	146.5	3.7	3707	1	PGBM_MOUSE	Q05793 mus musculus	521	129	3.3	235	1	VSP2_AGRBI	Q9psn3 agkistrodon
449	146	3.7	238	1	VSP1_AGRKA	P81176 agkistrodon	522	129	3.3	246	1	MCT4_RAT	P97592 rattus norv
450	146	3.7	256	1	TRVA_DROER	P54624 drosophila	523	128.5	3.3	232	1	VSP1_BOTJA	P81824 bothrops ja
451	145.5	3.7	598	1	FBLI_CERAE	Q8mj99 cercopithe	524	128.5	3.3	255	1	CATG_HUMAN	P08311 homo sapien
452	145	3.7	256	1	TRVA_DROME	P04814 drosophila	525	128.5	3.3	833	1	SRC2_MOUSE	P59222 mus musculus
453	145	3.7	260	1	VSP1_AGRKH	Q9vgj2 agkistrodon	526	128.5	3.3	2923	1	CLR2_HUMAN	Q9hcu4 homo sapien
454	145	3.7	372	1	LEM1_MOUSE	P18337 mus musculus	527	128	3.2	219	1	CA7_PIG	P80015 sus scrofa
455	144.5	3.7	246	1	MCT4_MOUSE	P21812 mus musculus	528	127.5	3.2	1389	1	LTBS_MOUSE	Q8cg18 mus musculus
456	144	3.7	260	1	VSP2_AGRKH	Q9vg16 agkistrodon	529	127.5	3.2	1713	1	LTBL_MOUSE	Q8cg19 mus musculus
457	143	3.6	234	1	VSP2_AGRKO	P82981 agkistrodon	530	127	3.2	258	1	GRAB_RAT	P49864 rattus norv
458	143	3.6	246	1	MCT2_SHEEP	P79204 ovie aries	531	127	3.2	1609	1	LMG1_HUMAN	P11047 homo sapien
459	143	3.6	258	1	VSP2_AGRKA	O42307 agkistrodon	532	127	3.2	3106	1	LM2_MOUSE	Q60675 mus musculus
460	143	3.6	3075	1	LM1_HUMAN	P25391 homo sapien	533	127	3.2	3110	1	LM2_MOUSE	P24043 homo sapien
461	142.5	3.6	247	1	MCT5_MOUSE	P21844 mus musculus	534	126.5	3.2	448	1	FBLS_RAT	Q9vvh8 rattus norv
462	142.5	3.6	258	1	VSP2_TRIJE	Q9df67 trimeresuru	535	126	3.2	257	1	VSP5_TRIMU	Q91511 trimeresuru
463	142	3.6	257	1	VSP2_BOTJA	O13069 bothrops ja	536	126	3.2	265	1	SER1_DROME	P17205 drosophila
464	141.5	3.6	310	1	ASTL_COTJA	P42662 coturnix co	537	126	3.2	272	1	SER3_DROME	P17207 drosophila
465	141.5	3.6	372	1	LEM1_HUMAN	P14151 homo sapien	538	126	3.2	330	1	FHR1_HUMAN	Q03591 homo sapien
466	141.5	3.6	372	1	LMG1_PANTR	Q95237 pan troglod	539	126	3.2	5147	1	FAT_DROME	P33450 drosophila
467	141.5	3.6	1581	1	LMG3_MOUSE	Q9r0b6 mus musculus	540	125.5	3.2	254	1	CTRL_HALRU	P35003 haliohis ru
468	141	3.6	246	1	GRAF_HUMAN	P20718 homo sapien	541	125.5	3.2	597	1	C4BP_HUMAN	P04003 homo sapien
469	140.5	3.6	246	1	MCT1_MOUSE	P11034 mus musculus	542	125	3.2	257	1	VSP3_TRIMU	Q91509 trimeresuru
470	140.5	3.6	372	1	LEM1_PONPY	Q95235 pongo pygma	543	125	3.2	443	1	FBLL_MOUSE	Q9vuj9 mus musculus
471	140.5	3.6	1234	1	CFAB_MOUSE	P06909 mus musculus	544	125	3.2	589	1	DLI3_RAT	O88671 rattus norv

545	125	3.2	1790	1	LMB1 DROME	P11046 drosophila	618	115.5	2.9	1679	1	FUR2 DROME	P30432 drosophila
546	124.5	3.2	248	1	GRAG MOUSE	P13366 mus musculus	619	115	2.9	133	1	AWN HORSE	P80720 equus caball
547	124.5	3.2	260	1	VSP1 TRIFL	P03620 trimeresuru	620	115	2.9	956	1	MTN2 HUMAN	P00339 homo sapien
548	124.5	3.2	268	1	TRYP STRGA	O54179 streptomyce	621	115	2.9	1207	1	EGP HUMAN	P01133 homo sapien
549	124	3.1	883	1	PGCB RAT	P55068 rattus norv	622	114.5	2.9	270	1	PHR2 HUMAN	P16980 homo sapien
550	124	3.1	1221	1	FBL2 MOUSE	P37889 mus musculus	623	114.5	2.9	443	1	FBL4 HUMAN	O95967 homo sapien
551	124	3.1	3333	1	PGCA CANFA	O28343 canis famil	624	114.5	2.9	816	1	NEL2 MOUSE	O61220 mus musculus
552	124	3.1	3333	1	LMA3 CANFA	O61789 mus musculus	625	114.5	2.9	1798	1	LMB2 HUMAN	P55268 homo sapien
553	123.5	3.1	259	1	CTRI ANOGA	O27289 anopheles g	626	114	2.9	255	1	VSPA BOTAT	P04971 bothriops at
554	123.5	3.1	370	1	LEMI BOVIN	P98131 bos taurus	627	114	2.9	846	1	ITBX DROME	P11584 drosophila
555	123.5	3.1	1184	1	FBL2 HUMAN	P98095 homo sapien	628	113.5	2.9	879	1	LDLR RAT	P35952 rattus norv
556	123.5	3.1	2144	1	CLR2 RAT	O90722 rattus norv	629	113.5	2.9	1712	1	LTBL RAT	O00818 rattus norv
557	123.5	3.1	2213	1	SORL RABIT	O95209 o sortilin-	630	113	2.9	250	1	CFBL CHICK	P81475 gallus gall
558	123	3.1	340	1	DAF PONFY	P49457 pongo pygma	631	113	2.9	462	1	KRM2 HUMAN	O8ncw0 homo sapien
559	123	3.1	798	1	FBL1 CAEEL	O77469 caenorhabdi	632	113	2.9	3301	1	CLR3 MOUSE	O91210 mus musculus
560	123	3.1	816	1	NEL CHICK	O90827 gallus gall	633	113	2.9	3312	1	CLR3 HUMAN	O9nyq7 homo sapien
561	122.5	3.1	603	1	CFAT MOUSE	O61129 mus musculus	634	113	2.9	4349	1	PAT2 HUMAN	O9nyq8 homo sapien
562	122	3.1	198	1	CABE BOVIN	O28066 bos taurus	635	112.5	2.9	264	1	CERC SCMA	P12546 schistosoma
563	122	3.1	257	1	VSP3 AGKAC	O918x0 agkistrodon	636	112.5	2.9	379	1	MCP CAVPO	P70105 cavia porce
564	122	3.1	257	1	VSP7 TRIMU	O9dg84 trimeresuru	637	112.5	2.9	643	1	CD93 RAT	O9et61 rattus norv
565	122	3.1	258	1	VSP2 AGKAC	O918x1 agkistrodon	638	112.5	2.9	1228	1	EMI4 HUMAN	Q13201 homo sapien
566	122	3.1	676	1	PRTS HUMAN	P07225 homo sapien	639	112.5	2.9	1247	1	NIDQ HUMAN	P14543 homo sapien
567	122	3.1	1808	1	TENA CHICK	P10039 gallus gall	640	112.5	2.9	1403	1	NID2 MOUSE	O88322 mus musculus
568	122	3.1	1955	1	AGRI CHICK	P31696 gallus gall	641	112	2.8	228	1	VSPA LACMU	P13589 lachesis mu
569	122	3.1	3313	1	CLR3 RAT	O88278 rattus norv	642	112	2.8	493	1	FBL3 HUMAN	Q12805 homo sapien
570	121.5	3.1	245	1	GILX HELHO	P43685 heloderma h	643	112	2.8	1125	1	TIE2 BOVIN	Q06807 bos taurus
571	121.5	3.1	610	1	C4BP BOVIN	O28065 bos taurus	644	112	2.8	3562	1	PGCV CHICK	O90953 gallus gall
572	121.5	3.1	5376	1	ZAN MOUSE	O88799 mus musculus	645	111.5	2.8	816	1	NEL2 RAT	Q62918 rattus norv
573	121	3.1	257	1	VSP2 TRIMU	O91508 trimeresuru	646	111.5	2.8	1328	1	AGRI DISOM	O90404 discopys o
574	121	3.1	1627	1	PAPA HUMAN	Q13219 homo sapien	647	111.5	2.8	1587	1	LMG3 HUMAN	O9v6n6 homo sapien
575	121	3.1	3396	1	PGCV HUMAN	P13611 homo sapien	648	111.5	2.8	4351	1	PAT2 RAT	O88277 rattus norv
576	120.5	3.1	247	1	MCT2 MERUN	P50341 meriones un	649	111	2.8	231	1	VSP1 AGKCO	P09872 agkistrodon
577	120.5	3.1	345	1	APOH CANFA	P33703 canis famil	650	111	2.8	254	1	PRN3 MOUSE	Q61096 mus musculus
578	120.5	3.1	646	1	PRTS RABIT	P98118 oryctolagus	651	110.5	2.8	234	1	VSP1 AGKRH	P26324 agkistrodon
579	120.5	3.1	728	1	HGF MOUSE	O80048 mus musculus	652	110.5	2.8	297	1	APOH RAT	P26644 rattus norv
580	120.5	3.1	1394	1	LTBS HUMAN	P22064 homo sapien	653	110.5	2.8	593	1	CFAT HUMAN	P05156 homo sapien
581	120.5	3.1	1595	1	LTBL HUMAN	Q14766 homo sapien	654	110.5	2.8	755	1	COMP MOUSE	O9r0g6 mus musculus
582	120.5	3.1	1801	1	LMB2 RAT	P15800 rattus norv	655	110.5	2.8	961	1	TSPA HUMAN	P35443 homo sapien
583	120	3.0	257	1	VSP1 TRIMU	Q15007 trimeresuru	656	110.5	2.8	1217	1	EGF MOUSE	P01132 mus musculus
584	120	3.0	493	1	FBL3 RAT	Q35568 rattus norv	657	110	2.8	258	1	VSP1 TRIGA	O13059 trimeresuru
585	120	3.0	644	1	CD93 MOUSE	O89103 mus musculus	658	110	2.8	569	1	PHRS HUMAN	O9bxr6 homo sapien
586	120	3.0	912	1	PGCB BOVIN	O28062 bos taurus	659	110	2.8	1124	1	TIE2 HUMAN	Q13751 homo sapien
587	120	3.0	1877	1	PKCS MOUSE	Q04592 mus musculus	660	109.5	2.8	2364	1	PGCA BOVIN	P13608 bos taurus
588	120	3.0	3358	1	PGCV MOUSE	Q62059 mus musculus	661	109.5	2.8	2920	1	CLR2 MOUSE	Q9r0m0 mus musculus
589	120	3.0	3381	1	PRTS BOVIN	P81282 bos taurus	662	109.5	2.8	4705	1	FAT2 DROME	O9vwl1 drosophila
590	119.5	3.0	675	1	PRTS BOVIN	P07224 bos taurus	663	109	2.8	379	1	WIFI MOUSE	O9vwal mus musculus
591	119.5	3.0	3579	1	STAN DROME	O9v5n8 drosophila	664	109	2.8	1172	1	LMB3 HUMAN	Q13751 homo sapien
592	119	3.0	258	1	VSP1 TRIST	Q91516 trimeresuru	665	108.5	2.8	773	1	AD11 MOUSE	O9r1v4 mus musculus
593	119	3.0	870	1	SRC2 HUMAN	Q969p6 homo sapien	666	108	2.7	251	1	CAP7 HUMAN	P20160 homo sapien
594	119	3.0	2738	1	PGCV RAT	Q9erb4 rattus norv	667	108	2.7	448	1	FBL5 HUMAN	O9ubx5 homo sapien
595	118.5	3.0	515	1	APX1 CAEEL	P41990 caenorhabdi	668	108	2.7	1321	1	PGCN HUMAN	O14594 homo sapien
596	118.5	3.0	728	1	HGF HUMAN	P14210 homo sapien	669	108	2.7	1450	1	SREJ STRPU	Q26627 strongyloce
597	118.5	3.0	728	1	HGF RAT	P17945 rattus norv	670	108	2.7	1700	1	BAR3 CHITE	Q03376 chironomus
598	118	3.0	133	1	AWN PIG	P26776 sus scrofa	671	108	2.7	2215	1	SORL MOUSE	O88307 m sortilin-
599	118	3.0	257	1	VSP4 TRIMU	Q91510 trimeresuru	672	108	2.7	2476	1	ZAN PIG	O28983 sus scrofa
600	118	3.0	374	1	WIFI XENLA	Q9w6f8 xenopus lae	673	107.5	2.7	331	1	PHR1 HUMAN	Q92496 homo sapien
601	118	3.0	883	1	PGCB MOUSE	Q61361 mus musculus	674	107.5	2.7	539	1	NTG1 MOUSE	Q8r490 mus musculus
602	118	3.0	931	1	ENR1 MOUSE	Q61549 mus musculus	675	107.5	2.7	769	1	AD11 HUMAN	O75078 homo sapien
603	117.5	3.0	188	1	KLK3 RAT	P15950 rattus norv	676	107.5	2.7	3014	1	CLR1 HUMAN	O9nyq6 homo sapien
604	117.5	3.0	649	1	PRTS MACMU	O28520 macaca mula	677	107.5	2.7	4289	1	TENX HUMAN	P22105 homo sapien
605	117.5	3.0	2214	1	SORL HUMAN	Q92673 h sortilin-	678	107.5	2.7	4544	1	LRP1 HUMAN	O07954 homo sapien
606	117.5	3.0	3375	1	UN52 CAEEL	Q96561 caenorhabdi	679	107	2.7	260	1	VSP1 TRILJE	O9df68 trimeresuru
607	117	3.0	704	1	FBL1 CHICK	Q97775 gallus gall	680	107	2.7	379	1	WIFI HUMAN	Q9y5w5 homo sapien
608	117	3.0	1639	1	LMG1 DROME	P15215 drosophila	681	106.5	2.7	165	1	TRY3 LUCCU	P35043 lucilia cup
609	116.5	3.0	377	1	MCP HUMAN	P15529 homo sapien	682	106.5	2.7	192	1	YD24 AQUAE	O67344 aquifex aeo
610	116.5	3.0	378	1	WIFI BRARE	O9w6f9 brachydanio	683	106.5	2.7	604	1	CFAT RAT	O9vuw3 rattus norv
611	116.5	3.0	443	1	FBL1 CRIGR	O50508 cricetus	684	106.5	2.7	755	1	COMP RAT	P35444 rattus norv
612	116.5	3.0	587	1	C08B ONCNY	Q90x85 oncorhynch	685	106.5	2.7	2813	1	VWF CANFA	Q28295 canis famil
613	116.5	3.0	1799	1	LMB2 MOUSE	Q61292 mus musculus	686	106	2.7	280	1	SLI1 HUMAN	Q13642 homo sapien
614	116	2.9	258	1	VSP3 TRIJE	Q9df66 trimeresuru	687	106	2.7	1133	1	EGF RAT	P07522 rattus norv
615	116	2.9	1375	1	NID2 HUMAN	Q41112 homo sapien	688	105.5	2.7	816	1	NEL2 HUMAN	O99435 homo sapien
616	115.5	2.9	256	1	PRN3 HUMAN	P24158 homo sapien	689	105	2.7	260	1	VSP2 VIPLE	O9pt40 vipera lebe
617	115.5	2.9	448	1	FBL5 MOUSE	O9vwh9 mus musculus	690	105	2.7	260	1	VSP6 TRIMU	Q9dgb3 trimeresuru

P01130 homo sapien
P41950 caenorhabdi
Q29116 sus scrofa
P24821 homo sapien
Q94933 homo sapien
Q9yrv4 brachydanio
Q01339 mus musculu
P98164 homo sapien
P97447 mus musculu
P17690 bos taurus

691 105 2.7 860 1 LDLR HUMAN
692 105 2.7 1107 1 YLK2 CAEL
693 105 2.7 1746 1 TENA_PIG
694 105 2.7 2201 1 TENA_HUMAN
695 105 2.7 2812 1 ZAN_HUMAN
696 104.5 2.6 322 1 FSA_BRARE
697 104.5 2.6 345 1 APOH_MOUSE
698 104.5 2.6 4655 1 LRP2_HUMAN
699 104 2.6 280 1 SLI1_MOUSE
700 104 2.6 345 1 APOH_BOVIN

ALIGNMENTS

RESULT 1

LFC_TACTR
ID_LFC_TACTR STANDARD; PRT; 1019 AA.
AC P28175;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Limulus clotting factor C precursor (PC 3.4.21.84) (FC).
OS Tachyploous tridentatus (Japanese horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OC Limulidae; Tachypieus.
OX NCBI_TaxID=6853;
[1]
RN SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND PARTIAL SEQUENCE.
RX MEDLINE=91177916; PubMed=2007602;
RA Ikohara Y., Iwanaga S.;
RA "Limulus factor C. An endotoxin-sensitive serine protease zymogen
RT with a mosaic structure of complement-like, epidermal growth
RT factor-like, and lectin-like domains.";
RL J. Biol. Chem. 266:6554-6561(1991).
CC -!- FUNCTION: This enzyme is closely associated with an endotoxin-
CC sensitive hemolymph coagulation system which may play important
CC roles in both hemostasis and host defense mechanisms. Its active
CC form catalyzes the activation of factor B.
CC -!- CATALYTIC ACTIVITY: Selective cleavage of 103-Arg-104 and
CC 124-Ile-Ile-125 bonds in Limulus clotting factor B to form
CC activated factor B. Cleavage of Pro-Arg-Xaa bonds in synthetic
CC substrates.
CC -!- ENZYME REGULATION: Activated by Gram-negative bacterial
CC lipopolysaccharides and chymotrypsin.
CC -!- SUBUNIT: Heterodimer of a light chain and a heavy chain linked by
CC a disulfide bond.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P28175-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=P28175-2; Sequence=VSP_005413, VSP_005414;
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 LCCL domain.
CC -!- SIMILARITY: Contains 5 Sushi (SCR) domains.

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EMBL; D90271; BAA14315.1; -;
EMBL; D90272; BAA14316.1; -;
PIR; A38738; A38738.
HSSP; P00763; LDPO.
MEROPS; S01.219; -.

DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; EGF.
DR InterPro; IPR004043; LCCL_dom.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF03815; LCCL; 1.
DR Pfam; PF00059; lectin_C; 1.
DR Pfam; PF00084; sushi_5.
DR Pfam; PF00089; trypsin_1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 5.
DR SMART; SM00034; CLECT; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00603; LCCL; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; FALSE_NEG.
DR PROSITE; PS00041; C_TYPE_LLECTIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00820; LCCL; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hemolymph clotting; Glycoprotein; Signal; Alternative splicing; Lectin;
KW Sushi; Repeat.
FT SIGNAL 1 25
FT CHAIN 26 1019 LIMULUS CLOTTING FACTOR C.
FT CHAIN 26 690 LIMULUS CLOTTING FACTOR C, HEAVY CHAIN.
FT CHAIN 691 1019 LIMULUS CLOTTING FACTOR C, LIGHT CHAIN.
FT CHAIN 691 762 LIMULUS CLOTTING FACTOR C, A CHAIN.
FT CHAIN 763 1019 LIMULUS CLOTTING FACTOR C, B CHAIN.
FT CHAIN 102 137 EGF-LIKE.
FT DOMAIN 142 195 SUSHI 1.
FT DOMAIN 200 254 SUSHI 2.
FT DOMAIN 260 321 SUSHI 3.
FT DOMAIN 325 421 LCCL.
FT DOMAIN 436 568 C-TYPE LECTIN.
FT DOMAIN 576 634 SUSHI 4.
FT DOMAIN 685 748 SUSHI 5.
FT DOMAIN 763 1019 SERINE PROTEASE.
FT ACT SITE 809 809 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 865 865 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 966 966 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT BINDING 960 960 SUBSTRATE (BY SIMILARITY).
FT DOMAIN 643 689 PRO-RICH.
FT DISULFID 106 118 BY SIMILARITY.
FT DISULFID 112 125 BY SIMILARITY.
FT DISULFID 127 136 BY SIMILARITY.
FT DISULFID 436 447 BY SIMILARITY.
FT DISULFID 464 564 BY SIMILARITY.
FT DISULFID 538 556 BY SIMILARITY.
FT DISULFID 794 810 BY SIMILARITY.
FT DISULFID 932 951 BY SIMILARITY.
FT DISULFID 962 996 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 740 740 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 767 767 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 912 912 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 492 498 LTTTWIG -> TDNVVAT (in isoform Short).
FT VARSPLIC 499 1019 /FTId=VSP_005413.
FT VARSPLIC 499 1019 Missing (in isoform Short).
FT VARSPLIC 1019 AA; 112346 MW; 5BC2864C6715289B CRC64;
SQ SEQUENCE 1019 AA; 112346 MW; 5BC2864C6715289B CRC64;
Query Match 17.0%; Score 672; DB 1; Length 1019;
Best Local Similarity 25.6%; Pred. No. 7.4e-43;

FT CHAIN 763 1019 LIMULUS CLOTTING FACTOR C, B CHAIN.
 FT DOMAIN 102 137 EGF-LIKE.
 FT 142 195 SUSHI 1.
 FT DOMAIN 200 254 SUSHI 2.
 FT 260 321 SUSHI 3.
 FT DOMAIN 325 421 LCCL.
 FT 436 568 C-TYPE LECTIN.
 FT DOMAIN 576 634 SUSHI 4.
 FT 685 748 SUSHI 5.
 FT DOMAIN 763 1019 SERINE PROTEASE.
 FT ACT SITE 809 809 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 865 865 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT 966 966 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT BINDING 960 960 SUBSTRATE (BY SIMILARITY).
 FT DOMAIN 643 689 PRO-RICH.
 FT 106 118 BY SIMILARITY.
 FT DISULFID 112 125 BY SIMILARITY.
 FT 127 136 BY SIMILARITY.
 FT DISULFID 436 447 BY SIMILARITY.
 FT 464 564 BY SIMILARITY.
 FT DISULFID 538 556 BY SIMILARITY.
 FT 794 810 BY SIMILARITY.
 FT DISULFID 932 951 BY SIMILARITY.
 FT 962 962 BY SIMILARITY.
 FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 624 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 740 740 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 767 767 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 912 912 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1019 AA; 112429 MW; 918A1EDB817B6C3 CRC64;
 SQ SEQUENCE 1019 AA; 16.9%; Score 665; DB 1; Length 1019;
 Query Match
 Best Local Similarity 25.4%; Pred. No. 2.5e-42;
 Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNIMCECEVDQIECVCPKRE-----VVGTYIPCCRNENECDCLIH 82
 DB 184 PNGQSNFPFKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RPSGDS----- 229
 QY 83 PGCTIFENCKSCR-NGSWGTL-----YPLNAHCETWTHA-----KPGFVI----- 103
 DB 230 PYYLIGQETLTQCGQWNGQIPQCKNLVFCPLDPVNAEHKVIQVGEQKYGQFPQGT 289
 QY 104 -----DDYVVGFCYACR--AGWYGG--DCNR-----CGQVLR-- 133
 DB 290 VTYTCGNYFLMGFDTLKCNPDGWSGSGQSCVKVADREVDCDSKAVDFLDVGPVRIH 349
 QY 134 APKQIILLES-----YPLNAHCETWTHA-----KPGFVI----- 162
 DB 350 CPAGCSLTAGTWGTAIYHELSSVCRAAIAHAKLPNSGGAVHVNNGPYSDPLGDLNGI 409
 QY 163 ---QRFVNLSEFDYM-----CQDYVEVRD-----GDNRDGQIIKRVCGN--E 202
 DB 410 KSEELKSLARSFRFDYVRSSTAGKSCPDGWFVEVDENCVYVTSKQAWERAQGVCTNMAA 469
 QY 203 RPAPQS---IGSLHLVLFHSDG-SKNFDGFH-----AYEETACSS 241
 DB 470 RLAVLDKQVIPSNTLTETLRGKLTWTWIGLHRLDAEKPFIEWLMDRNSNVVLDNLTFWAS 529
 QY 242 SPCFDHGTCLV---DKAGS--YKACLAGYTGRCENILLEEN---CSDPGGPPVNGYQKI 293
 DB 530 GPGFNETNCVYMDIQLOQSVWKTSCFOPSFACWMLDSLRNKAACDDPGSLENGHATL 589
 QY 294 TGGPGLINGRHAKIGITVWVFFCNNSVYLSGNKRTCCQNGEWSGKQPICIK--ACREPKI 351
 DB 590 HGQS--IDGFYA--GSSIRYSEVLHYLSGTETVCTTGTWTSAPKPRCIKVIITCONPV 645
 QY 352 SLIVRRVLPMQVSRETPLHQLYSNAFSKQKLO-----SAPTKKPLPFGD----- 398
 DB 646 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLAARAAKPPPKPRSSQPSSTVDLASK 702
 QY 399 --LPMGYQHLHTQLOVEICISPFVRLIGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455

DB 703 VKLPEGYRVGSRAIYTCESRYAYELLGSGQRCDNSNGWSPASCIPVCGRSPSPFP 762
 QY 456 -----KTQGLRWPMQAAIYRTSGVHDGSLHKGAWFLVCSGALVNERTVVAARHCVTDLG 510
 DB 763 IWNGNSTEIGQNPWQAGISRWLA-----DHNWFLQCGGSLNKKWIVTAACHVTYSA 815
 QY 511 KVTWIKTADLVKLVGKPYRDDDEKTIQSLQISAILHPNYDPILLDADIAIKLLDKA 570
 DB 816 TAEITDPNQFMYLGYKYRDDSDDDYVQVREALEIHWNPYDGNLNFIDIALIQLKTPV 875
 QY 571 RISTRVOPICLAASRDLSTSFQESH1-----TVAGWNLADVRSFGKNDTLRSVVSV 624
 DB 876 TLTRVOPICLPT--DIIT---REHLKEGTLAVVTGNG-----LNENNTYSETIOQAVLPV 926
 QY 625 VDSLLCEQHEHDGIPVSDTNDMFCASWEPTAPSDICTAETGGIAAVSFGRASPEPRWH 684
 DB 927 VAASTCEEGYKEADPLTVTENMFCAGYK-KGYDACSDDSGG--PLVFADDSRTERRWV 983
 QY 685 LMGVLVSWSYDKTCSH-RLSTAFYTKVLFPKQWIER 717
 DB 984 LEGIVSWGSPSGCGKANQYGGFTKVNVLFWIRQ 1017

RESULT 3

CHAR HUMAN
 ID CRAR_HUMAN STANDARD; PRT; 699 AA.
 AC P48740; O95570; Q9UF09;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Complement-activating component of Ra-reactive factor precursor
 DE (EC 3.4.21.-) (Ra-reactive factor serine protease p100) (RaRF)
 DE (Mannan-binding lectin serine protease 1) (Mannose-binding protein
 DE associated serine protease) (MASP-1).
 GN MASP1 OR CRARF OR CRARF1 OR PRSS5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94055062; PubMed=8240317;
 RA Takada F., Takayama Y., Hattuse H., Kawakami M.;
 RT "A new member of the C1s family of complement proteins found in a
 RT bactericidal factor, Ra-reactive factor, in human serum.";
 RL Biochem. Biophys. Res. Commun. 196:1003-1009(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=94289349; PubMed=8018603;
 RA Sato T., Endo Y., Matsushita M., Fujita T.;
 RT "Molecular characterization of a novel serine protease involved in
 RT activation of the complement system by mannose-binding protein.";
 RL Int. Immunol. 6:665-669(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97079701; PubMed=8921412;
 RA Endo Y., Sato T., Matsushita M., Fujita T.;
 RT "Exon structure of the gene encoding the human mannose-binding
 RT protein-associated serine protease light chain: comparison with
 RL complement C1r and C1s genes.";
 RL Int. Immunol. 8:1355-1358(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99402590; PubMed=10475605;
 RA Takayama Y., Takada F., Nowatari M., Kawakami M., Matsura N.;
 RT "Gene structure of the P100 serine-protease component of the human Ra-
 RT reactive factor.";
 RL Mol. Immunol. 36:505-514(1999).
 CC -!- FUNCTION: Component of the bactericidal ra-reactive factor rarf

which specifically binds to RA and R2 polysaccharides expressed by certain enterobacteria. It triggers the activation of complement cascade by activating the C4 and C2 components. It activates the C4 component by cleaving the alpha-chain of C4.

-1- SUBUNIT: RARF consists of a complement-activating component (CRARF) and a polysaccharide-binding (mannose-binding) component. CRARF is an heterodimer of a heavy (p70) and a light chain (p29) linked by a disulfide bond.

-1- DOMAIN: CRARF has a module organization similar to C1r and C1s.

-1- SIMILARITY: Belongs to peptidase family S1.

-1- SIMILARITY: Contains 2 CUB domains.

-1- SIMILARITY: Contains 1 EGF-like domain.

-1- SIMILARITY: Contains 2 Sushi (SCR) domains.

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EMBL; D17525; BAA04477.1; --
EMBL; D28593; BAA05928.1; --
EMBL; D61695; BAA34864.1; --
EMBL; AB010822; BAA34864.1; JOINED.
EMBL; AB010813; BAA34864.1; JOINED.
EMBL; AB010814; BAA34864.1; JOINED.
EMBL; AB010815; BAA34864.1; JOINED.
EMBL; AB010816; BAA34864.1; JOINED.
EMBL; AB010817; BAA34864.1; JOINED.
EMBL; AB010818; BAA34864.1; JOINED.
EMBL; AB010819; BAA34864.1; JOINED.
EMBL; AB010820; BAA34864.1; JOINED.
EMBL; AB010821; BAA34864.1; JOINED.
EMBL; D61690; BAA34864.1; JOINED.
EMBL; D61691; BAA34864.1; JOINED.
EMBL; D61692; BAA34864.1; JOINED.
EMBL; D61693; BAA34864.1; JOINED.
EMBL; D61694; BAA34864.1; JOINED.
EMBL; AB007617; BAA89206.1; --
EMBL; AB007602; BAA89206.1; JOINED.
EMBL; AB007603; BAA89206.1; JOINED.
EMBL; AB007604; BAA89206.1; JOINED.
EMBL; AB007605; BAA89206.1; JOINED.
EMBL; AB007606; BAA89206.1; JOINED.
EMBL; AB007607; BAA89206.1; JOINED.
EMBL; AB007608; BAA89206.1; JOINED.
EMBL; AB007609; BAA89206.1; JOINED.
EMBL; AB007610; BAA89206.1; JOINED.
EMBL; AB007611; BAA89206.1; JOINED.
EMBL; AB007612; BAA89206.1; JOINED.
EMBL; AB007613; BAA89206.1; JOINED.
EMBL; AB007614; BAA89206.1; JOINED.
EMBL; AB007615; BAA89206.1; JOINED.
EMBL; AB007616; BAA89206.1; JOINED.
PIR; I54763; I54763.
HSSP; P00736; LAPO.
MEROPS; S01.198; --
Genow; HGNC:6901; MASPL.

MIN; 600521; --
GO; GO:0004252; F:serine-type endopeptidase activity; TAS.
GO; GO:0006956; P:complement activation; TAS.
InterPro; IPR000152; Asx hydroxyl_S.

InterPro; IPR000859; CUB_Ser_trypsin.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF-like.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR000436; Sushi_SCR_CCP.
Pfam; PF00431; CUB; 2.
Pfam; PF00084; sushi; 2.

DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00032; CCP; 2.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00020; TRY_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS0240; TRYPSIN_HIS; 1.
DR PROSITE; PS00134; TRYPSIN_SER; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Complement pathway; Serine protease; Protease;
KW Glycoprotein; Sushi; Repeat; Signal; EGF-like domain; Hydroxylation.
FT SIGNAL 1 19
FT CHAIN 20 699
FT CHAIN 20 448
FT CHAIN 449 699
FT CHAIN 20 138
FT DOMAIN 139 182
FT DOMAIN 185 297
FT DOMAIN 300 363
FT DOMAIN 366 433
FT DOMAIN 449 699
FT ACT_SITE 490 490
FT ACT_SITE 552 552
FT ACT_SITE 646 646
FT MOD_RES 159 159
FT DISULFID 73 91
FT DISULFID 143 157
FT DISULFID 153 166
FT DISULFID 168 181
FT DISULFID 185 212
FT DISULFID 242 260
FT DISULFID 301 349
FT DISULFID 329 362
FT DISULFID 367 414
FT DISULFID 397 432
FT DISULFID 436 572
FT DISULFID 614 631
FT DISULFID 642 672
FT CARBOHYD 49 49
FT CARBOHYD 178 178
FT CARBOHYD 385 385
FT CARBOHYD 407 407
FT CONFLICT 235 235
FT CONFLICT 285 285
FT CONFLICT 499 499
FT CONFLICT 499 499
FT CONFLICT 527 527
FT CONFLICT 543 543
FT CONFLICT 552 552
FT CONFLICT 643 643
SQ SEQUENCE 699 AA; 79258 MW; ADD9697AE6AB01B5 CRC64;
Query Match 12.1%; Score 478; DB 1; Length 699;
Best Local Similarity 24.6%; Pred. No. 2.1e-28;
Matches 176; Conservative 93; Mismatches 217; Indels 228; Gaps 38;
QY 69 CRNEECDSCLHPGCTIFENCKSRNGSWGTLDDFYVKGFGYCAECRAGWY----GGD 124
Db 143 CKEREDEELSCDHY-----CHN-----YIGGYICS-CRFGYILHTDNR 180
QY 125 C-MRCQVLRAPKGOILL-----ESYPLNAHCWTTHAKPGFVIOIRFVMSLEFYM-- 176
Db 181 CRVECDNLFTQRTGVITSPDFPNPKSSECDYITIELEGFMVNLQFEDI----FDIQDH 237
QY 177 ----COYDYVEVRDGNRDGQIKIKVCNRPAPIQISGLSHLVFHSKGNKFDGFHAI 232
Db 238 PEVPCPYDIKIKVGP-----KVLGPGCGEKAPEPISTQSHSVLILFHSNDAENRGWRL- 292

FT	DISULFID	372	419	POTENTIAL.
FT	DISULFID	402	437	POTENTIAL.
FT	DISULFID	441	577	INTERCHAIN (POTENTIAL).
FT	DISULFID	619	636	POTENTIAL.
FT	DISULFID	647	677	POTENTIAL.
FT	CARBOHYD	54	54	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	183	183	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	390	390	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	412	412	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	704 AA;	71F44F3012D2C67F CRC64;	
Query Match 12.0%; Score 475; DB 1; Length 704;				
Best Local Similarity 23.3%; Pred. No. 3.5e-28;				
Matches 196; Conservative 109; Mismatches 256; Indels 280; Gaps 46;				
QY	11	LTEQLQLLSL	-----PREYTV-INE-----ACPG-----	-----AEWNIMCRE----- 44
DB	4	LSFWRLLLHALCLALPEVSAHVELNEMFGQIQSPGYPDSYSDSEVTWNIIVPGFRI		63
QY	45	-----CCREYDQIE-----CVC-----	-----PGKREV-----	61
DB	64	KLYFMHFNLESSYLCEYDYVVKETEDQVLATFCGRETTEQTQPGQEVLSPTGFMFMTVF		123
QY	62	-----VGTIFCCNEEENECCLIHPCCTIFENCKSCNCGSWGGLTD		104
DB	124	RSDFSNEERTGFDHAYMAVDVDECKERDEELSCDHY-----	-----CHN-----	164
QY	105	DFYVKGPGYACACRAGWY-----GGDC-MRC-GQVLRAPKGOILL-----	-----ESYPLNAHCEWTI	154
DB	165	--YIGGYCS-CHFGYILHNDNTRCVCESGNLFTQRTGTITSPDPNPNPKSSECSYII		221
QY	155	HAKPGFVIQRLFVMSLEFD-----YMCQDYVEVRDGNDRDQIIXKVCNERNPAPIQ		208
DB	222	DLEEGFMVSLQFEDI-----FDIEDHPVPCPYDIKIKAGSKWGP-----CGEKSPEPIS		274
QY	209	SIGSSLHLVPHSDGSKNFDGFHAIYEITACSSPCFHDCTCVLDKAGSYKCAACLAGYTG		268
DB	275	TQTHSVQILFRSDNSGNGWRL-----	-----SYRAA-----	303
QY	269	QRCEENLEERNCDPGPVNGYQKITGGPGLNGRHAIGITVVSFFCNNSY-VLSGNE--		325
DB	304	NECPKL-----QP--PV--YKIEPSSQAVS--FKQOVLVS--CDTGYKVLKONGVM		347
QY	326	---KRTCCQNGEWGKQIPIC- IKACREPKISDLVRRRVLPMQVQSRETPHLQIYSAPSK		381
DB	348	DTFQIECLKDGANSKIPTCKIVDCGAP-----	-----AGLK	379
QY	382	QKLOAPTCKPALPFCDLPMGYQHLHTQLOVEICISPYRELGSRR--RTCLRTGKWSGRA		439
DB	380	HGLVTFSTRNLTTY-----XSEIRYSCQPPYKMLHNTTGYVTCSAHGTWTKV		429
QY	440	-----PSCIPICG-----KIENI--TAPKTQGLRWPQQAIIYRRTSGVHDGSLHKGAW		485
DB	430	LKESLPTCLVCGVPKFSRQISRIENGRPAQKG-TMPWTAML-----	-----SHLNGQP	478
QY	486	FLVCSGALVNERVTWVAACHV-----TDLGKVTMIKTADLKVLVGLKPY-RDDRDEK		536
DB	479	F--CGSLLGSNVMVLAACHLHOSLDPEEPTLHSSYLLSPDFFKIIMGKHWRRSDEDE-		535
QY	537	TIOSLOISAILHPNVDPIILLDIALIKLKDARISTRVOPICLAASRDLSFQESH		596
DB	536	--QHLHVKRTTLPLYNPSTFENDGLGVLSESPRLNDFWNPCLPE-----QSTSGTMV		599
QY	597	TVAGWNVLDVRSPFGKNDLRSQVSVVDSLLCEOEHEHDGIPVSVTNNMFCASWEPTA		656
DB	590	IVSGWKGQFLQRP-----ENLMEIEIPIVNSDTCQEAATP--LKKKYTKDMICAG-EKEG		642
QY	657	PSDICTABTCGIAAVSPGGRASPRHLMGLVSWSYDKTCSHRLSTAFKVLVFPKDWIE		716
DB	643	GKDACAGDSGGPMVT-----KDAERDQWLVGVWSWGEDCGKDRYG-VYSYIYFNKDWIQ		697
QY	717	R 717		

DB	698	R 698
RESULT 5		
ID	CIR_HUMAN	STANDARD; PRT; 705 AA.
AC	P00736;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	01-AUG-1988 (Rel. 08, Last sequence update)	
DT	15-MAR-2004 (Rel. 43, Last annotation update)	
DE	Complement C1r component precursor (EC 3.4.21.41).	
GN	C1r.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	SEQUENCE FROM N.A.
RP	MEDLINE=87026566; PubMed=3021205;	
RX	Leytus S.P., Kurachi K., Sakariassen K.S., Davie E.W.;	
RA	"Nucleotide sequence of the cDNA coding for human complement C1r.;"	
RT	Biochemistry 25:4855-4863(1986).	
RN	[2]	SEQUENCE FROM N.A. AND VARIANT LEU-152.
RP	MEDLINE=87156625; PubMed=3030286;	
RX	Journet A., Tosi M.;	
RA	"Cloning and sequencing of full-length cDNA encoding the precursor of	
RT	human complement component C1r.;"	
RL	Biochem. J. 240:783-787(1986).	
RN	[3]	SEQUENCE OF 18-463.
RP	MEDLINE=87241248; PubMed=3036070;	
RX	Arlaud G.J., Willis A.C., Gagnon J.;	
RA	"Complete amino acid sequence of the A chain of human complement-	
RT	classical-pathway enzyme C1r.;"	
RL	Biochem. J. 241:711-720(1987).	
RN	[4]	SEQUENCE OF 454-705.
RP	MEDLINE=83204782; PubMed=6303394;	
RX	Arlaud G.J., Gagnon J.;	
RA	"Complete amino acid sequence of the catalytic chain of human	
RT	complement subcomponent C1r.;"	
RL	Biochemistry 22:1758-1764(1983).	
RN	[5]	SEQUENCE OF 152-186, AND HYDROXYLATION.
RP	MEDLINE=88005128; PubMed=2820791;	
RX	Arlaud G.J., van Dorsselaer A., Bell A., Mancini M., Aude C.,	
RA	Gagnon J.;	
RT	"Identification of erythro-beta-hydroxyasparagine in the EGF-like	
RL	domain of human C1r.;"	
FEBS	FEBS Lett. 222:129-134(1987).	
RN	[6]	SEQUENCE OF 133-137; 187-211 AND 609-613, AND PHOSPHORYLATION.
RP	MEDLINE=96221263; PubMed=8635594;	
RX	Pelloux S., Thielens N.M., Hudry-Clergeon G., Petillot Y., Filhol O.,	
RA	Arlaud G.J.;	
RT	"Identification of a cryptic protein kinase CK2 phosphorylation site	
RL	in human complement protease C1r, and its use to probe intramolecular	
FEBS	FEBS Lett. 386:15-20(1996).	
RN	[7]	STRUCTURE BY NMR OF 140-192.
RP	MEDLINE=98138432; PubMed=9477945;	
RX	Bersch B., Hernandez J.-F., Marion D., Arlaud G.J.;	
RA	"Solution structure of the epidermal growth factor (EGF)-like module	
RT	of human complement protease C1r, an atypical member of the EGF	
RL	family.;"	
Biochemistry	37:1204-1214(1998).	
-I- FUNCTION:	C1r B chain is a serine protease that combines with C1q	
and C1s to form C1, the first component of the classical pathway		
of the complement system.		
-I- CATALYTIC ACTIVITY:	Selective cleavage of Lys(or Arg)- -Ile bond	
in complement subcomponent C1s to form the active form of C1s		

(EC 3.4.21.42).
 - SUBUNIT: C1 is a calcium-dependent trimolecular complex of C1q, C1r and C1s in the molar ratio of 1:2:2. C1r is a dimer of identical chains, each of which is activated by cleavage into two chains, A and B, connected by disulfide bonds.
 - SIMILARITY: Belongs to peptidase family S1.
 - SIMILARITY: Contains 2 CUB domains.
 - SIMILARITY: Contains 1 EGF-like domain.
 - SIMILARITY: Contains 2 Sushi (SCR) domains.
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 EMBL; X04701; CAA28407.1; -;
 DR EMBL; M14058; AAM51851.1; -;
 DR PIR; A24170; C1HURB.
 DR PDB; 1APQ; 17-SEP-97.
 DR PDB; 1GPZ; 31-JUL-02.
 DR MEROPS; S01.192; -;
 DR GenSeq; HGNC:1246; C1r.
 DR MIM; 216950; -;
 DR GO; GO:0003815; F:complement component C1r activity; TAS.
 DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
 DR GO; GO:0006955; P:immune response; TAS.
 DR InterPro; IPR000152; Asx_hydroxyl_s.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001881; EGF_CA.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR000436; Sushi_SCR_CCP.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00084; sushi; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00032; CCP; 2.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00020; TRYP_SPC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS00022; EGF_1; FALSE_NEG.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Complement pathway; plasma; Glycoprotein; Serine protease; Hydrolase;
 KW Hydroxylation; Phosphorylation; Sushi; Repeat; Signal;
 KW EGF-like domain; 3D-structure; Polymorphism.
 DR SIGNAL 1 17
 FT CHAIN 18 463 COMPLEMENT C1R HEAVY CHAIN.
 FT CHAIN 464 705 COMPLEMENT C1R LIGHT CHAIN.
 FT DOMAIN 18 141 CUB 1.
 FT DOMAIN 142 190 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 193 305 CUB 2.
 FT DOMAIN 308 372 SUSHI 1.
 FT DOMAIN 375 448 SUSHI 2.
 FT DOMAIN 464 705 SERINE PROTEASE.
 FT ACT_SITE 502 502 CHARGE RELAY SYSTEM.
 FT ACT_SITE 557 557 CHARGE RELAY SYSTEM.
 FT ACT_SITE 654 654 CHARGE RELAY SYSTEM.
 FT MOD_RES 167 167 HYDROXYLATION.
 FT MOD_RES 206 206 PHOSPHORYLATION (BY CK2).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 514 514 N-LINKED (GLCNAC. . .).

FT CARBOHYD 581 581 N-LINKED (GLCNAC. . .).
 FT DISULFID 71 89 PROBABLE.
 FT DISULFID 146 165
 FT DISULFID 161 174
 FT DISULFID 176 189
 FT DISULFID 193 220 PROBABLE.
 FT DISULFID 250 268 PROBABLE.
 FT DISULFID 309 358 PROBABLE.
 FT DISULFID 338 371 PROBABLE.
 FT DISULFID 376 429 PROBABLE.
 FT DISULFID 406 447 PROBABLE.
 FT DISULFID 451 577 INTERCHAIN (PROBABLE).
 FT DISULFID 620 639 POTENTIAL.
 FT DISULFID 650 680 POTENTIAL.
 FT VARIANT 152 152 S -> L (in dbSNP:1801046).
 FT TURN 145 147 /FTid=VAR_016103.
 FT TURN 150 152
 FT TURN 160 161
 FT STRAND 164 168
 FT TURN 169 170
 FT STRAND 171 175
 FT TURN 178 179
 FT STRAND 181 182
 FT TURN 184 185
 FT STRAND 189 190
 SQ SEQUENCE 705 AA; 80173 MW; 5CBCCC0201061463 CRC64;
 Query Match 10.2%; Score 403.5; DB 1; Length 705;
 Best Local Similarity 22.9%; Pred. No. 8.9e-23;
 Matches 178; Conservative 96; Mismatches 259; Indels 245; Gaps 41;
 QY 44 ECRYDQIEC-----VC-----PGKREVVGYTIPCC-----RNEECDC 77
 Db EGCFFDYVYKISADKSLGRFCGQLGSLGNPPGKKEFMSQGNKMLTFHTDFSEEN--G 126
 QY 78 SCLHPGCTIF---ENCKSCENGSGGTLD-----DFYVKGFFCAECRAG----- 120
 Db TIMFYKFLAYQAVDLDECASRSKSGEEDPQOCQHLCHNYGVGYPCS-CRPGELOED 185
 QY 121 ---YGGDCMRGQVLRAPKQI-LLE---SYPLNAHCEWTTHAKPGFVIQIRFVMSLEF 173
 Db RHSCQAECSSELYTEASGYISSLEYPRSYPPDLRCNYSIRVERGLTLHLKLE---PF 240
 QY 174 D-----YMCQYDYVVEVDGNRDGQIIKRVCGNERPAPIOSIGSSSLHLVLFHSDGSKNF 227
 Db DIDDHQVHCYPDQIQI---YANGKNIGFCGKQRPDLDTSSNAVDLLFTFDESQDSR 296
 QY 228 GFHAIY-EEITACSSSPCFHDGTCLVDKAGSYKACLAGYTGQRCENLEERNCSDPGP 286
 Db GWKURYTTEIIKCPQPKTLDFTTIQNLQPOYQ---FRDYFIATCK----- 339
 QY 287 VNGYQKITGGPGLINGRHAQIGTVVSPFCNNYSYVLGSGNEKRTCOQNGSWGKQPIK- 345
 Db QGYQLLIEGNQVL-----HSFT-----AVCQDDGTWHRAMPCKIKD 375
 QY 346 CREPKISDLVRRVLPQVQSRFPLHQLYSAAFSKQLQSAPTYKPAKLPAGDL-----PM 401
 Db CGQPR-----CGQPR-----NLPNGDFRYTTM 393
 QY 402 GVOHLHLOQYECISPFYR---RLGSSRR---TCLRTGKWSG-----RAPSCIPICGK 448
 Db GUNYKARIQYTCHEPYKQYKQTRAGSRESEGVYCTAAGIWKQKQKEKIPCLIPVCGK 453
 QY 449 IEN-----ITAPKTQGLRWPQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNRVTV 500
 Db PWPVPEQRQRIIGGQKAKMGFPWQV-----FTNIHG-----GGALLDRWIL 498
 QY 501 VAAHCVTLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQ-----ISAILLPNY-- 552
 Db TAAHTLPKHEAQ-SNASLDVFLG-----HTNVEELMKLGNHPIRRVSHPDYRQ 548
 QY 553 -DPILLDADIAILKLDKARISTRVQPICLAASRDLSLTSFQESHI-TVAGWNVLAD----- 606

Db 549 DESVNEFDIALLELENSVTLGPNLLPICLP---DNDTFYDLGLMGVSGFGVMEKIAH 605
Qy 607 ---VSPGKNDTLRSGVVVVDLLCERQEDHGIPVSVTDNMFCSWEPTAPSDICT 662
Db 606 DLRFVRLP-----VANPQACEWLKGRKRMVFSQNMFCAG-HPSLKQDACQ 651
Qy 663 AETGGIAAVFPGRASPEPRHMLGLVSWSYDKTCSHRLSTAFKVLFPKDWIERNMK 720
Db 652 GDSGGVFAVRDPN----TDRWATGIVSWGIG--CS-RGYGFTKVLNLYVDWIKEME 702

RESULT 6
MAS2 HUMAN
ID MAS2 HUMAN STANDARD; PRT; 686 AA.
DT 00187; 075754; Q9BZH0; OSUBP3; Q9Y270;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mannan-binding lectin serine protease 2 precursor (EC 3.4.21.-)
DE (Mannose-binding protein associated serine protease 2) (MASP-2)
DE (MBL-associated serine protease 2).
GN MASP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Liver;
RX MEDLINE=97242412; PubMed=9087411;
RA Thiel S., Jensen T.V., Stover C.M., Schwaebler W.J., Laursen S.B.,
RA Poulsen K., Willis A.C., Eggleton P., Hansen S., Holmskov U.,
RA Reid K.B.M., Jensenius J.C.;
RT "A second serine protease associated with mannan-binding lectin that
RT activates complement.";
RL Nature 386:506-510(1997).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Thiel S., Vorup-Jensen T., Stover C.M., Schwaebler W., Laursen S.B.,
RA Poulsen K., Willis A.C., Eggleton P., Hansen S., Holmskov U.,
RA Reid K.B.M., Jensenius J.C.;
RT "Identification and characterization of a novel protein of the human
RT complement system, mannan-binding lectin-associated serine protease-2
RT (MASP-2).";
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Liver;
RX MEDLINE=99192764; PubMed=10092804;
RA Stover C.M., Thiel S., Thelen M., Lynch N.J., Vorup-Jensen T.,
RA Jensenius J.C., Schwaebler W.J.;
RT "Two constituents of the initiation complex of the mannan-binding
RT lectin activation pathway of complement are encoded by a single
RT structural gene.";
RL J. Immunol. 162:3481-3490(1999).
[4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=99262289; PubMed=10330290;
RA Takahashi M., Endo Y., Fujita T., Matsushita M.;
RT "A truncated form of mannose-binding lectin-associated serine
RT protease (MASP)-2 expressed by alternative polyadenylation is a
RT component of the lectin complement pathway.";
RL Int. Immunol. 11:859-863(1999).
[5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Park D., Kim B., Baek K., Yoon J.;
RT "Structure of human MASP-2 gene.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Trypsin protease that presumably plays an important role
CC in the initiation of the mannose-binding lectin (MBL) complement
CC activation pathway. After activation it cleaves C4 generating C4a
CC and C4b.

CC -1- SUBUNIT: Isoform 2 binds to MASP-1.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O00187-1; Sequence=Displayed;
CC Name=2; Synonyms=MAP19, Small MBU-associated protein, sMAP;
CC IsoId=O00187-2; Sequence=VSP_005383, VSP_005384;
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 2 Sushi (SCR) domains.
CC
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CC
CC EMBL; Y09926; CAA71059.1; -
CC EMBL; X98400; CAA67050.1; -
CC EMBL; Y18281; CAB50728.1; -
CC EMBL; Y18283; CAB50730.1; -
CC EMBL; Y18284; CAB50731.1; -
CC EMBL; Y18286; CAB50732.1; -
CC EMBL; Y18286; CAB50733.1; -
CC EMBL; Y18287; CAB50734.1; -
CC EMBL; Y18287; CAB50735.1; -
CC EMBL; A5008047; BAA78616.1; -
CC EMBL; A5033742; BAA85658.1; -
CC EMBL; AF321562; AAG50274.1; -
CC EMBL; AF321558; AAG50274.1; JOINED.
CC EMBL; AF321559; AAG50274.1; JOINED.
CC EMBL; AF321560; AAG50274.1; JOINED.
CC EMBL; AF321561; AAG50274.1; JOINED.
CC EMBL; AF321558; AAG50275.1; -
CC PIR; A59271; A59271.
CC HSP; P00763; IDPO.
CC MEROPS; S01.229; -
CC Genew; HGNC:6902; MASP2.
CC MIM; 605102; -
CC GO; GO:0004252; F-serine-type endopeptidase activity; TAS.
CC GO; GO:0006960; P-antimicrobial humoral response (sensu Inver. . . ; TAS.
CC GO; GO:0006956; P-complement activation; TAS.
CC InterPro; IPR000152; Axx_hydroxyl_S.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR01881; EGF_Ca.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00084; sushi; 2.
CC PRINTS; PR00089; trypsin; 1.
CC SMART; SM00032; CCP; 2.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00179; EGF_Ca; 1.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS01187; EGF_Ca; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Complement pathway; Serine protease; Protease;
KW Glycoprotein; Sushi; Repeat; Signal; EGF-like domain; Hydroxylation;
KW Alternative splicing.
FT SIGNAL 1 15 POTENTIAL.
FT CHAIN 15 686 MANNAN-BINDING LECTIN SERINE PROTEASE 2.

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FT CHAIN 16 444 MANNAN-BINDING LECTIN SERINE PROTEASE 2 A
FT PT CHAIN 445 686 CHAIN.
FT PT CHAIN 445 686 MANNAN-BINDING LECTIN SERINE PROTEASE 2 B
FT PT CHAIN 445 686 CHAIN.
FT PT DOMAIN 16 137 CUB 1.
FT PT DOMAIN 138 181 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
FT PT DOMAIN 184 296 CUB 2.
FT PT DOMAIN 299 362 SUSHI 1.
FT PT DOMAIN 365 431 SUSHI 2.
FT PT DOMAIN 445 686 SERINE PROTEASE.
FT PT ACT SITE 483 483 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT PT ACT SITE 532 532 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT PT ACT SITE 633 633 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT PT MOD_RES 158 158 HYDROXYLATION (POTENTIAL).
FT PT DISULFID 72 90 POTENTIAL.
FT PT DISULFID 142 156 POTENTIAL.
FT PT DISULFID 152 165 POTENTIAL.
FT PT DISULFID 167 180 POTENTIAL.
FT PT DISULFID 241 259 POTENTIAL.
FT PT DISULFID 300 348 POTENTIAL.
FT PT DISULFID 328 361 POTENTIAL.
FT PT DISULFID 366 412 POTENTIAL.
FT PT DISULFID 396 430 POTENTIAL.
FT PT DISULFID 434 552 INTERCHAIN (POTENTIAL).
FT PT DISULFID 598 618 POTENTIAL.
FT PT DISULFID 629 660 POTENTIAL.
FT PT VARSPLIC 182 185 ALCS -> EOSL (in isoform 2).
FT PT VARSPLIC 186 686 /FID=VSP 005383.
FT PT CONFLICT 361 362 Missing (in isoform 2).
FT PT CONFLICT 371 371 MISSING (in isoform 2).
FT PT CONFLICT 372 372 D -> Y (IN REF. 5).
FT PT CONFLICT 442 442 L -> LCS (IN REF. 3).
FT PT CONFLICT 447 447 G -> E (IN REF. 5).
FT PT CONFLICT 461 462 G -> E (IN REF. 5).
FT PT CONFLICT 473 473 MISSING (IN REF. 3).
FT PT CONFLICT 473 473 L -> LIL (IN REF. 3).
FT PT CONFLICT 473 473 L -> LIL (IN REF. 3).
FT PT SEQUENCE 686 AA; 75685 MW; 4E34DED159448A2A CRC64;

Query Match
Best Local Similarity 10.2%; Score 400.5; DB 1; Length 686;
Matches 173; Conservative 78; Mismatches 245; Indels 267; Gaps 34;

QY 128 CQOVL--APK-----GQILLESVP-----LNAHCETHAKPGVQLRFVWLSLEFDY 175
DB 11 CGSVATPLGPKWPEVFGRLASGPPGEYANDQERRWTLTAPPGYRLRLYTFHFDLELSH 70
QY 176 MCQYDVEVRDGNRDGQIIKVCNNE-----RPAP-----IQSIGSLHLVLFHSDGS--KN 225
DB 71 LCEYDFVKLSG-----AKVLATLCGOESTDTERAPGKDTFFSLGSSLDITFRSDYSNEKP 126
QY 226 FQGFUAIY--EETACSSSP-----CFHDGTCVLDKAGSYKACLAGLYGTQR-----CENL 274
DB 127 FTGFEPAYAEIDECQAVAPGAETCDH---CHNHLGGFYSCRAGYVYLNHKTCSAL 183
QY 275 -----LEE----- 277
DB 184 CSGQVQFQSGELSPPEPRYPKLSCTYSISLEGFSVLDFVESFDVETHPETLCPY 243
QY 278 -----RNCSDP 283
DB 244 DFLKIQTDREBHPFGCKTLPHRIETKSNVTITFTVDSBGHTGKWIHYTSTAACVPY 303
QY 284 GGVNAGYQKITGGPLNGRHAH--IGTVSVFFCNNSY--VLSG-----NEKTCQONGEW 335
DB 304 MAPNGH-----VSPQAKYILKDSFSIFCETGYELLOGLPLKSFATAVCQKDGSW 354
QY 336 SGKQPTC--KACREPKISDLVRRVRLPMQVQSRRETPHLQLYSAAPSKQLQAPKPKPAL 394
DB 355 DRPMFACSVDCGPP--DDLPSGRV-----EYITGP----- 383
QY 395 PFGDLPMGQHLHTQLQYECISPPY--RLGSSRRCTCLRTGKWSG-----RAPSCIPICK 448

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RESULT 7

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CASP_MESAU
ID CASP_MESAU STANDARD; PRT; 695 AA.
AC P15156;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Calcium-dependent serine proteinase precursor (EC 3.4.21.-) (CASP).
OS Mesocricetus auratus (Golden Hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-50 AND 446-472.
RC TISSUE=Fibroblast;
RX MEDLINE=89325606; PubMed=2753140;
RA Kinoshita H., Sakiyama H., Tokunaga K., Imajob-Ohmi S., Hamada Y.,
RA Isono K., Sakiyama S.;
RT "Complete primary structure of calcium-dependent serine proteinase
RT capable of degrading extracellular matrix proteins."
RL FEBS Lett. 250:411-415(1989).
CC -1- FUNCTION: Capable of degrading extracellular matrix proteins.
CC CASP degrades type I and IV collagen and fibronectin in the
CC presence of calcium.
CC -1- SUBUNIT: Heterodimer, consisting of heavy and light chains with
CC disulfide bonds. The heavy chain is expected to be a regulatory
CC subunit and the light chain contains the catalytic site.
CC -1- DOMAIN: The Glu-rich region in the N-terminal region may be gamma
CC carboxylated and function as a calcium-binding site.
CC -1- SIMILARITY: TO BLOOD COAGULATION FACTORS SUCH AS IX, X AND AN
CC ANTICOAGULATION FACTOR, PROTEIN C.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 2 Sushi (SCR) domains.
CC -----
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CC -----
DR EMBL; X16160; CRA34286.1; -
DR PIR; S05008; S05008.
DR HSP; P00763; 1DPO.
DR MEROPS; S01.193; -.

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RP SEQUENCE FROM N.A.
RX MEDLINE=2238257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klauer R.D., Collins F.S., Wegner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-329 FROM N.A.
RX TISSUE=Peripheral blood leukocytes;
RX MEDLINE=99008558; PubMed=9794427;
RA Endo Y., Takahashi M., Nakao M., Saiga H., Sekine H., Matsushita M.,
RA Nonaka M., Fujita T.,
RT "Two lineages of mannose-binding lectin-associated serine protease
RT (MASP) in vertebrates.";
RL J. Immunol. 161:4924-4930(1998).
RN [6]
RP SEQUENCE OF 291-688 FROM N.A.
RX MEDLINE=90040704; PubMed=2553984;
RA Tosi M., Duponchel C., Meo T., Couture-Tosi E.,
RT "Complement genes C1r and C1s feature an intronless serine protease
RT domain closely related to haptoglobin.";
RL J. Mol. Biol. 208:709-714(1989).
RN [7]
RP SEQUENCE OF 16-61; 168-219; 287-334 AND 384-445.
RX MEDLINE=86164350; PubMed=3007145;
RA Spycher S.E., Nick H., Rickli E.E.,
RT "Human complement component C1s. Partial sequence determination of
RT the heavy chain and identification of the peptide bond cleaved during
RT activation.";
RL Eur. J. Biochem. 156:49-57(1986).
RN [8]
RP SEQUENCE OF 438-500; 503-534; 542-601; 617-623 AND 626-656.
RX MEDLINE=84104122; PubMed=6362661;
RA Carter P.E., Dunbar B., Fothergill J.B.,
RT "The serine proteinase chain of human complement component C1s.
RT Cyanogen bromide cleavage and N-terminal sequences of the
RT fragments.";
RL Biochem. J. 215:565-571(1983).
RN [9]
RP PARTIAL SEQUENCE.
RX TISSUE=Plasma;
RX MEDLINE=91308095; PubMed=1854725;
RA Illy C., Thielens N.M., Gagnon J., Arlaud G.J.,
RT "Effect of lactoperoxidase-catalyzed iodination on the Ca(2+)-
RT dependent interactions of human C1s. Location of the iodination
RT sites.";
RL Biochemistry 30:7135-7141(1991).
RN [10]
RP DISULFIDE BONDS.
RX MEDLINE=91175725; PubMed=2007122;
RA Hess D., Schaller J., Rickli E.E.,
RT "Identification of the disulfide bonds of human complement C1s.";
RL Biochemistry 30:2827-2833(1991).
RN [11]
RP PARTIAL SEQUENCE, AND 3D-STRUCTURE MODELING OF CATALYTIC DOMAIN.
RX MEDLINE=95298736; PubMed=7779774;

RA Rossi V., Gaboriaud C., Lacroix M., Ulrich J., Pontecilla-Camps J.C.,
RA Gagnon J., Arlaud G.J.,
RT "Structure of the catalytic region of human complement protease C1s:
RT study by chemical cross-linking and three-dimensional homology
RT modeling.";
RL Biochemistry 34:7311-7321(1995).
RN [12]
RX MEDLINE=21286517; PubMed=11390518;
RA Dragon-Durey M.-A., Quartier P., Fremaux-Bacchi V., Blouin J.,
RA de Barace C., Prieur A.-M., Weiss L., Fridman W.-H.,
RT "Molecular basis of a selective C1s deficiency associated with early
RT onset multiple autoimmune diseases.";
RL J. Immunol. 166:7612-7616(2001).
CC -|- FUNCTION: C1s B chain is a serine protease that combines with C1q
CC and C1r to form C1, the first component of the classical pathway
CC of the complement system. C1r activates C1s so that it can, in
CC turn, activate C2 and C4.
CC -|- CATALYTIC ACTIVITY: Cleaves component C4 to C4a and C4b (Arg-|-Ala
CC bond), and component C2 to C2a and C2b (Lys(or Arg)-|-Lys bond).
CC -|- SUBUNIT: C1 is a calcium-dependent trimolecular complex of C1q,
CC C1r and C1s in the molar ratio of 1:2:2. Activated C1s is an
CC disulfide-linked heterodimer of a heavy chain and a light chain.
CC -|- DISEASE: Defects in C1S are the cause of selective C1s deficiency
CC [MIM:120580]; that is associated with early onset multiple
CC autoimmune diseases.
CC -|- SIMILARITY: Belongs to peptidase family S1.
CC -|- SIMILARITY: Contains 2 CUB domains.
CC -|- SIMILARITY: Contains 1 EGF-like domain.
CC -|- SIMILARITY: Contains 2 Sushi (SCR) domains.
CC -----
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CC -----
DR EMBL; X06596; CAA29817.1; -;
DR EMBL; J04080; AAA51852.1; -;
DR EMBL; M18767; AAA51853.1; -;
DR EMBL; BC056903; AAU56903.1; -;
DR EMBL; AB009076; BA86864.1; -;
DR PDB; 1ELV; 14-MAR-01.
DR MEROPS; S01.193; -;
DR SWISS-2DPAGE; P09871; HUMAN.
DR Genew; HGNC:1247; C1S.
DR MIM; 120580; -;
DR GO; GO:0003816; P:complement component C1s activity; TAS.
DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR01881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00084; eushi; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Complement pathway; Plasma; Glycoprotein; Serine protease; Hydrolase;

Hydroxylation; Sush1; Repeat; Signal; EGF-like domain;
Calcium-binding; Polymorphism; 3D-structure.

SIGNAL 1 15
CHAIN 16 437 COMPLEMENT C1S HEAVY CHAIN.
CHAIN 438 688 COMPLEMENT C1S LIGHT CHAIN.
DOMAIN 16 130 CUB 1.
DOMAIN 131 172 EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
DOMAIN 175 290 CUB 2.
DOMAIN 293 355 SUSH1 1.
DOMAIN 358 422 SUSH1 2.
DOMAIN 438 688 SERINE PROTEASE.
ACT_SITE 475 475 CHARGE RELAY SYSTEM.
ACT_SITE 529 529 CHARGE RELAY SYSTEM.
ACT_SITE 632 632 CHARGE RELAY SYSTEM.
MOD_RES 149 149 HYDROXYLATION (PROBABLE).
CARBOHYD 174 174 N-LINKED (GLCNAC. . .).
CARBOHYD 406 406 N-LINKED (GLCNAC. . .).
DISULFID 65 83
DISULFID 135 147

Query Match 8.5%; Score 334; DB 1; Length 688;
Best Local Similarity 21.7%; Pred. No. 1.5e-17;
Matches 163; Conservative 83; Mismatches 246; Indels 260; Gaps 37;

QY 137 GOILL-----ESYPLNAHCEHTIAKPGFVQLRPVMSLEFDYMCQDYVEVRDGNRDG 192
DB 21 GEILSPNPOAYPSEVEKSDIEVPEGYGHLFTHLDIELSENCAVDSVQIISGDTGEE 80
QY 193 QIIKRVCGNERPAPI-----QSIGSLHVLPHSDGS--KNFDGPHAIY--BEITACS--S 241
DB 81 RLCCQRSSNPHFIVPEEPQVFNKLVQIFKSDFSNEERTGTGAAYVATDINECTDFVD 140
QY 242 SPCFHDGTCLVDKAGSYKCACLAGY----- 266
DB 141 VPCSHFCNFI--GGYFCPCPEYFLHDDMKGVNCSGDVFTALIGETASPNPKPY 197
QY 267 TGORCNELL-----FERNCS-----PGPVGNGQKIT 294
DB 198 ENSRCQYIRLEKGFQVYVTLRDEDFVEAADSAGNCLDSLAVAGDRQPGPYCGH----- 253
QY 295 GGPGLIN-----GRHAK--I 307
DB 254 GFQPLNIETKSNALDIIFQDTLITGQKWKGLRYHGDPMCPKEDTPNSWVEAKAYVF 313
QY 308 GTVVSFPNNYS-VLSG-----NEKRTQQQNGWSGK-----QPICAKACREPISDLVRR 357
DB 314 RDVVQITCLDGFVEVGRVCGATSFYSTCQNGKWSNKLKCPV--DCGIP----- 362
QY 358 RVLPMQVQSRTEPLHQLYSAPFKSKQLQSAFTKPP-ALPFGDLPNGVQHLHTQLQYECIS 416
DB 363 -----ESIENGKVEDPESTLFGSV-----IRYTCEE 388
QY 417 PFY--RRLLSSRRTLCTLTKWSGRA-----PSCIPICGKIENITAPKTQGLRWPWQAAIY 469
DB 389 PYYMENGSGGEYHCAGNSWNEVLGPPLKCPVCG-----VP-----RPFPEK-- 435
QY 470 RRTSGVHDSGLHGANFLV-----CSGALVNERVTVVAAHCVTDLKGVTMIKTADLKVL 524
DB 436 QRIIGSDADIKNPPQVFPDNPWAGGALINEYVLTAAHVGEGRPTM-----YV 487
QY 525 GKFRDDEKTKTQSLQISAILHPNYDPILL-----DADIALKLLDKARISTRVQ 577
DB 488 GSTSVQTSRLAKS-KMLTPHFVTHPGWKLEVPPEGRNTFNDIALVRLKDPVYKMGPTVS 546
QY 578 PICLAASRDLSFQESHITVAGWNLVADVRSPGFKN-----TLRSGVSVVSDLSLCEQH 634
DB 547 PICLPGTSSDYNLMDGLGLISGW-----RTE--KEDRAVRLKARLPVAPLRKCKEVK 599
QY 635 EDHGIPVS-----VTDMFCASWEPTAPSDICTAETGTGTAASFPGRASPERPWHLMGL 688
DB 600 VEK--PTADAAYVFTPNMT-CAGE--KGMDSCKGDSGGAFVQDP---NDKTKFVAAGL 652
QY 689 VSNYSYDKTCSHRLSTAFTKVLPFKDMIERNNK 720

DB 653 VSWG--PQCG--TYGLYTRVKYVDWIMTMQ 680

RESULT 9
ENTK_HUMAN
ID ENTK_HUMAN STANDARD; PRT; 1019 AA.
AC P98073;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Enteroproteptidase precursor (EC 3.4.21.9) (Enterokinase).
GN PRSS7 OR ENTK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Duodenum;
RX MEDLINE=95234679; PubMed=7718557;
RA Kitamoto Y., Veille R.A., Denis-Keller H., Sadler J.E.;
RT "cDNA sequence and chromosomal localization of human enterokinase,
RL Biochemistry 34:4562-4568 (1995)."
RN [2]
RP SEQUENCE FROM N.A., AND DISEASE.
RX MEDLINE=21606074; PubMed=11719902;
RA Holzinger A., Maier E.M., Buck C., Mayerhofer P.U., Kappler M.,
RA Haworth J.C., Moroz S.P., Hadorn H.-B., Sadler J.E., Roscher A.A.;
RT "Mutations in the proenteroproteptidase gene are the molecular cause of
RL congenital enteroproteptidase deficiency.";
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Sasaki T., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordliek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Rieselmann L., Dagand E.,
RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehrach H., Reinhardt R., Vaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319 (2000).
RN [4]
RP SEQUENCE OF 749-1019 FROM N.A.
RC TISSUE=Duodenum;
RX MEDLINE=94329561; PubMed=8052624;
RA Kitamoto Y., Yuan Q., Wu Q., McCourt D.W., Sadler J.E.;
RT "Enterokinase, the initiator of intestinal digestion, is a mosaic
RL protease composed of a distinctive assortment of domains.";
RN Proc. Natl. Acad. Sci. U.S.A. 91:7588-7592 (1994).
CC -I- FUNCTION: Responsible for initiating activation of pancreatic
CC proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase
CC A). It catalyzes the conversion of trypsinogen to trypsin which in
CC turn activates other proenzymes including chymotrypsinogen,
CC procarboxypeptidases, and proelastases.
CC -I- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
CC trypsinogen.
CC -I- SUBUNIT: Heterodimer of a catalytic (light) chain and a
CC multi-domain (heavy) chain linked by a disulfide bond.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -I- TISSUE SPECIFICITY: Intestinal brush border.
CC -I- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS
CC CLEAVED BY A TRYPSIN-LIKE PROTEASE.
CC -I- DISEASE: Defects in PRSS7 are a cause of enterokinase deficiency
CC [MIM:236200]; a life-threatening intestinal malabsorption disorder

252 LDKAGSYKC--ACLA-----GYTORCENLLEERNCSDPGPNVNGYKQITGGPGLNG 302
644 --KADHFOCKNGECVPLVNLCDGHL--HCBGDSDEADC-----VRFNGTNNNGLVRF 693
303 RHAKIGTVVSFFCNCNSVLSGNEKRTCOQNGESGKQPCIKACREPKISDLVRRVLPM 362
694 RIQSIW-----HTACAEWNTQISNDVC-----QLLGL 721
363 QVQSRRTPLHQLYSAAFSKOKLOSAPTYPKLPALFGLPMGYOHLHTQLOVEICISPFYRL 422
722 GSGNSSKPIFSTGGPF--VKLNTAPD-----GHLILTPSQOCLQDSLRL 765
423 GSRRTCLRTGKSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSLHK 482
766 QCNHSC-----GKLLAAQDITPKI--VGSNAKEGAPWVVGLY-----YGR--- 807
483 GANFLVCSGALVNERVTVAHAHCVTDLGKVTMTKADLKVLGKFRDDBDKTQSLQ 542
808 ----LLCGASLVSDWLVSAAHCV--YGR--NLEPSKWTAILGLHMKSNLTSQTVPRL- 858
543 ISAILHPNYDPIILDADIAILKLLDKARISTRVQPCICLAASRDLSFQESHITVAGWN 602
859 IDEIVINPHYNNRRKNDIAHMLPEKKNVTDYIQCIPLEENQVPPGR--NCSIAAGWG 916
603 VLADVSPGPNITLRSVGVSVVDSLLCEQHDHGIPVSVDNMFCASWEPTAPSDICT 662
917 T---VYQGTANTILQEADVLLSLNRCQQQMEY----NITENMICAGYE-EGGIDSCQ 968
663 AETGGIAAVSPGRASPEPWHMLGLVMSYDNTCSHRLSTFTKVLPPFKDWIE 716
969 GDSGG-----PLMCQENNRWFLAGVTSFGYKALPNR-PGVYARVSRFTENIQ 1015
[1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TTSUE=Duodenal mucosa;
RA Matsushima M., Ichinose M., Yahagi N., Kakei N., Tsukada S.,
Miki K., Kurokawa K., Tashiro K., Shiohara K., Shinomiya K.,
Uneyama H., Inoue H., Takahashi T., Takahashi K.;
RT "Structural characterization of porcine enteropeptidase";
J. Biol. Chem. 269:19976-19982(1994).
CC -1- FUNCTION: Responsible for initiating activation of pancreatic
proteolytic proenzymes (trypsin, chymotrypsin and carboxypeptidase
A). It catalyzes the conversion of trypsinogen to trypsin which in
turn activates other proenzymes including chymotrypsinogen,
procarboxypeptidases, and proelastases.
CC -1- CATALYTIC ACTIVITY: Selective cleavage of 6-Lys-|-Ile-7 bond in
trypsinogen.
CC -1- SUBUNIT: Heterotrimer of a catalytic (light) chain, a multidomain
(heavy) chain, and a mini chain.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -1- PTM: THE CHAINS ARE DERIVED FROM A SINGLE PRECURSOR THAT IS
CLEAVED BY A TRYPSIN-LIKE PROTEASE.
CC -1- PTM: THE MINI CHAIN MAY BE CLEAVED BY ELASTASE.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 2 LDL-receptor class A domains.
CC -1- SIMILARITY: Contains 1 MAM domain.
CC -1- SIMILARITY: Contains 1 SEA domain.

CC -1- SIMILARITY: Contains 1 SRCR domain.

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or send an email to license@isb-sib.ch).

CC EMBL; D30799; BAA06459.1; -;
CC HSP; P00763; IDPO.
CC MEROPS; S01.156; -;
DR InterPro; IPR000859; CUB.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000998; MAM domain.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR000082; SEA_domain.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00057; ldl_recept_a; 2.
DR Pfam; PF00629; MAM; 1.
DR Pfam; PF01390; SEA; 1.
DR Pfam; PF00330; SRCR; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PRINTS; PR00020; MAMDOMAIN.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00192; LDLA; 2.
DR SMART; SM00137; MAM; 1.
DR SMART; SM00200; SEA; 1.
DR SMART; SM00202; SR; 1.
DR SMART; SM00020; TYP_SPC; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01209; LDLRA_1; 2.
DR PROSITE; PS00068; LDLRA_2; 2.
DR PROSITE; PS00740; MAM_1; 1.
DR PROSITE; PS00060; MAM_2; 1.
DR PROSITE; PS00024; SEA; 1.
DR PROSITE; PS00420; SRCR_1; FALSE_NEG.
DR PROSITE; PS0287; SRCR_2; 1.
DR PROSITE; PS0240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
DR Signal-anchor; Glycoprotein; Myristate; Hydrolase; Serine protease;
KW Zymogen; Transmembrane; Repeat; Lipoprotein.
FT CHAIN 52 117 NON-CATALYTIC M CHAIN (MINI CHAIN).
FT CHAIN 118 799 NON-CATALYTIC H CHAIN (HEAVY CHAIN).
FT CHAIN 800 1034 CATALYTIC L CHAIN (LIGHT CHAIN).
FT DOMAIN 1 18 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 19 47 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 48 1034 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 52 169 SEA.
FT DOMAIN 197 238 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 240 349 CUB 1.
FT DOMAIN 357 519 MAM.
FT DOMAIN 539 649 CUB 2.
FT DOMAIN 656 694 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 693 786 SRCR.
FT DOMAIN 800 1034 SERINE PROTEASE.
FT ACT_SITE 840 840 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 891 891 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 986 986 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT LIPID 2 2 N-myristoyl glycine (Potential).
FT DISULFID 199 212 BY SIMILARITY.
FT DISULFID 206 225 BY SIMILARITY.
FT DISULFID 219 236 BY SIMILARITY.
FT DISULFID 658 670 BY SIMILARITY.
FT DISULFID 665 683 BY SIMILARITY.

FT DISULFID 677 911 BY SIMILARITY. INTERCHAIN (BY SIMILARITY).
FT DISULFID 787 911 BY SIMILARITY.
FT DISULFID 825 841 BY SIMILARITY.
FT DISULFID 925 932 BY SIMILARITY.
FT DISULFID 956 971 BY SIMILARITY.
FT DISULFID 982 1010 BY SIMILARITY.
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 343 343 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 455 455 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 485 485 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 518 518 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 549 549 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 645 645 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 697 697 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 701 701 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 721 721 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 740 740 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 761 761 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 804 804 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 863 863 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 902 902 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 964 964 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1034 AA; 114776 MW; 0388C64CF64CC368 CRC64;
Query Match 8.4%; Score 330.5; DB 1; Length 1034;
Best Local Similarity 22.9%; Pred. No. 4.6e-17;
Matches 137; Conservative 86; Mismatches 224; Indels 151; Gaps 27;
QY 143 SYPLNAHCETTHAKPGFVIQRLVFLSLEFPMQCYDYVEVRDGDNRDGIKRVCGNE 202
DB 560 NYPNQAFVWNLNAQKGNQLHFE----EPDENIADVEIRDEEDSLLAVYTG-- 613
QY 203 RPAPQSTGSS---LHVLFSHDS-----KNP-DGFHAIYEETACSSSPCFHD---- 247
DB 614 -PGPVEDVFSTTRMTVLFTITDALTGKGFKANFTTGVHLGIPE-----PKCEDNFQC 665
QY 248 --GTCVLDKAGSKACLAGYTGQRCENLBERNCSDPGGPNVYQKITGGGLINGHA 305
DB 666 ENGECVL-----LVNLCDFSHCKGSDAHCVRFUNGANSGLVQFRIQ 711
QY 306 KIGTVVFFCNNSYVLSGNEKTKCOQNGSWGKQPCIKACREPKISDLVRRRVLPQVQ 365
DB 712 SIW-----HTACAEWTTQTSDVDC-----QLLGLGTG 739
QY 366 SRETPHLQLYSAFQKQKQLOAPTKKPPALPGDLPNGVQLHTQLOECISPFYRLGSS 425
DB 740 NSSMPFFSGGGGPF--VKLNTAPNGSLILITASE-----OCFEDSLILLQCN 783
QY 426 RTCLRTGKWSGRAPSCIPICIKIENITAPKTQGLR-----WPWQALYRTSGVHDS 479
DB 784 HKSC---GK-----KQVAQEVSPKIVGNDSEGAWPVVALY-----YNGQ 822
QY 480 LHKGAFLVCSGALVNERTVVAHVCHVTDLGKVITKTLADLVLGKVFYRDDRDEKTIQ 539
DB 823 -----LLCGASLVSRDLVSAACHCV--YGR--NLEPSKWKAILG-LHMTSNLTSPOIV 870
QY 540 SLQISAILHPNYPDILLADAILKLLDKARISRTVQIPICLAASRDLSQFESHI-TV 598
DB 871 TRLIDEIVNPHNRRKSDSIAMHLEPKVNYTYDIOICILPENQV---PPGRIGSI 927
QY 599 AGWNLADVRSFGKNDTLRSGVSVVDSLLCEQHEHDGIPVSVTDNNFCAWSBPAPS 658
DB 928 AGWKVYOGSPA---DILQADVPLLSNEKCCQOMPEY-----NITENMWCAGYE-EGGI 979
QY 659 DICTATGTGIAVSPFGRASBPERRHMLGLVSNWYDKTCSHRLSTAFKVLFPKDWIE 716
DB 980 DSCQGDGSG-----PLMCLENNRLLAGVTSGFYQCALPNR-PGVYARVPKFTIEWIQ 1030

RESULT 11
CSM1_HUMAN STANDARD; PRT; 3565 AA.
ID Q96PZ7; Q96QU9; Q96RM4;
AC 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, last sequence update)
DE 15-MAR-2004 (Rel. 43, last annotation update)
DE CUB and esushi multiple domains protein 1 precursor (UNQ5952/PRO19863).
GN CSMD1 OR KIAA1890.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=21365705; PubMed=11472063;
RA Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant B.C.,
RA Sunwoo J.B., Gollin S.M., Scholnick S.B.;
RA "Transcript map of the 8p23 putative tumor suppressor region.";
RL Genomics 75:17-25(2001).
RN [2]
RP SEQUENCE OF 1319-3565 FROM N.A. (ISOFORM 3).
RX TISSUE=Brain;
RA Wakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Ota T., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isano Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Suzuki Y., Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RA "NEDO human cDNA sequencing project.";
RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 825-3565 FROM N.A. (ISOFORM 4).
RX MEDLINE=22887296; PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RN [4]
RP SEQUENCE OF 966-2013 FROM N.A. (ISOFORM 4), AND TISSUE SPECIFICITY.
RX TISSUE=Brain;
RA MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RA "Prediction of the coding sequences of unidentified human genes. XXI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins.";
RL DNA Res. 8:179-187(2001).
RN [5]
RP DISEASE.
RX MEDLINE=22581359; PubMed=12696061;
RA Toomes C., Jackson A., Maguire K., Wood J., Gollin S., Ishwad C.,
RA Paterson I., Prime S., Parkinson K., Bell S., Woods G., Markham A.,
RA Oliver R., Woodward R., Sloan P., Dixon M., Read A., Thakker N.;
RA "The presence of multiple regions of homozygous deletion at the CSMD1
RT locus in oral squamous cell carcinoma question the role of CSMD1 in
RT head and neck carcinogenesis.";
RL Genes Chromosomes Cancer 37:132-140(2003).
RN [6]
RP DISEASE.
RX MEDLINE=22868729; PubMed=14506705;
RA Scholnick S.B., Richter T.M.;
RA "The role of CSMD1 in head and neck carcinogenesis.";

Genes Chromosomes Cancer 38:281-283(2003).

CC -1- FUNCTION: Potential suppressor of squamous cell carcinomas.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=4;

CC Name=1;

CC IsoId=Q96P27-1; Sequence=Displayed;

CC Name=2; Synonyms=Short;

CC IsoId=Q96P27-2; Sequence=VSP_009034, VSP_009035;

CC Name=3;

CC IsoId=Q96P27-3; Sequence=VSP_009030, VSP_009031;

CC Note=No experimental confirmation available;

CC Name=4;

CC IsoId=Q96P27-4; Sequence=VSP_009032, VSP_009033;

CC -1- TISSUE SPECIFICITY: Weakly expressed in most tissues, except in brain. Expressed at intermediate level in brain, including cerebellum, substantia nigra, hippocampus and fetal brain.

CC -1- DISEASE: Defects in CSMD1 may be a cause of oral and oropharyngeal squamous cell carcinomas (OSCCs). Ref.5 and Ref.6 are however in disagreement: while Ref.6 considers CSMD1 as a strong candidate for OSCCs, Ref.5 thinks it is not.

CC -1- SIMILARITY: Belongs to the CSMD family.

CC -1- SIMILARITY: Contains 14 CUB domains.

CC -1- SIMILARITY: Contains 28 Sushi (SCR) domains.

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CC -----

DR EMBL; AF333704; AAK73475.2; -

DR EMBL; AY017307; AAG52948.1; -

DR EMBL; AK126936; BAC86754.1; ALT_INIT.

DR EMBL; AY358174; AAG88541.1; ALT_INIT.

DR EMBL; AB067477; BAB67783.1; -

DR Genew; HGNC:14026; CSMD1.

DR InterPro; IPR000859; CUB.

DR InterPro; IPR000436; Sushi_SCR_CCP.

DR Pfam; PF00431; CUB; 14.

DR Pfam; PF00084; sushi; 27.

DR SMART; SM00032; CCP; 24.

DR SMART; SM00042; CUB; 14.

DR PROSITE; PS01180; CUB; 14.

DR Repeat; Signal; Transmembrane; Sushi; Alternative splicing.

FT SIGNAL 1 26

FT CHAIN 27 3565

FT DOMAIN 27 3488

FT TRANSMEM 3489 3509

FT DOMAIN 3510 3565

FT DOMAIN 32 140

FT DOMAIN 145 202

FT DOMAIN 208 312

FT DOMAIN 349 407

FT DOMAIN 412 523

FT DOMAIN 528 581

FT DOMAIN 585 693

FT DOMAIN 698 755

FT DOMAIN 759 867

FT DOMAIN 874 927

FT DOMAIN 931 1041

FT DOMAIN 1046 1101

FT DOMAIN 1105 1213

FT DOMAIN 1218 1274

FT DOMAIN 1278 1387

FT DOMAIN 1392 1448

FT DOMAIN 1452 1560

FT DOMAIN 1565 1622

FT DOMAIN 1626 1734

FT DOMAIN 1742 1799

FT DOMAIN 1803 1911

FT SIGNAL 1 26

FT CHAIN 27 3565

FT DOMAIN 27 3488

FT TRANSMEM 3489 3509

FT DOMAIN 3510 3565

FT DOMAIN 32 140

FT DOMAIN 145 202

FT DOMAIN 208 312

FT DOMAIN 349 407

FT DOMAIN 412 523

FT DOMAIN 528 581

FT DOMAIN 585 693

FT DOMAIN 698 755

FT DOMAIN 759 867

FT DOMAIN 874 927

FT DOMAIN 931 1041

FT DOMAIN 1046 1101

FT DOMAIN 1105 1213

FT DOMAIN 1218 1274

FT DOMAIN 1278 1387

FT DOMAIN 1392 1448

FT DOMAIN 1452 1560

FT DOMAIN 1565 1622

FT DOMAIN 1626 1734

FT DOMAIN 1742 1799

FT DOMAIN 1803 1911

FT	DOMAIN	1916	1971	SUSHI 11.
FT	DOMAIN	1975	2083	CUB 12.
FT	DOMAIN	2088	2143	SUSHI 12.
FT	DOMAIN	2147	2258	CUB 13.
FT	DOMAIN	2259	2316	SUSHI 13.
FT	DOMAIN	2320	2431	CUB 14.
FT	DOMAIN	2433	2491	SUSHI 14.
FT	DOMAIN	2496	2553	SUSHI 15.
FT	DOMAIN	2558	2618	SUSHI 16.
FT	DOMAIN	2623	2676	SUSHI 17.
FT	DOMAIN	2681	2734	SUSHI 18.
FT	DOMAIN	2739	2797	SUSHI 19.
FT	DOMAIN	2802	2855	SUSHI 20.
FT	DOMAIN	2863	2916	SUSHI 21.
FT	DOMAIN	2921	2975	SUSHI 22.
FT	DOMAIN	2980	3035	SUSHI 23.
FT	DOMAIN	3040	3093	SUSHI 24.
FT	DOMAIN	3098	3151	SUSHI 25.
FT	DOMAIN	3159	3213	SUSHI 26.
FT	DOMAIN	3218	3273	SUSHI 27.
FT	DOMAIN	3276	3331	SUSHI 28.
FT	CARBOHYD	40	40	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	57	57	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	588	588	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	687	687	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	956	956	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1016	1016	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1035	1035	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1185	1185	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1198	1198	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1400	1400	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1455	1455	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1573	1573	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1645	1645	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1793	1793	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1806	1806	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1883	1883	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2019	2019	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2150	2150	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2155	2155	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2188	2188	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2359	2359	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2395	2395	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2401	2401	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2446	2446	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2471	2471	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2504	2504	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2606	2606	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2751	2751	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2762	2762	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2796	2796	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2895	2895	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	2964	2964	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3023	3023	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3057	3057	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3106	3106	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3229	3229	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3261	3261	N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match

8.4%; Score 329.5; DB 1; Length 3565;

Best Local Similarity 20.8%; Pred. No. 2.6e-16;

Matches 163; Conservative 93; Mismatches 239; Indels 287; Gaps 34;

QY 48 YDQIEVCVP-----GKREVGVYIP--C-----CRNEEEDCDLHPGTTIFENCK 92

Db 693 FGQNECHDPGIPNGRRFGDFLLGSSVSFHCDDGFVKTQGSSEITCILQDG----- 744

QY 93 SCENGSGGTLDDFYVKGFCACRAGWYGGDCMRGCVLRAPKGOILLESYP-----LNA 148

Db 745 ---NVVWSSTV-----PCGHLTASSGVILPPGWYKDSL 783

QY 149 HCEWTHAKPGFVIQLRFVWLSLEFDYMCQDYVEVRDGDNRDQGIKRVCGNERPAPIQ 208

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Db 784 HCEWIEIAKPGHSIRKWTDFRQTEVN-----YDTEVRDGPASSPLIGYHGTOAQOFLI 839
QY 209 STGSLHLVHSDGSKNFDGHAIEYEITACSSSPCFHDGTCVLDKAGSYKACLAGVTG 268
Db 840 STGNFWYLLFTDNRSGSIGFLIHESVT----- 868
QY 269 QRCENLLEBRNCSDPGGPNVGQKTTGGFLNGHAKIGTVSPFCNNSVYLSGNEKRT 328
Db 869 -----LESDSCLDPGIPVNGHR-----HGDGFGIRSTVTIPSCDPGYTSLSDPELV 913
QY 329 COONGEMSKQPCIKAC----- 346
Db 914 CERNHOMNHALPSCDALCGYITQKSGTVLSPGFFDYPNSLNCWTWTEVSHGKGVQMP 973
QY 347 -----REPKISDLVRR---RVLPQMVQ-----SRETFLHQL 374
Db 974 HTFHLESSHDXLLITEDGGSFSEPVARTGSLVPHITKAGLFGNFTQAQLRPFISDFSISVEG 1033
QY 375 YSAATSKQLQSAPTKALPGDLPNGYQH-LHTQLQVEICISPPYRLGSSRRRTCLRTG 433
Db 1034 FNITSEYDLE--PCDDPGVPAPSRRIQGFHFGVGDLSLTFSCFLG-YRLEGATKLTCLGGG 1090
QY 434 K--WGRAPSCPIGCKTIENTAPKTQGLRWFPWQAAIYRRTSGVHDGSLHKGAWFLVCSG 491
Db 1091 RRVNSAPLPRCVAECG-----ASV-----KG----- 1111
QY 492 ALVNERTVVV-----AAHCV---TDLGKVTMIKTADLKVLVG---RKYRDDDRDE 535
Db 1112 ---NEGTLSPNFPNSYNDTHCIVKITEAGKGIHLRTSRFQEGDTLKVYDGKSS 1168
QY 536 K---TIQSLQISAILHPNYDIPLLDADIAILKLDKARISTRVOPICLAASRDLSFQ 592
Db 1169 RPLGFTTKNELGLILNSTNHLWLEFN-----TNGSDTDQGFQ 1207
QY 593 ESHITVAGNVLADVRSPGKNDTLR-----SGWSVWVDSLLCEEQHDHGIPVSVTDNNF 648
Db 1208 ---LYTFSF-LVKCEDGIPVNYGIRDEGHFTDTVLVYSCNPGVAMHG-----SNLT 1258
QY 649 CAS-----WEPTAPSDICTAETGG---IAVSG-----FPGRASP-EPRHMLGLVWSYDKT 696
Db 1259 CLSGDRRVMDKPLPS--CIAECGGQIHAATSGRILSPGYPAPYDNNLHCTWIIIEADPGKT 1316
QY 697 CS 698
Db 1317 IS 1318

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RESULT 12

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CSM1_MOUSE
ID CSM1_MOUSE STANDARD; PRT; 3564 AA.
AC Q92L3; Q8BUV1; Q8BYQ3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE CUB and euehi multiple domains protein 1 precursor.
GN CSM1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6;
RX MEDLINE=21365705; PubMed=11472063;
RA Sun P.C., Uppaluri R., Schmidt A.P., Pashia M.E., Quant E.C.,
RT Sunwoo J.B., Gollin S.M., Scholnick S.B.;
RL "Transcript map of the 8p23 putative tumor suppressor region.";
RN Genomics 75:17-25(2001).
RP SEQUENCE FROM N.A. (ISOFORM 3), AND SEQUENCE OF 3250-3564 FROM N.A.
RP (ISOFORM 2).
RC STRAIN=C57BL/6J; Tissue=Cerebellum, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;

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RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaio I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami H., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriell L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Clothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer J.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Meglath D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagasima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hata A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q92L3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q92L3-2; Sequence=VSP_009037;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q92L3-3; Sequence=VSP_009036;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Belongs to the CSM1 family.
CC -!- SIMILARITY: Contains 14 CUB domains.
CC -!- SIMILARITY: Contains 28 Sushi (SCR) domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; AY017475; AAGS4083.1;
CC EMBL; AK038679; BAC30095.1; ALT_INIT.
CC EMBL; AK082377; BAC38482.1;
CC MGD; MGI:2137383; GsmDI.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR000436; Sushi_SCR_CCP.
CC Pfam; PF00431; CUB; 14.
CC Pfam; PF00084; sushi; 28.
CC SMART; SM00032; CCP; 28.
CC SMART; SM00042; CUB; 14.
CC PROSITE; PS01180; CUB; 14.
CC Repeat; Signal; Transmembrane; Sushi; Alternative splicing.
FT SIGNAL 1 29
FT CHAIN 30 3564
FT DOMAIN 30 3487
FT TRANSMEM 3488 3508
FT DOMAIN 3509 3564
FT DOMAIN 32 140
FT DOMAIN 145 202
FT DOMAIN 208 312
FT DOMAIN 349 406

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FT DOMAIN 411 522 CUB 3. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 527 580 SUSHI 3. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 584 692 CUB 4. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 697 754 SUSHI 4. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 758 866 CUB 5. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 873 926 SUSHI 5. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 930 1040 CUB 6. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1045 1100 SUSHI 6. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1104 1212 CUB 7. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1217 1273 SUSHI 7. (GLCNAC. . .) (POTENTIAL).
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 FT DOMAIN 1391 1447 SUSHI 8. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1451 1559 CUB 9. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1564 1621 SUSHI 9. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1625 1733 CUB 10. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1741 1798 SUSHI 10. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1802 1910 CUB 11. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1915 1970 SUSHI 11. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1974 2082 CUB 12. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2087 2142 SUSHI 12. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2146 2257 CUB 13. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2258 2315 SUSHI 13. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2319 2430 CUB 14. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2432 2490 SUSHI 14. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2495 2552 SUSHI 15. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2557 2617 SUSHI 16. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2622 2675 SUSHI 17. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2680 2733 SUSHI 18. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2738 2791 SUSHI 19. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2796 2854 SUSHI 20. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2859 2912 SUSHI 21. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2920 2973 SUSHI 22. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 2978 3032 SUSHI 23. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 3037 3092 SUSHI 24. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 3097 3150 SUSHI 25. (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 3155 3208 SUSHI 26. (GLCNAC. . .) (POTENTIAL).
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 Query Match 8.3%; Score 329; DB 1; Length 3564;
 Best Local Similarity 21.3%; Pred. No. 2.8e-16;
 Matches 159; Conservative 95; Mismatches 226; Indels 266; Gaps 33;
 QY 48 YQIECVCP-----GKREVVGVTIP--C---CRNEECCDCLIHGCTIPENCK 92
 DB 692 FQNECHDFGIPVNGRRFGDRFLGSSVSFCHDDGFVKQTQGESITCIIQDG----- 743
 QY 93 SCRNGSWGOTLDDFFVYKGYCAECRAGWYGCRCGQVLRAPKQIILLESYP-----L 146
 DB 744 ---NVWSSSTV-----PRCEA-----PCGHLTASSGVILPPGWPFGYKDSL 782
 QY 147 NAHCEWTIHAKGDFVQLRFVMSLEFDYMCQYDVYVVRDGDNRDQIITKRVCGNERBAP 206
 DB 783 N--CEWVIEAKPGHSIKITDFRQTEVN---YDLEVRDGTSSPLIGEVHGTQAPQ 836
 QY 207 IQSIGSSHLVHFDGSKNFDGFHAIYEITACSSSPCHDGTCLVDKAGSYKCACLAGY 266
 DB 837 LISTGNMYLLFTDSSRASVGLIHESVT----- 867
 QY 267 TQORCNLEERNCSDPGPGVNGYKQITGGPLNGRHAKIGTVVSFFCNNSVVLGNK 326
 DB 868 -----LESCLDPGIPVNGQR-----HGSNFGIRSTVTFTSCDPGYTSLDDEP 910
 QY 327 RTCOONGEWSGKOPICIKAC----- 346
 DB 911 LVCEKQHNHALPSCDALCGGYHKGSTVLSPPGPDYFNSLNTWTIEVSHGKGVQM 970
 QY 347 -----REPKISDLVRR---RVLPQVQV-----SRETPLH 372
 DB 971 NFHTPHLESSHDYLLITEDGSFSEPVARLTGSLVPHTIKAGLFGNFTAQLRFISDFSISY 1030
 QY 373 QLYSAFQKQKQOSAPTKPALPFGDLPMGYQH-LHTQLOVEICISFFYRLGSSRTCLR 431
 DB 1031 EGFNITFAEYDLE--PCDDPGVPAPFRRIGFCFGVGDTLAFTCFQG-YRLEGATKLTCLG 1087
 QY 432 TGG--WSGRAPSCIPICIKIENITAPKTQGLRWPMQAAIYRRTSGVHDGSLHKGAWFLVC 489
 DB 1088 GGRVWSAPLPRCAECG-----ASV-----KG----- 1110
 QY 490 SGALVNERTVW---VAAH-----CV-----TDLGKVTMIKTADLKVVLGKFYRDDDRDEK 536
 DB 1111 ----NEGTLSPNPPSHYDNNHECIYKETEAGKGIHLRARTFQLFEGDTLKVYDGKDS 1165
 QY 537 TQSLOISAIILHPNDPILLADTAIILKDKARISTRVQVICLA-ASRDLSTSFQESH 595
 DB 1166 SRSRL---GVFTRSEFPMGLVNSTNYLLEFNTNGSDTAQGFQLTFTYTFDL-VKCEDPG 1221
 QY 596 ITVAGNVVLADVRSFGKNDTLRSVVSVVSDLLCEOHEDHGIPVSVTDNNMPCAS---- 651
 DB 1222 IPNYGYR---IRDDGHFTDTV-----VLYS--CNPGYAMHG-----SSTLTCLSGDRR 1264
 QY 652 -WEPTAPSDICTAETGGIAAVSFPGR 676
 DB 1265 VNDKPMPS--CVABCGGLVHAATSGR 1288

RESULT 13
 ST14_HUMAN
 ID ST14_HUMAN STANDARD; PRT; 855 AA.
 AC Q9Y5Y6; Q9BS01; Q9H350; Q9HB36; Q9HCA3;
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Matrptase) (Membrane-
 DE type serine protease 1) (MT-SP1) (Prostatin) (Serine protease TADG-15)
 DE (Tumor associated differentially-expressed gene-15 protein).
 GN ST14 OR PRS14 OR SMC19 OR TADG15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP MEDLINE=99303581; PubMed=10373424;
 RX MEDLINE=99303581; PubMed=10373424;
 RA Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
 RT "Molecular cloning of cDNA for matrptase, a matrix-degrading serine
 RT protease with trypsin-like activity."
 RL J. Biol. Chem. 274:18231-18236(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99432178; PubMed=10500122;
 RA Takeuchi T., Shuman M.A., Craik C.S.;
 RT "Reverse biochemistry: Use of macromolecular protease inhibitors to
 RT dissect complex biological processes and identify a membrane-type
 RT serine protease in epithelial cancer and normal tissue."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Yamaguchi N., Mitsui S.;
 RT "Molecular cloning of a novel transmembrane serine protease expressed
 RT in human prostate."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Tanimoto H., Underwood L.J., Wang Y., Shigemasa K., Parmley T.H.,
 RA O'Brien T.J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood, and Muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Klapper R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zensberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Schmorc A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 340-664 FROM N.A.
 RA Cao J., Fan W., Zheng S.;
 RT "Genomic analysis of a novel human serine protease SMC19."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP CHARACTERIZATION.
 RC TISSUE=Milk;
 RX MEDLINE=99303582; PubMed=10373425;
 RA Lin C.Y., Anders J., Johnson M., Dickson R.B.;
 RT "Purification and characterization of a complex containing matrptase
 RT and a Kunitz-type serine protease inhibitor from human milk."
 RN [8]

RL J. Biol. Chem. 274:18237-18242(1999).
 CC -!- FUNCTION: Degrades extracellular matrix. Proposed to play a role
 CC in breast cancer invasion and metastasis. Exhibits trypsin-like
 CC activity as defined by cleavage of synthetic substrates with Arg
 CC or Lys as the P1 site.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 2 CUB domains.
 CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
 CC -----
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 CC -----
 DR EMBL; AF118224; AAD42765.2; -;
 DR EMBL; AF133086; AAF00109.1; -;
 DR EMBL; AB030036; BAB20376.1; -;
 DR EMBL; AF057145; AAG15395.1; -;
 DR EMBL; BC005826; AAH05826.1; -;
 DR EMBL; BC030532; AAH30532.1; -;
 DR EMBL; AF283256; AAG13949.1; -;
 DR HSSP; P00763; LDPO. -;
 DR Genew; HGNC:11344; ST14.
 DR MIM; 606797; -;
 DR MEROPS; S01.302; -;
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_SIA.
 DR Pfam; PF00431; CUB; 2.
 DR Pfam; PF00057; ldl_recept_a; 4.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR SMART; SM00042; CUB; 2.
 DR SMART; SM00192; LDLA; 3.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS01180; CUB; 2.
 DR PROSITE; PS01209; LDLRA_1; 2.
 DR PROSITE; PS00068; LDLRA_2; 4.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Signal-anchor; Glycoprotein; Hydrolase; Serine protease;
 KW Transmembrane; Repeat.
 FT DOMAIN 1 55
 FT TRANSMEM 56 76
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT CUB 1.
 FT CUB 2.
 FT LDL-RECEPTOR CLASS A 1.
 FT LDL-RECEPTOR CLASS A 2.
 FT LDL-RECEPTOR CLASS A 3.
 FT LDL-RECEPTOR CLASS A 4.
 FT SERINE PROTEASE.
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT FEA -> GTR (IN REF. 5; AAH05826).
 FT R -> S (IN REF. 4).
 FT CONFLICT 381

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FT CONFLICT 674 674 A -> V (IN REF. 3).
SQ SEQUENCE 855 AA; 94769 MW; 26143132C01F99C9 CRC64;

Query Match 8.3%; Score 328; DB 1; Length 855;
Best Local Similarity 21.4%; Pred. No. 5.7e-17;
Matches 143; Conservative 70; Mismatches 224; Indels 230; Gaps 27;

QY 128 CGOVLRAPKGQI-----LLSEYPLNAHCEWTHAKPGFVIQLRPFVMSLSLEFDYM-----176
DB 340 CGGLRKAQAGTNSPYPGHYPPNIDCTWNIEVPNNQHVKVRP-----KFFYLLEPGVPA 394

QY 177 --COYDYVEVRDGNRDGQIKKVCNRPAPIQSIGSSHLVLFHSDGSKNPDGHEHAIYE 234
DB 395 GTCPKDYVEING-----EKYCGERSQFVTSNSKITVRHFSQDSQYTDGTFLAEX- 444

QY 235 EITACSSSPCFDGTG-----VLDKAGSYKCACLAGY-----266
DB 445 -LSYSDSDPCPGOCTRTGRCIRKELRCDCGWADCTDHSDELNCSCDAGHFTCKNKFCXP 503

QY 267 -----TGRCENLBERNCSDPGPVNGYQKITGGFGLNGHAKIGTVVSPFCNNSV 320
DB 504 LFWCVDSVNDGNSDEQGCSCP-----AQTPRCNSGKC 537

QY 321 LSG-----NEKRTCOQNGESGKQPIKACREPKISDLVRRVLPVQVQSRETFPLHOLYS 376
DB 538 LSKSQOCNGKDDCGDSDSEACPKVNVTC-----567

QY 377 AAFSKQKLOSAPTKPALPGDLPMGVQHLHTQYECISPFYRRLGSSRRRTCLRTGRWS 436
DB 568 -----TK-----HT-----YRCLNGL-----CLSKGN-- 584

QY 437 GRAPSCIPCGKIENTAPKTQ-----GLR-----HPWQAAYRRYS 473
DB 585 -----PECDGKEDCSDGSDKDCGLRSFTRQARVVGTDADGEGWPMQVSLHALGQ 637

QY 474 GVHDGSLHKGANFLVCSGALVNERTVVAACHVTDLGKVTMTADLKVLGKFRYDDDR 533
DB 638 G-----H-----ICASLISNWLVSAAHYIDRGRFYSPDPTWAPLG-LHQDSQR 684

QY 534 DEKTIQSLQISAILHPNYDPIILDADIALKLLDKARISTRVQPICLAAASRLDSTFSQE 593
DB 685 SAFGVQERRLKRIISHPFNDFTFDYDIALLEKPAEYSWVRPCLP--DASHVPEA 741

QY 594 SH-ITVAGNVNLDVRSPPGKNTDLGSGVSVVDSLLCERQHDHGIPVSVTNNMCASW 652
DB 742 GKAIWVTGW---GHTQYGGTGALILQKGEIRVINQTTCNL-----LPQQITPRMMCVGP 793

QY 653 EPTAPSDICTAETGG-IAAVSFPRGRASPRHMLGLVSWSDYKTCSHRLSTAFTKVLPF 711
DB 794 -LSGGVDSVSCGDSGGPLUSSVEADGRI-----FQAGVVSNG-DGCAQRNKPQVYTRPLPF 845

QY 712 KDWIERN 718
DB 846 RDWIKEN 852

RESULT 14
PRTC_MOUSE STANDARD; PRT; 461 AA.
AC P33587; O35498;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
DE (Autoproteolysis II) (Anticoagulant protein C) (Blood coagulation factor XIV).
GN PROC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC TISSUE=Liver;
RX MEDLINE=92316897; PubMed=1618739;
RT Tada N., Sato M., Teujimura A., Iwase R., Hashimoto-Gotoh T.;
RL "Isolation and characterization of a mouse protein C cDNA.";
RN J. Biochem. 111:491-495(1992).
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=98152576; PubMed=9493582;
RT Jallbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
RN Castellino F.J.;
RA "Nucleotide structure and characterization of the murine gene encoding
RT anticoagulant protein C.";
RT Thromb. Haemost. 79:310-316(1998).
RN [3]
RP SEQUENCE OF 274-434 FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=8043441;
RA Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
RT "A comparative study of partial primary structures of the catalytic
RN region of mammalian protein C.";
RL Br. J. Haematol. 86:590-600(1994).
CC -!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
CC regulates blood coagulation by inactivating factors Va and VIIIa
CC in the presence of calcium ions and phospholipids.
CC -!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
CC and VIIIa.
CC -!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved
CC into a light chain and a heavy chain held together by a disulfide
CC bond. The enzyme is then activated by thrombin, which cleaves a
CC tetradecapeptide from the amino end of the heavy chain; this
CC reaction, which occurs at the surface of endothelial cells, is
CC strongly promoted by thrombomodulin.
CC -!- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
CC -!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu
CC residues allows the modified protein to bind calcium.
CC -!- MISCELLANEOUS: Calcium also binds, with stronger affinity to
CC another site, beyond the GLA domain. This GLA-independent binding
CC site is necessary for the recognition of the thrombin-
CC thrombomodulin complex.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -----
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CC -----
CC EMBL; D10445; BAA01235.1; -.
CC EMBL; AF034569; AAC33795.1; -.
CC EMBL; D43755; BAA07812.1; -.
CC PIR; JX0210; JX0210.
CC HSSP; P04070; 1PCU.
CC MEROPS; S01.218; -.
CC MGD; MGI:97771; Proc.
CC InterPro; IPR000152; Asx hydroxyl S.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC InterPro; IPR000294; VitK_dep_GLA.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00594; gla; 1.
CC Pfam; PF00889; Crypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00001; GLABLOOD.
CC SMART; SM00179; EGF_CA; 1.
CC SMART; SM00069; GLA; 1.
```



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RP SEQUENCE FROM N.A.
RA Wallis J., Brown A.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnorrich A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 2542-3487 FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins."
RL DNA Rep. 8:179-187(2001).
CC -1- ALTERNATIVE PRODUCTS:
CC Name=1;
CC IsoId=Q72408-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q72408-2; Sequence=VSP_009038, VSP_009039, VSP_009040,
CC VSP_009041, VSP_009042;
CC Note=No experimental confirmation available;
CC Name=3;
CC IsoId=Q72408-3; Sequence=VSP_009043, VSP_009044, VSP_009045,
CC VSP_009046;
CC Note=No experimental confirmation available;
CC -1- TISSUE SPECIFICITY: Weakly expressed in most tissues, except in
CC brain. Expressed at intermediate level in brain, including
CC cerebellum, substantia nigra, hippocampus and fetal brain.
CC Overexpressed in some head and neck cancer cell lines.
CC -1- SIMILARITY: Belongs to the CSMD family.
CC -1- SIMILARITY: Contains 14 CUB domains.
CC -1- SIMILARITY: Contains 26 Sushi (SCR) domains.
CC -1- CAUTION: Ref.3 sequence differs from that shown due to a
CC frameshift in position 939 that shortens the protein by 1021
CC residues in its N-terminus. It is unknown whether the sequence
CC shown exists or whether Ref.3 is right, shortening the sequence in
CC its N-terminus.
CC -1- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC gene model prediction.
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EMBL; AY210418; AAC34701.1; -
EMBL; AK095627; BAC04593.1; ALT_INIT.

```

FT	CARBOHYD	34	34	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	51	51	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	581	581	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	680	680	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	949	949	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	983	983	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1009	1009	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1028	1028	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1158	1158	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1178	1178	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1194	1194	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1393	1393	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1566	1566	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1638	1638	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1786	1786	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1799	1799	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1876	1876	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	2012	2012	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	2185	2185	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	2190	2190	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	2223	2223	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	2394	2394	N-LINKED	(GLCNAC. . .)	(POTENTIAL).
Query Match 8.1%; Score 318; DB 1; Length 3487;						
Best Local Similarity 22.6%; Pred. No. 1.8e-15;						
Matches 159; Conservative 70; Mismatches 236; Indels 240; Gaps 28;						
QY	57	GKREVVGYTIPCRNEENECDSLIHPGCTIPENCKSCRNGS-WGGTLDLDFYVKGFCYCAE	115			
DB	675	GKR---GFNITFTFRHNECPD---PGVPV-----NGKRFQDLSQLQSGSSISFLCDE	719			
QY	116	CRAGWYGGDCMR-----CGQVLRAPKGOILLESYP-----LNAH	149			
DB	720	GLTGQSETITCVLKEGVSVMNSAVLRCEAPCGGHLTSPSGTILSPGWPFGYKDAL	777			
QY	150	CEWTIRAKFGFVQLRFVMSLEFDYMCQDYVEVRDGDNRDQIIRKVCGNERPAPIQS	209			
DB	778	CAWIEAQFGYPIKITFDRKTEVN---YDLEVRDGRYTSAPLIGVHGTQVQFPLIS	833			
QY	210	IGSSLHLVPHSDGSKNPFQFHAIEYBITACSSPCFHDGTCVLDKAGSYKCACLAGYTGQ	269			
DB	834	TSNYLYLFTSDKSHSDIGQLRYETIT-----	861			
QY	270	RCENLLEERNCSPPGGPVNGYQKITGGPGLINGRHAIGITVVSFFCNSYVLSGNEKRTC	329			
DB	862	-----LQSDHCLDPGIPVNGQR-----HGNDYFVGALVTFSCDGYTILSDGEPLEC	907			
QY	330	QQGEWSGKQPICIKAC-----REPKISDLVRRR-----	358			
DB	908	EPNFQHSRALPSCALCGGFIQSSGTLSPGFPDPYPPNNLNTWIIETSHGKGVFFTH	967			
QY	359	-----VLPQVQSRRTPLHQL-----Y	375			
DB	968	TFHLESGHDYLLITENGSTFQPLRLTQSLRGLPAPISAGLYGNFTAQVRFISDFSMSEYGF	1027			
QY	376	SAAFSKQKLOSAPTKKPPALPGPLNGYOH-LHTQLQYECISPFYRLGSSRRTCL--RT	432			
DB	1028	NITFSYDLE--PCEBFEVPAYSIRKQLQFGVGDTLTFSCF-PGYRLEGARITCLGRRR	1084			
QY	433	GKWSGRAPSCIPICGK-----IENITAPKTQGLRWPWQAAI	468			
DB	1085	RLWSSPLPRCAECGNSVTGTQTLSPNPPVNNNNHCEIYSIQTPGKGIQ--LKARA	1142			
QY	469	YRTSG-----VHDGSLHKGAWFLVCS-----GALVNERTVVVAHCVTD-----	508			
DB	1143	FELSEGDVLKVDGNNNNSARLLGVFSHSEMMGVTLNSTSSSLWLDFTDAENTSKGFELH	1202			
QY	509	LGVVTMIKTADLVVLGKF--YRDDRDDEKTIQSLQISAILIHENYDPILLDADIAIKLL	567			
DB	1203	FSSFELIKCEDPGT--PKFGYKVHDEGHFAGGSVSFSC---DFGYS---LRGSEELICLS	1254			
QY	568	DKARISTRVQPICLAASRDLSSTFSQESHITVAGWNLADVRSFGF	612			

Db 1255 GERTWDRPLPTCVA-----ECGGTVRG-EVSGQVLSPGY 1288

Search completed: August 18, 2004, 16:24:06
Job time : 19 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	949	24.1	181	2	T08805	hypothetical prote
2	672	17.0	1019	2	A38738	coagulation factor
3	482	12.2	699	1	I54763	Ra-reactive factor
4	403	10.2	705	1	C1HURB	complement subcomp
5	400.5	10.2	686	1	A52771	Ra-reactive factor
6	378.5	9.6	695	1	S05008	complement subcomp
7	354	9.0	1524	2	T30337	polyprotein - Afri
8	340.5	8.6	694	2	JC5554	complement subcomp
9	334	8.5	688	1	C1HUS	complement subcomp
10	331.5	8.4	1019	1	A56318	enteropeptidase (E
11	330.5	8.4	1034	1	A53663	enteropeptidase (E
12	320	8.1	461	1	JX0210	protein C (activat
13	317.5	8.0	1035	1	A43090	enteropeptidase (E
14	314.5	8.0	475	1	EXCH	coagulation factor
15	313	7.9	655	2	JC7731	membrane-bound arg
16	310.5	7.9	461	1	KXHU	protein C (activat
17	299.5	7.6	443	2	I46932	coagulation factor
18	293.5	7.4	407	1	KFBO7	coagulation factor
19	292	7.4	461	1	S18994	protein C (activat
20	285.5	7.2	452	1	A30351	coagulation factor
21	283.5	7.2	482	1	EXRT	coagulation factor
22	282	7.1	456	1	KXBO	protein C (activat
23	281.5	7.1	558	2	JCS878	plasma hyaluronan-
24	281	7.1	492	1	EXBO	coagulation factor
25	280.5	7.1	264	2	I38136	chymotrypsin-like
26	280	7.1	562	1	KFHU7	t-plasminogen acti
27	278.5	7.1	466	1	UKHU7	coagulation factor
28	278	7.0	488	1	EXHU	coagulation factor
29	278	7.0	1113	2	JE0315	low-density lipopr

103	223.5	5.7	274	2	S35339	trypsin (EC 3.4.21)	176	199.5	5.1	2555	2	A40043	notch protein homo
104	223.5	5.7	348	1	HPHUR	haptoglobin-relate	177	198.5	5.0	229	1	TRBTR	trypsin (EC 3.4.21)
105	222.5	5.6	417	1	S00845	hepsin (EC 3.4.21)	178	198.5	5.0	232	1	KOPG	tissue kallikrein
106	222.5	5.6	434	1	A35005	u-plasminogen acti	179	198.5	5.0	237	2	S53378	serine proteinase
107	222.5	5.6	790	1	PLPG	plasmin (EC 3.4.21)	180	198	5.0	250	2	S68424	allergen Der f III
108	222	5.6	269	2	A26823	pancreatic elastase	181	198	5.0	270	2	B29934	pancreatic elastase
109	222	5.6	275	2	B35863	trypsin (EC 3.4.2)	182	198	5.0	760	1	C2MS	classical compleme
110	221.5	5.6	2531	2	S18188	notch protein homo	183	197.5	5.0	250	2	T01779	trypsin (EC 3.4.21)
111	221	5.6	231	2	S31778	trypsin (EC 3.4.21)	184	197.5	5.0	258	2	I36947	haptoglobin Hpp -
112	220.5	5.6	274	2	A45754	trypsin (EC 3.4.2)	185	196.5	5.0	269	2	C36823	pancreatic elastase
113	220.5	5.6	1057	1	A39288	dorsal-ventral pat	186	196.5	5.0	570	2	A48836	fibropellin C prec
114	220	5.6	275	2	A35863	trypsin (EC 3.4.2)	187	196.5	5.0	767	2	T30018	hypothetical prote
115	219.5	5.6	235	2	H42696	thrombin (EC 3.4.2)	188	196.5	5.0	2524	2	A35844	notch protein - Af
116	219.5	5.6	271	2	A25528	pancreatic elastase	189	196	5.0	3623	2	T08618	intrinsic factor-B
117	219.5	5.6	761	1	BBMS	complement factor	190	195.5	5.0	271	2	I46580	factor IX - pig (f
118	219	5.6	343	1	A57014	proctasin (EC 3.4.)	191	195	4.9	432	1	S18932	u-plasminogen acti
119	218	5.5	271	2	S41308	serine proteinase (192	194.5	4.9	246	1	TR8T1	trypsin (EC 3.4.21)
120	217.5	5.5	243	2	A56338	venom proteinase	193	194	4.9	261	2	A25606	tissue kallikrein
121	217	5.5	239	2	A27207	tissue kallikrein	194	194	4.9	267	2	S40006	trypsin (EC 3.4.21)
122	217	5.5	268	2	S68825	pancreatic elastase	195	193.5	4.9	249	2	A55634	granzyme M (EC 3.4
123	217	5.5	273	2	A47246	trypsin (EC 3.4.2)	196	193.5	4.9	347	1	HPRT	haptoglobin precu
124	217	5.5	603	2	S28941	coagulation factor	197	193.5	4.9	2471	2	A49128	cell-fate determin
125	217	5.5	2703	1	A24420	notch protein - fr	198	193	4.9	240	1	CB0A3	procarboxypeptidas
126	216.5	5.5	236	2	I42696	thrombin (EC 3.4.2)	199	193	4.9	246	1	DSHU	complement factor
127	216.5	5.5	346	2	I36942	haptoglobin - chlm	200	191.5	4.9	247	1	A25852	trypsin (EC 3.4.21)
128	216.5	5.5	2616	1	PLHU	nudel protein prec	201	191.5	4.9	281	2	T13596	trypsin homolog -
129	216	5.5	810	1	TRDG	plasmin (EC 3.4.21)	202	191.5	4.9	830	2	A30359	P-selectin precurs
130	215.5	5.5	247	1	S50666	trypsin (EC 3.4.21)	203	190.5	4.8	579	2	JG7629	membrane-type friz
131	215.5	5.5	248	2	S50666	trypsin (EC 3.4.21)	204	190.5	4.8	768	2	A42755	P-selectin precurs
132	215	5.4	241	2	S39048	trypsin (EC 3.4.21)	205	190.5	4.8	1064	2	A40136	fibropellin fa - 8
133	215	5.4	268	2	S68826	pancreatic elastase	206	189.5	4.8	266	2	S54146	trypsin (EC 3.4.21)
134	214.5	5.4	247	2	S13813	trypsin (EC 3.4.21)	207	189.5	4.8	1737	2	T00209	MEGF8 protein - hu
135	214.5	5.4	366	2	JE0105	testicular serine	208	189	4.8	246	2	JQ1472	trypsin (EC 3.4.21)
136	214.5	5.4	593	2	S45281	coagulation factor	209	189	4.8	247	2	S05494	trypsin (EC 3.4.21)
137	214	5.4	275	2	C35963	trypsin (EC 3.4.2)	210	189	4.8	253	2	A53968	serine proteinase
138	213.5	5.4	225	2	D42696	thrombin (EC 3.4.2)	211	189	4.8	258	4	S70439	pancreatic elastase
139	213.5	5.4	232	2	T30201	Notch homolog prot	212	189	4.8	267	4	A56615	probable pancreati
140	212	5.4	260	2	I56559	neuropain - mouse	213	189	4.8	646	2	UN0473	P-selectin precurs
141	212	5.4	455	2	A61545	plasmin (EC 3.4.21)	214	188.5	4.8	282	2	I84621	coagulation factor
142	211	5.3	237	2	S68702	trypsin (EC 3.4.2)	215	188	4.8	263	2	S15686	tissue kallikrein
143	211	5.3	276	2	A38654	mast cell proteina	216	187.5	4.8	250	2	S55493	serine proteinase
144	210.5	5.3	1220	2	A56136	jagged protein pre	217	187.5	4.8	259	2	I38363	trypsin (EC 3.4.21)
145	210	5.3	2437	2	S42612	transmembrane prot	218	187.5	4.8	304	2	S33496	trypsin (EC 3.4.21)
146	209	5.3	433	1	UKMS	u-plasminogen acti	219	187	4.7	246	2	JQ1471	trypsin (EC 3.4.21)
147	208.5	5.3	258	2	I36945	haptoglobin Hp - c	220	187	4.7	261	2	S45303	tissue kallikrein
148	207.5	5.3	239	2	G42696	trypsin (EC 3.4.2)	221	187	4.7	271	2	S29239	chymotrypsin (EC 3
149	207.5	5.3	269	2	B26823	pancreatic elastase	222	186	4.7	1594	2	T30549	hensin - rabbit
150	207	5.2	238	1	TRW5Y	trypsin-like prote	223	185.5	4.7	711	1	A47136	macrophage-stimula
151	206.5	5.2	246	1	TRR12	trypsin (EC 3.4.21)	224	185.5	4.7	927	1	JQ0948	A5 antigen precurs
152	206.5	5.2	256	2	T10109	serine proteinase	225	185	4.7	256	1	NGMSA	7S nerve growth fa
153	206	5.2	430	1	A24702	apoptein(a) (EC	226	183.5	4.7	1372	2	T25933	hypothetical prote
154	206	5.2	4548	1	S00657	mastocytoma protei	227	183	4.6	265	1	KQRTP	serine proteinase
155	205.5	5.2	269	2	B32410	plasmin (EC 3.4.21)	228	183	4.6	392	1	A30100	E-selectin - pig
156	205.5	5.2	460	2	B61545	testicular serine	229	182.5	4.6	482	2	JC5092	DELTA-like 1 - mou
157	204.5	5.2	367	2	JE0104	complement C2 prec	230	182.5	4.6	722	2	I48324	notch homolog - se
158	204.5	5.2	752	1	C2HU	Notch B protein -	231	182.5	4.6	2531	2	T31070	tissue kallikrein
159	204.5	5.2	1203	2	A49175	trypsin (EC 3.4.21)	232	182	4.6	261	1	TRMSM5	granzyme B (EC 3.4
160	203.5	5.2	247	1	B25852	complement factor	233	181.5	4.6	247	1	TRMSCL	trypsin (EC 3.4.21)
161	203.5	5.2	263	1	I55608	coagulation factor	234	181.5	4.6	247	2	S12764	serine proteinase
162	203.5	5.2	285	2	I48144	coagulation factor	235	181.5	4.6	258	2	A45161	acrosin (EC 3.4.21)
163	203.5	5.2	309	2	B49878	coagulation factor	236	181.5	4.6	437	1	S18407	7S nerve growth fa
164	203.5	5.2	3623	2	T09456	intrinsic factor-B	237	181	4.6	261	1	NGMSG	acrosin (EC 3.4.21)
165	203	5.1	403	2	C82228	probable trypsin v	238	181	4.6	418	2	A37344	hypothetical prote
166	202	5.1	240	2	S39047	trypsin (EC 3.4.21)	239	181	4.6	1291	2	T21694	trypsin (EC 3.4.21)
167	202	5.1	2321	2	S78549	notch3 protein - h	240	180.5	4.6	248	2	S55067	factor IX - rabbit
168	201.5	5.1	246	2	B25528	trypsin (EC 3.4.21)	241	180.5	4.6	275	2	I46712	trypsin (EC 3.4.21)
169	200.5	5.1	226	1	KCUF	bradykinin (EC 3.4	242	180.5	4.6	437	2	JX0172	acrosin (EC 3.4.21)
170	200.5	5.1	231	1	TRP6TR	trypsin (EC 3.4.21)	243	180	4.6	254	2	S49329	trypsin-like prote
171	200.5	5.1	810	2	B30848	plasmin (EC 3.4.21)	244	180	4.6	261	2	S01971	tissue kallikrein
172	199.5	5.1	247	2	A27547	trypsin (EC 3.4.21)	245	180	4.6	275	2	S40005	trypsin (EC 3.4.21)
173	199.5	5.1	257	2	S33772	tissue kallikrein	246	179.5	4.6	243	2	A35871	trypsin (EC 3.4.21)
174	199.5	5.1	258	2	G02959	haptoglobin - rhes	247	179.5	4.6	259	1	WMMS28	complement factor
175	199.5	5.1	275	2	S40007	trypsin (EC 3.4.21)	248	179.5	4.6	274	2	I47078	coagulation factor

249	179.5	4.6	728	2	I50719	C-Delta-1 - chicke	322	161.5	4.1	250	2	S31384	trypsin (EC 3.4.21
250	179.5	4.6	1047	2	A55617	masquerade precurs	323	161.5	4.1	261	2	S40162	cathepsin G (EC 3.
251	179	4.5	266	1	BLPG	pancreatic elastas	324	161.5	4.1	265	2	T15451	hypothetical prote
252	179	4.5	612	2	B42755	E-selectin precurs	325	161.5	4.1	832	2	A31246	neurogenic protein
253	178.5	4.5	402	2	JH0403	procollagen I C-pr	326	161.5	4.1	880	2	S00670	neurogenic repetit
254	177.5	4.5	248	2	A43520	natural killer cel	327	161.5	4.1	1025	1	A43526	complement C3d/Eps
255	177.5	4.5	420	2	A55283	acrosin (EC 3.4.21	328	161	4.1	1827	2	T34288	hypothetical prote
256	177.5	4.5	1964	2	T09059	notch4 - mouse	329	160.5	4.1	661	1	KFHU13	coagulation factor
257	177	4.5	268	2	JQ1473	pancreatic elastas	330	160	4.1	302	1	A31372	granzyme A (EC 3.4
258	177	4.5	473	2	A56175	adhesive plaque pr	331	160	4.1	3002	2	A47221	fibrillin-1 precur
259	177	4.5	747	2	I51579	complement factor	332	159.5	4.0	1722	2	E89753	protein Fl1C7.4 fi
260	176.5	4.5	1091	1	PL0009	complement C3d/Eps	333	159	4.0	244	2	A42884	tissue kallikrein
261	176	4.5	261	1	A31136	tissue kallikrein	334	159	4.0	261	2	A28062	gamma-amin (EC 3.
262	176	4.5	261	2	A29745	tissue kallikrein	335	159	4.0	2907	2	A57278	fibrillin-2 precur
263	176	4.5	264	2	A32794	trypsin-like prote	336	158.5	4.0	247	2	S59135	mast cell proteina
264	176	4.5	2318	2	S45306	notch 3 protein -	337	158.5	4.0	385	2	S53718	homotetic protein d
265	175.5	4.4	274	2	S40004	trypsin-related pr	338	158.5	4.0	833	2	S19087	gene Delta protein
266	175	4.4	270	2	A29934	pancreatic elastas	339	158	4.0	610	2	T16761	hypothetical prote
267	175	4.4	421	1	S11674	acrosin (EC 3.4.21	340	158	4.0	2918	2	A54105	fibrillin-2 precur
268	174.5	4.4	232	2	S32398	serine proteinase	341	157.5	4.0	579	2	A56740	sperm-egg recognit
269	174.5	4.4	246	1	TRDGC	trypsin (EC 3.4.21	342	157.5	4.0	907	2	T27317	hypothetical prote
270	174	4.4	259	2	A29746	tissue kallikrein	343	157	4.0	261	2	JE0236	tissue kallikrein
271	174	4.4	261	1	KQMS1	tissue kallikrein	344	157	4.0	610	2	A35046	E-selectin precurs
272	174	4.4	1295	2	A32901	glpi protein precu	345	156.5	4.0	252	2	A36172	procytotoxic T-lym
273	173.5	4.4	548	2	D82175	probable trypsin v	346	156.5	4.0	275	2	JC8506	tumor necrosis fac
274	173	4.4	229	1	TRDFS	trypsin (EC 3.4.21	347	156.5	4.0	1429	2	S06434	homotetic protein 1
275	173	4.4	768	2	I53821	p-selectin - rat	348	156.5	4.0	3635	2	T10053	laminin alpha 5 ch
276	172.5	4.4	248	1	PRMSC2	granzyme C (EC 3.4	349	156	4.0	259	1	KQRTTN	tonin (EC 3.4.21 -
277	172.5	4.4	277	2	S35340	trypsin (EC 3.4.21	350	156	4.0	261	2	A29586	tissue kallikrein
278	172.5	4.4	431	2	S47538	acrosin (EC 3.4.21	351	156	4.0	702	2	T16832	hypothetical prote
279	172.5	4.4	449	2	A55362	procollagen I C-pr	352	155.5	3.9	213	2	S17537	fibrinolytic prote
280	172	4.4	254	2	S65465	trypsin-like prote	353	155.5	3.9	485	2	S36772	E-selectin - bovin
281	172	4.4	261	2	A24378	tissue kallikrein	354	155.5	3.9	533	2	JC7985	brain-specific CUB
282	172	4.4	415	1	A34170	acrosin (EC 3.4.21	355	155	3.9	250	2	S15685	kallikrein, glandu
283	171.5	4.3	230	2	A27802	hypodermin C (EC 3	356	155	3.9	2489	2	I73012	complement C3b/C4b
284	171.5	4.3	262	1	KQHU	tissue kallikrein	357	154.5	3.9	252	2	A34877	C4b-binding protei
285	171.5	4.3	2403	2	A59386	sanko - human	358	154	3.9	689	2	S65551	factor H - bovine
286	171	4.3	257	2	B45061	granzyme A (EC 3.4	359	153.5	3.9	251	2	JC2125	chymase (EC 3.4.21
287	171	4.3	260	2	A45061	granzyme A (EC 3.4	360	153.5	3.9	387	2	B49175	Notch A protein -
288	171	4.3	266	1	ELRT1	pancreatic elastas	361	153.5	3.9	551	2	I46709	endothelial leukoc
289	171	4.3	273	2	S40003	trypsin-related pr	362	153.5	3.9	1786	1	MMWSB1	laminin beta-1 cha
290	171	4.3	2139	2	A35672	crumbs protein - f	363	153	3.9	152	2	A53274	complement factor
291	170	4.3	248	2	S33756	granzyme-like prot	364	153	3.9	254	1	TRWV3Y	trypsin-like prote
292	170	4.3	266	2	JC4850	trypsin-like prote	365	153	3.9	2871	2	A55567	fibrillin-1 - bovi
293	169.5	4.3	251	1	T10262	mast cell serine p	366	152.5	3.9	248	1	S01007	granzyme F (EC 3.4
294	169.5	4.3	261	1	S35711	semenogelase (EC 3	367	152.5	3.9	264	2	S65663	granzyme 3 (EC 3.4
295	169.5	4.3	421	2	S29599	acrosin (EC 3.4.21	368	152.5	3.9	385	2	A54785	preadipocyte facto
296	169.5	4.3	214	2	T16833	hypothetical prote	369	152.5	3.9	422	1	KXHUZ	plasma protein Z p
297	169	4.3	214	2	S17680	fibrinolytic prote	370	152	3.9	281	1	A61021	Granzyme B (EC 3.4
298	169	4.3	246	2	S64707	chymase (EC 3.4.21	371	152	3.9	686	2	JC7569	Delta-4 protein -
299	169	4.3	259	2	B31136	tissue kallikrein	372	151.5	3.8	261	2	A40332	tissue kallikrein
300	169	4.3	504	2	S56745	mucin (clone pgM31	373	151.5	3.8	716	1	A40332	macrophage-stimula
301	168.5	4.3	248	2	S33755	granzyme-like prot	374	151.5	3.8	977	2	I52657	seizure-related pr
302	168	4.3	597	2	S71352	metalloproteinase	375	151	3.8	249	1	A35842	chymase (EC 3.4.21
303	168	4.3	2014	2	I36936	complement recepto	376	151	3.8	261	2	A41020	tissue kallikrein
304	167.5	4.2	261	1	A32297	semenogelase (EC 3	377	151	3.8	1620	2	T27283	hypothetical prote
305	167.5	4.2	383	2	S53716	delta-like homoteti	378	150.5	3.8	248	2	S43259	granzyme-like prot
306	167	4.2	247	2	S45113	granzyme-like prot	379	150.5	3.8	277	2	A41735	hyaluronate-bindin
307	167	4.2	260	2	A37938	tissue kallikrein	380	150.5	3.8	285	2	T35195	probable serine pr
308	166	4.2	265	2	T10495	chymotrypsin (EC 3	381	150.5	3.8	685	2	JC7570	Delta-4 protein -
309	165	4.2	2043	2	T18524	scavenger receptor	382	150.5	3.8	1053	2	S46199	probable complemen
310	164.5	4.2	449	1	NBHUS	complement factor	383	150	3.8	263	1	WMVZSP	apolipoprotein H h
311	164.5	4.2	1231	1	NBHUH	complement factor	384	150	3.8	267	1	ELHUL	leukocyte elastase
312	164	4.2	230	2	I48685	mast cell proteina	385	150	3.8	601	2	B36346	fibrulin 1 precurs
313	164	4.2	613	2	S15468	complement C3b/C4b	386	150	3.8	770	2	T00203	LDL receptor-relat
314	164	4.2	2871	2	A55624	fibrillin-1 precur	387	150	3.8	3712	2	S18253	laminin alpha-1 ch
315	163	4.1	868	2	T20239	hypothetical prote	388	149.5	3.8	236	1	A32121	snake venom factor
316	162.5	4.1	276	2	A47290	TSG-6 homolog P84	389	149.5	3.8	259	1	TRSMG	trypsin (EC 3.4.21
317	162.5	4.1	1290	2	A57190	ebnerin precursor	390	149.5	3.8	13288	2	T03099	mucin, submaxillar
318	162.5	4.1	2083	2	T42721	CRP-ductin-alpha p	391	149	3.8	216	1	KYVH20	chymotrypsin (EC 3
319	162	4.1	261	1	EGMSB	tissue kallikrein	392	149	3.8	683	2	C36346	fibrulin 1 precurs
320	161.5	4.1	226	2	S69370	duodenase - bovine	393	149	3.8	770	2	T00204	LDL receptor relat
321	161.5	4.1	248	2	S01006	cytotoxic T-lympho	394	149	3.8	1408	2	S16148	gene serrate prote

395	148	3.8	218	1	KYH2C	chymotrypsin (EC 3	468	134	3.4	3034	2	T14119	seven-pass transme
396	148	3.8	668	2	A46013	coagulation factor	469	133.5	3.4	154	2	S35207	proteinase 7 - buf
397	148	3.8	1469	2	B36665	slit protein 2 pre	470	133.5	3.4	1687	2	T30176	EGF repeat transme
398	148	3.8	1480	2	A36665	slit protein 1 pre	471	133.5	3.4	3507	2	T34513	hypothetical prote
399	147.5	3.7	244	2	A34910	mast cell proteina	472	133	3.4	810	2	T10756	Nel-homolog protei
400	147.5	3.7	244	2	A46721	chymase (EC 3.4.21	473	132.5	3.4	331	2	T27906	hypothetical prote
401	147.5	3.7	597	1	S53711	C4BP alpha chain p	474	132	3.3	246	2	A38678	mast cell proteina
402	147.5	3.7	1786	1	MMHUB1	laminin beta-1 cha	475	132	3.3	372	2	JCS377	L-selectin precurs
403	147.5	3.7	4391	2	A38096	perlecan precursor	476	132	3.3	558	2	S57953	C4BP protein alpha
404	147	3.7	236	2	A28566	T-cell suppressor	477	132	3.3	2109	1	I50421	aggregran precursor
405	147	3.7	259	2	D23863	tissue kallikrein	478	132	3.3	3871	2	T22812	hypothetical prote
406	147	3.7	262	1	JC4803	venombin A (EC 3.4	479	131.5	3.3	302	1	WMBE1E	secretory compleme
407	147	3.7	716	1	JCS061	macrophage-stimula	480	131.5	3.3	1268	2	S52781	neurocan - mouse
408	147	3.7	1557	2	T28811	hypothetical prote	481	130.5	3.3	1257	2	S28764	neurocan precursor
409	147	3.7	3084	1	MMMSA	laminin alpha-1 ch	482	130.5	3.3	3672	2	T23433	hypothetical prote
410	146.5	3.7	236	1	B32121	snake venom factor	483	130.5	3.3	3704	2	T37316	probable laminin a
411	146.5	3.7	3707	2	S18252	heparan sulfate pr	484	129.5	3.3	233	1	JG0169	venombin A (EC 3.4
412	146	3.7	263	2	T28450	hypothetical prote	485	129.5	3.3	376	2	JC4892	L-selectin precurs
413	145	3.7	256	1	TRPF	trypsin-like prote	486	129.5	3.3	381	1	B36359	decay-accelerating
414	145	3.7	263	1	C36838	complement control	487	129.5	3.3	440	2	A26359	decay-accelerating
415	145	3.7	372	2	A32375	L-selectin precurs	488	129	3.3	235	1	S65621	venombin AB (EC 3.
416	145	3.7	782	2	A61625	tenascin-like prot	489	128.5	3.3	255	2	A27122	cathepsin G (EC 3.
417	144.5	3.7	246	2	B38578	mast cell proteina	490	128.5	3.3	321	2	T33161	hypothetical prote
418	144.5	3.7	303	2	T13598	trypsin homolog -	491	128	3.2	219	1	TRPGA2	azurocidin - pig
419	144.5	3.7	360	2	T42321	complement control	492	128	3.2	5147	1	IJFFTM	cadherin-related t
420	144	3.7	283	2	B72152	Bi8L protein - var	493	127.5	3.2	1531	2	T42218	slit-1 protein hom
421	144	3.7	685	2	S78040	fibulin, splice fo	494	127	3.2	258	2	S62220	tryptase 2 - rat
422	143.5	3.6	247	2	S23504	chymase (EC 3.4.21	495	127	3.2	1609	1	MMHUB2	laminin gamma-1 ch
423	143	3.6	3075	2	S14458	laminin alpha-1 ch	496	127	3.2	1751	1	MMHUMH	laminin alpha-2 ch
424	142.5	3.6	260	2	S26043	chymase (EC 3.4.21	497	127	3.2	3106	1	S53868	laminin alpha-2 ch
425	142	3.6	272	2	JC4170	trypsin-like prote	498	126.5	3.2	1025	2	T42626	secreted leucine-r
426	141.5	3.6	310	2	S41055	metalloproteinase	499	126	3.2	265	2	J50260	serine proteinase
427	141.5	3.6	385	1	A34015	L-selectin precurs	500	126	3.2	265	2	A38894	serine proteinase
428	141	3.6	225	2	S45356	probable serine pr	501	126	3.2	330	2	I56100	complement factor
429	141	3.6	246	1	A46504	cytotoxic T-lympho	502	126	3.2	642	2	S53433	plasma protein S p
430	140.5	3.6	246	1	A36504	chymase (EC 3.4.21	503	125.5	3.2	254	2	S35585	chymotrypsin-like
431	140.5	3.6	1234	1	NBM5H	complement factor	504	125.5	3.2	265	2	I48679	neutrophil elastase
432	140.5	3.6	2406	2	A54148	od2 protein - frul	505	125.5	3.2	597	1	NHUC4	C4b-binding protei
433	140.5	3.6	2515	2	S47008	tenascin-like prot	506	125	3.2	152	2	S35209	serine proteinase
434	140.5	3.5	396	1	KXBOZ	plasma protein Z -	507	125	3.2	323	1	S09702	L-selectin precurs
435	139.5	3.5	258	1	S44184	chymotrypsin (EC 3	508	125	3.2	1790	1	MMFFB1	laminin beta-1 cha
436	139.5	3.5	288	2	T33224	hypothetical prote	509	124.5	3.2	248	2	A33412	cytotoxic T-lympho
437	139.5	3.5	319	2	I51569	UVS-2 protein - Af	510	124.5	3.2	548	2	T16642	hypothetical prote
438	139	3.5	1820	2	A55494	latent transformin	511	124	3.1	330	2	T46256	brevican - human (
439	138.5	3.5	244	2	S26042	chymase (EC 3.4.21	512	124	3.1	710	1	I51283	hepatocyte growth
440	138.5	3.5	247	1	KYHUCM	chymase (EC 3.4.21	513	124	3.1	883	2	S49126	brevican precursor
441	138.5	3.5	705	2	S34968	fibulin, splice fo	514	124	3.1	1221	2	A49457	fibulin-2 precurs
442	138.5	3.5	1111	2	T26972	hypothetical prote	515	124	3.1	1523	2	T13953	MEGF5 protein - ra
443	137.5	3.5	191	2	S54115	complement factor	516	124	3.1	1584	2	T22674	hypothetical prote
444	137.5	3.5	88	2	D35069	complement factor	517	124	3.1	2180	2	T29764	hypothetical prote
445	137	3.5	288	2	S57960	C4BP protein beta	518	123.5	3.1	151	2	S35205	proteinase 5 - buf
446	137	3.5	372	2	S23936	L-selectin precurs	519	123.5	3.1	259	1	S49129	chymotrypsin (EC 3
447	137	3.5	2823	2	T23064	hypothetical prote	520	123.5	3.1	370	2	S22124	L-selectin precurs
448	137	3.5	2823	2	F87908	protein T22A3.8 [i	521	123.5	3.1	699	2	T33375	hypothetical prote
449	137	3.5	3102	2	T43291	laminin alpha chai	522	123.5	3.1	1184	2	A55184	fibulin-2 precurs
450	136.5	3.5	247	1	PRRTG	mast cell proteina	523	123	3.1	248	2	S49323	chymotrypsin (EC 3
451	136.5	3.5	1274	2	T42017	cysteine rich prot	524	123	3.1	308	2	JC7125	epidermal growth f
452	136	3.4	360	1	WMBE2E	membrane-bound com	525	123	3.1	340	2	I56234	decay-accelerating
453	136	3.4	676	2	A45900	complement C3b rec	526	123	3.1	798	2	T22793	hypothetical prote
454	136	3.4	1574	2	T13954	MEGF6 protein - ra	527	123	3.1	2844	2	S28291	hypothetical prote
455	136	3.4	1607	1	MMMSB2	laminin gamma-1 ch	528	122.5	3.1	1081	2	T31329	receptor tyrosine
456	135.5	3.4	226	2	JE0151	myonase (EC 3.4.-	529	122	3.1	152	2	S35206	serine proteinase
457	135.5	3.4	372	2	T29359	hypothetical prote	530	122	3.1	198	2	I46002	C4BP beta chain -
458	135.5	3.4	452	2	A35068	complement factor	531	122	3.1	676	1	KXHUS	plasma protein S p
459	135.5	3.4	469	1	NBMSC4	C4b-binding protei	532	122	3.1	1810	1	A32230	tenascin precursor
460	135	3.4	159	2	I84615	coagulation factor	533	122	3.1	1955	1	AGCH	agrin precursor -
461	135	3.4	343	2	G35070	apolipoprotein H-r	534	121.5	3.1	245	2	A48598	kallikrein-like se
462	135	3.4	345	1	NBRU	apolipoprotein H p	535	121.5	3.1	416	2	T20448	hypothetical prote
463	135	3.4	3051	2	S42373	hypothetical prote	536	121.5	3.1	610	1	I46001	C4b-binding protei
464	134.5	3.4	601	2	T22025	hypothetical prote	537	121.5	3.1	576	2	T42215	zonadhesin - mouse
465	134.5	3.4	601	2	D89711	protein F40E10.4 [538	121	3.1	647	2	A43902	tenascin - associat
466	134	3.4	232	1	A54361	venombin A (EC 3.4	539	121	3.1	1627	2	S65464	pregnancy-associat
467	134	3.4	2824	2	T22759	hypothetical prote	540	121	3.1	2409	1	A60979	versican precursor

541	120.5	3.1	247	2	564708	chymase (EC 3.4.21	614	112	2.8	228	1	S35689	venombin A (EC 3.4
542	120.5	3.1	252	2	T46247	hypothetical prote	615	112	2.8	918	2	JC4361	scavenger receptor
543	120.5	3.1	345	1	JN0465	apolipoprotein H p	616	112	2.8	1125	1	S57846	protein-tyrosine k
544	120.5	3.1	497	2	JC2054	complement regulat	617	112	2.8	1353	1	JH0675	restriccin precurs
545	120.5	3.1	646	2	S38819	plasma protein S -	618	112	2.8	1639	1	MW6FB2	laminin gamma-1 ch
546	120.5	3.1	689	2	T42760	fibulin, splice fo	619	112	2.8	3562	2	A47171	chondroitin sulfat
547	120.5	3.1	712	2	T42990	fibulin 1, splice	620	112	2.8	4307	2	T20721	hypothetical prote
548	120.5	3.1	728	1	A60185	hepatocyte growth	621	111.5	2.8	159	2	S35202	proteinase 2 - buf
549	120.5	3.1	1394	2	A35626	transforming growt	622	111.5	2.8	370	2	JC7592	spinal cord-derive
550	120.5	3.1	1801	1	NWRTS	laminin beta-2 cha	623	111.5	2.8	651	2	T19477	hypothetical prote
551	120	3.0	257	1	JC2479	venombin B (EC 3.4	624	111.5	2.8	1328	2	T43060	agrin - electric r
552	120	3.0	363	2	B45900	complement C3d/Eps	625	111.5	2.8	1797	2	A55677	tenascin precursor
553	120	3.0	493	2	JC5621	epidermal growth f	626	111.5	2.8	2019	1	JQ1322	hypothetical prote
554	120	3.0	589	2	T43210	fibulin-ID precurs	627	111.5	2.8	2531	2	T16743	MEGF1 protein - ra
555	120	3.0	912	2	A54423	brevican precursor	628	111.5	2.8	4351	2	T00252	venombin A (EC 3.4
556	120	3.0	1548	2	S34593	serine proteinase	629	111	2.8	231	2	A60468	hypothetical prote
557	120	3.0	1643	2	T14274	versican precursor	630	111	2.8	915	2	T21773	venombin A (EC 3.4
558	120	3.0	2397	1	A55535	versican precursor	631	110.5	2.8	234	1	S20407	apolipoprotein H p
559	120	3.0	3381	2	T42389	versican precursor	632	110.5	2.8	237	1	NBRT	hypothetical prote
560	119.5	3.0	161	2	T48158	coagulation factor	633	110.5	2.8	408	2	T22801	complement factor
561	119.5	3.0	482	2	A34924	complement C3b/C4b	634	110.5	2.8	583	2	A29154	growth arrest-spec
562	119.5	3.0	675	1	KXBOS	plasma protein S p	635	110.5	2.8	678	2	B48089	hypothetical prote
563	119.5	3.0	835	2	JP0076	nel protein - chic	636	110.5	2.8	692	2	T32980	thrombospondin 4 p
564	119.5	3.0	1247	1	MWJUND	nidogen precursor	637	110.5	2.8	961	1	TSHUP4	epidermal growth f
565	119.5	3.0	1506	2	T30886	integumentary muc	638	110.5	2.8	1217	1	EGMSMG	plexin 1 precursor
566	119	3.0	258	2	A57290	venom plasminogen	639	110.5	2.8	1894	2	JC4980	hypothetical prote
567	119	3.0	513	2	D88991	protein apx-1 (imp	640	110	2.8	266	2	T19292	protein-tyrosine k
568	118.5	3.0	674	2	I55476	growth potentiatin	641	110	2.8	1124	1	I58388	Plexin - African c
569	118.5	3.0	728	1	JH0579	hepatocyte growth	642	110	2.8	1905	2	I51553	cytotoxic T-lympho
570	118.5	3.0	728	1	A35644	hepatocyte growth	643	109.5	2.8	198	2	S06176	LR11 protein - mou
571	118	3.0	133	2	S21114	spermadhesin AWN -	644	109.5	2.8	2215	2	T00348	hypothetical prote
572	118	3.0	196	2	T08808	hypothetical prote	645	109	2.8	661	2	T42754	hypothetical prote
573	118	3.0	293	2	B26637	neurogenic repetit	646	109	2.8	2610	2	T15099	hypothetical prote
574	118	3.0	838	2	T20125	hypothetical prote	647	109	2.8	2802	2	T20968	hypothetical prote
575	118	3.0	883	2	S57653	brevican precursor	648	108.5	2.8	236	1	A41456	venombin A (EC 3.4
576	117.5	3.0	188	2	B32340	tissue kallikrein	649	108.5	2.8	2825	2	T14271	Doc4 protein, stre
577	117.5	3.0	259	2	T21011	hypothetical prote	650	108	2.7	221	1	TRHUAZ	azurocidin precurs
578	117.5	3.0	642	2	S53434	plasma protein S p	651	108	2.7	1450	2	T30273	hypothetical prote
579	117.5	3.0	996	2	J02037	apolipoprotein E r	652	108	2.7	1700	2	S08167	Balbiani ring 3 pr
580	117.5	3.0	1160	2	F88369	protein unc-52 (im	653	108	2.7	2476	2	T34022	zonadhesin - pig
581	117.5	3.0	2295	2	C88369	protein unc-52 (im	654	107.5	2.7	640	2	T19346	hypothetical prote
582	117.5	3.0	3375	2	T19821	hypothetical prote	655	107.5	2.7	670	2	I65967	disintegrin-like m
583	116.5	3.0	256	1	PRH03	proteinase 3 (EC 3	656	107.5	2.7	3566	1	A40701	tenascin-X precurs
584	116.5	3.0	377	2	I54479	membrane cofactor	657	107.5	2.7	4544	1	S02392	alpha-2-macroglobu
585	116.5	3.0	378	2	B59180	Wnt inhibitory fac	658	107	2.7	280	2	G02741	skeletal muscle LI
586	116.5	3.0	384	2	S01896	membrane cofactor	659	107	2.7	497	2	T27827	hypothetical prote
587	116.5	3.0	1170	2	A53612	laminin B1k chain	660	106.5	2.7	192	2	E70414	hypothetical prote
588	116	2.9	1376	2	G00043	osteonidogen - hum	661	106.5	2.7	362	2	JC5194	membrane cofactor
589	115.5	2.9	440	2	A43519	complement recepto	662	106.5	2.7	369	2	JC5138	hypothetical prote
590	115.5	2.9	1474	2	D88550	protein ZC84.6 (im	663	106.5	2.7	616	2	T29234	cartilage oligomer
591	115.5	2.9	1680	2	A43434	furin (EC 3.4.21.7	664	106.5	2.7	755	2	A44315	hypothetical prote
592	115	2.9	279	2	JG0164	LIM protein, FHL4	665	106	2.7	417	2	T33376	hypothetical prote
593	115	2.9	1207	1	EGHU	epidermal growth f	666	106	2.7	657	2	T00859	hypothetical prote
594	114.5	2.9	270	2	T37278	complement factor	667	106	2.7	927	2	T12772	epidermal growth f
595	114.5	2.9	349	2	G02913	sperm CD46 - human	668	106	2.7	1133	1	EGRT	hypothetical prote
596	114.5	2.9	369	2	I57998	membrane cofactor	669	106	2.7	1142	2	T30272	protein T22F7.3 [1
597	114.5	2.9	1798	2	S38169	laminin beta-2 cha	670	106	2.7	1522	2	H88380	hypothetical prote
598	114	2.9	255	1	A28163	venombin A (EC 3.4	671	106	2.7	1805	2	T21888	hypothetical prote
599	114	2.9	741	2	T46488	hypothetical prote	672	106	2.7	2195	2	T4264	hypothetical prote
600	114	2.9	846	2	A30889	integrin beta chai	673	105.5	2.7	346	2	T46914	hypothetical prote
601	114	2.9	1069	2	T42681	hypothetical prote	674	105.5	2.7	596	2	A45664	variant-specific s
602	113.5	2.9	293	2	T22919	hypothetical prote	675	105.5	2.7	673	2	A48089	growth arrest-spec
603	113.5	2.9	502	2	T00130	hypothetical prote	676	105	2.7	860	1	QRHULD	LDL receptor precu
604	113.5	2.9	558	2	T17324	hypothetical prote	677	105	2.7	1107	2	T15884	hypothetical prote
605	113.5	2.9	574	2	B88465	protein B0244.8 [i	678	105	2.7	1746	1	S19694	tenascin precursor
606	113.5	2.9	879	1	Q8RTLD	LDL receptor precu	679	105	2.7	2201	2	A32160	tenascin-C - human
607	113.5	2.9	1712	2	A38261	masking protein pr	680	104.5	2.6	345	1	NBMS	apolipoprotein H p
608	112.5	2.9	161	2	I62744	coagulation factor	681	104.5	2.6	1360	2	T33922	hypothetical prote
609	112.5	2.9	264	2	A28942	pancreatic elastas	682	104	2.6	343	1	NBBO	apolipoprotein H p
610	112.5	2.9	370	2	JC7591	spinal cord-derive	683	104	2.6	360	1	A55198	transcription fact
611	112.5	2.9	677	2	C42125	trophozoite cystei	684	104	2.6	379	2	A59180	Wnt inhibitory fac
612	112.5	2.9	1228	2	A57384	multimerin, endoth	685	104	2.6	473	2	T23226	hypothetical prote
613	112.5	2.9	1797	2	T1889	hypothetical prote	686	104	2.6	2101	2	S57245	insulin receptor (

Qy 456 -KTQGLRWPQAIIYRRTSGVHDGSLHKGAWFLVCSGALVNRVTVAHVCTDLGKVTM 514
 Db 767 NSTEIGQWPQAGISRWLA-----DHNWFLQCGSLLNKKWIVTAHCVTSATAEI 819
 Qy 515 IKTADLVKVLGKVRDRDRDEKTIQSLQISAILHNPYDILLDADTALIKLADKARIST 574
 Db 820 IDPSQFKYLGKYYRDRDRDDVYVQREALIEHVPNPYDGNLNFDFALIQLTPTVLT 879
 Qy 575 RVOPICLAARDLSTSPQESHI-----TVAGWNVLADVRSPGKNDLRSVVVVDSL 628
 Db 880 RVOPICLPT-DITT--REHLREGTLAVTGWG---LNENNTYSEMIQAVLPVVAAS 930
 Qy 629 LCEQEDHGHIPSVTONMFCASWEPTAPSDICTAETGGIAAASFPGASPERHLMGL 688
 Db 931 TCBEYKADLPLVTENMFECAGY-KRGYDACSDDSGG--PLVAFDDSRSTRRWVLEGI 987
 Qy 689 VSMYDKTCSH-RLSTAFKTVLPFKDWIER 717
 Db 988 VSMGSPSGCKANQYGGFTKVNFLSIQ 1017

RESULT 3
 I54763
 Na/Alternative factor (EC 3.4.21.-) 1 precursor - human
 C/Specios: Homo sapiens (man)
 C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
 C/Accession: J54763; JN0883
 R/Sato, T.; Endo, Y.; Matsushita, M.; Fujita, T.
 Int: Immunol. 6, 665-669, 1994
 A/Title: Molecular characterization of a novel serine protease involved in activation of
 A/Reference number: I54763; MUID:94289349; PMID:8018603
 A/Accession: I54763
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-699 <SAT>
 A/Cross-references: GB:028593; NID:9790963; PIDN:BA05928.1; PID:9471128
 R/Takada, F.; Takayama, Y.; Hatae, H.; Kawakami, M.
 Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
 A/Title: A new member of the C1s family of complement proteins found in a bactericidal f
 A/Reference number: JN0883; MUID:94059062; PMID:8240317
 A/Accession: JN0883
 A/Molecule type: mRNA
 A/Residues: 1-234, 'E', 236-284, 'G', 286-498, 'K', 500-542, 'K', 544-642, 'S', 644-699 <TAK>
 A/Cross-references: DBJ:DI7525; NID:9433712; PIDN:BA04477.1; PID:9433713
 A/Experimental source: liver
 C/Comment: This is a serum bactericidal factor that activates complement C4 and C2 compo
 C/Genetics:
 A/Gene: GDB:MSP1; GDB:CRAPF; CRAPF1; PRSS5; MASP
 A/Cross-references: GDB:361104; GDB:330954; OMIM:600521
 A/Map position: 3q27-3q28
 C/Superfamily: complement
 C/Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hydro
 F/1-17/Domain: signal sequence #status predicted <SIG>
 F/18-448,449-699/Product: Ra-reactive factor #status predicted <MAT>
 F/19-135/Domain: C1r/C1s repeat homology <C1r1>
 F/143-181/Domain: EGF homology <EGF>
 F/185-294/Domain: C1r/C1s repeat homology <C1R2>
 F/301-362/Domain: complement factor H repeat homology <FHL>
 F/367-432/Domain: complement factor H repeat homology <FH2>
 F/449-651/Domain: trypsin homology <TRY>
 F/49,178,407/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/73-91,143-157,153-166,168-181,185-212,242-260,301-349,359-362,367-414,397-432,436-572,
 F/159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 F/448-449/Cleavage site: Arg-Ile (autolytic) #status predicted
 F/490,552,646/Active site: His, Asp, Ser #status predicted

Query Match 12.2%; Score 482; DB 1; Length 699;
 Best Local Similarity 24.9%; Pred. No. 1.2e-24;
 Matches 178; Conservative 93; Mismatches 228; Gaps 39;
 Qy 69 CRNENECDCLIHGCTIPENCCKSRNGSGTLDLPVYKGFYCAECRAGWY---GGD 124

Db 143 CKREDEBELSCDHY-----CHN-----YIGGYCS-CRFGYILLTNDRT 180
 Qy 125 C-MRCQVLRAPKQILL-----ESYPLNAHCWTHAKPGFVIQIRFVMLSLEFDYM-- 176
 Db 181 CRVECDNLFTQRTGVTITSPDPNPPYKSKSECLYITIELEGFMVNLQFEDI---FDIQH 237
 Qy 177 ----COYDVVEVDGNRGGQIIKRVCGNERPAPIOSIGSSLLHVLPHSDGSKNDFDHAI 232
 Db 238 PEVPCFYDIKIKVGP-----KVLGPFCKGKAPETSTQSHSVLILPHSDNSAENRWRL- 292
 Qy 233 YEBITACSSPPCHDGTCLVLDKAGSYKCACTAGYTGQRCENLEERNCSDPGPGVNGYQK 292
 Db 293 -----SYRAA-----GNECPCL-----QP-PVH----- 309
 Qy 293 ITGGPLINGRHAHIGTVVSFF-----CNNSY-VLSGNEKR-----TCQNGENSGKQ 339
 Db 310 ----GKIPSOAKY-----FFKQDVLVSCDTGYKVLKDNVEMDTFOIECLDKGTWSNKI 359
 Qy 340 PIC-IKACREPKISDLVRRVLPQVQSRETPLHQLYSAAFSKQKLOSAFTKKPALPFGD 398
 Db 360 PTCKIVDCRAP-----OLOYECISPFVRRILGSSR--RTCLRTGKWS---GRA-PSC 442
 Qy 399 LPMGYQLHT-----OLOYECISPFVRRILGSSR--RTCLRTGKWS---GRA-PSC 442
 Db 373 LEGLITFTSTRNLTKYKSEIKYSCQEPYKMLNNTGIYCSAQGVWNNKVLGRSLPTC 432
 Qy 443 IPICG-----KIENITAPKTQGLRWPQAIIYRRTSGVHDGSLHKGAWFLVCSGA 492
 Db 433 LPVGLPKFSRKLWARIEN-GRPAQKGT-PTIAML-----SHLNGQPF--CGGS 478
 Qy 493 LVNERTVVAACHV---TDLGKVT-----MIKTADLVKVLGKPYRDDDRDEKTIQSLQIS 544
 Db 479 LIGSSWIVTAACHLQSLDPGDTLRSLLSPDFKILILGRHW--LRSDENEQHLGVK 536
 Qy 545 AIIHPNYDPIILDADIAILKLDKARISTRVOPICLAASRDLSFQE-SHITVAGWNV 603
 Db 537 HTLHRQYDPTENDVALVELLESPLNANFNPICLPBPQ-----QEGAMVIVSGWK 591
 Qy 604 LADVRSPGKNDTLRSVSVVSDSLCEQEDHGHIPSVVDNMFCASWEPTAPSDICTA 663
 Db 592 QFLQRF-----ETLMEIPIVDHSTQKAYAP--LKKKVTTRDMICAG-EKEGKDKACAG 644
 Qy 664 ETGIAAVSPGASPERHLMGLYSVDKTCSHLSTAFKTVLPFKDWIER 717
 Db 645 DSGGPMVTLNRERG-----QWLVGTVSGWDDCKKDRYG-VYSYIHHNKDWIOR 693

RESULT 4
 C1HURB
 Complement subcomponent C1r (EC 3.4.21.41) precursor [validated] - human
 C/Species: Homo sapiens (man)
 C/Date: 15-Nov-1984 #sequence_revision 30-Jun-1991 #text_change 28-Jul-2003
 C/Accession: A24170; A29768; A29769; S02422; A00916; A37820; S68830
 R/Leytus, S.P.; Kurachi, K.; Sakariassen, K.S.; Davie, E.W.
 Biochemistry 25, 4855-4863, 1986
 A/Title: Nucleotide sequence of the cDNA coding for human complement C1r.
 A/Reference number: A24170; MUID:87026586; PMID:3021205
 A/Accession: A24170
 A/Molecule type: mRNA
 A/Residues: 1-705 <LEY>
 A/Cross-references: GB:M14058; NID:G179643; PIDN:AAA51851.1; PID:G179644
 R/Journet, A.; Tosi, M.
 Biochem. J. 240, 783-787, 1986
 A/Title: Cloning and sequencing of full-length cDNA encoding the precursor of human comp
 A/Reference number: A29768; MUID:87156625; PMID:3030286
 A/Accession: A29768
 A/Molecule type: mRNA
 A/Residues: 1-151, 'L', 153-705 <JOU>
 A/Cross-references: GB:X04701; NID:G29538; PIDN:CRA28407.1; PID:G29539
 R/Arlaud, G.J.; Willis, A.C.; Gagnon, J.
 Biochem. J. 241, 711-720, 1987
 A/Title: Complete amino acid sequence of the A chain of human complement-classical-pathwa
 A/Reference number: A29769; MUID:87241248; PMID:3036070

Query Match	9.6%	Score 378.5	DB 1	Length 695	
Best Local Similarity	21.8%	Pred. No. 1e-17			
Matches 168	Conservative	81	Mismatches 227	Indels 293	Gaps 35
QY	137	GOILL	---BSYPLNAHCEWTHAKPGFVIQLRVLMLSLEDFYMCQYDVVEVRDGNRDG	192	
DB	27	GEILSPNYPOAYPNEMEKTWIEVPEGGRVRLYFTHLDMELSENCEYDSVQIISGGVEEG	86		
QY	193	QIIKRVCGNERP	---API---OSIGSSLHVLFHSDGS--KNFDGFHAIY-----EET 237		
DB	87	---RLCGORTSKNANSPIVEEFOIPYNNKQLOVIFRSDFSNERRFTGFAAYYAIDNECT	142		
QY	238	ACSSSPCFHDGTCVLDRKAGSYKCACLAGY	---266		
DB	143	DFTDVPCHFCNNPI	---GGYFCSPPEYFLHDDMRNCVNCVGNVFTALIGEISPNYP 199		
QY	267	---TGORCEN--LLEE	---RNCSDP-----283		
DB	200	NPYPENSRCEYQILLEEGFQVVVTIQREDFDVEPADSQNCQDSLLFAAKNRQFGPFCGN	259		
QY	284	---	---GGPUNGQYKITGGP-----297		
DB	260	GFGPLTIETHSNTLDIVQDTLQKQGWKLRYHGDPIPCPEKITANSVWAPEKAKYVF	319		
QY	298	---	---GLINGRHAKIGTVGSFFCNCNSYVLSGNEXRTCOQNGWSGK---QBICIKACR 347		
DB	320	KDVVKISCVDGFEAVGNVGSTFFYS	---TCQNGQWSNSRLRCQPV---DCG 366		
QY	348	EPKISDLVRRLVPMQVSRTPPLHOLYSAAPSKOKLQSAPTKKPALPGDLPNGVQHLH	407		
DB	367	IPE	-----PIQNGKVDPPENTLFGSV-----387		
QY	408	TQLOYECISPPY	---RRLGSSRTCLRTGKWSG---RAPSCIPICGKIENITAPKTQ 458		
DB	388	--THYSCEEPYYMEHAHGEYR--CAANGSVNDELGIELPKCFVCG	---VPTE 437		
QY	459	GLRWFQAAIYRRRTSGVHDGSLHGAW	-----FLVCSGALVNERTVVVAACHVTDLGKVT 513		
DB	438	PFR	---IQQRIFGGFPFAKIQFPWPQVFFEPFRAGGALIGEHWLVTAAHVVEGNSDPS 491		
QY	514	M-IKTADLKVGLGYFRDDDDREKTIQSLQISAIILHPNYDP	-----ILLDADIAILK 565		
DB	492	MYVGSTSRM	-----ENLANVQKLTDRVIIHPGKPGDDLSTRTNFNDIALVR 541		
QY	566	LLDKARISTRVQPTCLAAASRLDSTSFSQSH	---ITVAGH-----NVLADVRSPPGKNDT 616		
DB	542	LKQPVKMGPTVSPICLPGT	---SSEYSESGDLGISGWRTERNNIVQLR-----590		

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492  MYGVSTVRM-----ENLVNQKLTTDRVIIHPGWKFGDDLSRTNFNDIALVR 541
Db

566  LLKARISTRVQPTCLAASRDLSFQESH---ITVAGH-----NVLADVRSPGFKNDT 616
QY

542  LKQPKVKGPTVSPICLPQT---SSEYERSEGLHISGWRTERNNIVQLR----- 590
Db

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QY 617 LRSQVSVVVDLSL-----LCEQHEHGHGIPSVVTDNMFCAWBPETAPSDICTAETGIAAV 671
 DB 591 ---GAKLPVTSLEKCRQVKEENPKARADDVFTSNMICAEGKV---DSCQDGSQGFAL 644
 QY 672 SPGRASPPRHLWGLVSWSDKTSRHLSTAFKTLVLPKDWIERNMK 720
 DB 645 PVFN--VRDPKPYVAGLVSWG--KKCG--TYGIYTKVRNWKDWILQTMQ 687

RESULT 7
 T30337
 polypeptide - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003
 C:Accession: T30337
 R:Yang, J.C.; Lindsey, L.L.; Hedrick, J.L.
 A:Description: cDNA cloning of ovocytinase, a chymotrypsin-like protease released from X.
 A:Reference number: Z20829
 A:Accession: T30337
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1524 <YAN>
 A:Cross-references: EMBL:U81290; NID:G2981640; PID:G2981641; PIDN:AAC24717.1
 C:Superfamily: tryosin related polypeptide; trypsin homology

Query Match 9.0%; Score 354; DB 2; Length 1524;
 Best Local Similarity 22.3%; Pred. No. 1.1e-15;
 Matches 166; Conservative 101; Mismatches 260; Indels 216; Gaps 39;

QY 55 CRGKRVGY-----TIPCRNEECDSCLHPGCTIFENCKSRNGSWGTLDDFFVK 109
 DB 214 CHAVLEPIGHVLDLTMCAFGPEGMDACQDGSQGFV---CRR-RSGVW-----FLA 263
 QY 110 GFVCAB-----CRAGW-----YGGDCMRCGQVLRAP 135
 DB 264 G--CVSWGLGCGRSWGAQIIRSQSPALFRRVSVLDLFRPPKLTGCSKSGRTITGK 321
 QY 136 KQOI---LLESYPLNAHCWTHAKPGFVQLRFLVMSLEFDMYQDYVVRDGNRGG 192
 DB 322 NGTVRYPLSGNYSINVCRWMLAVQAKTIEIRFLQDIEDHATCTFDLSFTVNE--- 377
 QY 193 QIIKVCNGNERAPTIQSGSLHLVPHSDGNKFGPHAIYEITACSSSPCFHDTGCVL 252
 DB 378 KMIRKVCSTIPSLVLRNKNVTTFSDGTGTFGRGFEIQFALPTKASAC--GSAKIL 435
 QY 253 DKAGSYKACLAGYTGRCENLLEERNCSDP-----GGPVNGYQKITGGPGLIN 301
 DB 436 KKKG-----MIYSNPDPYPRLTKCSMIIEAPENHIVKLKFEDEFVE 478
 QY 302 GRHAKIGTVSPFCNNYSYVLSGNEKRTCCQNGEWSGKQPCIKACREPKISDLVRR---R 358
 DB 479 YGHGCIYDAVE-----VYDGAEEK-----QLIARLCGY 506
 QY 359 VLPQVQSR-----TPLHQLYSAFSAKQLQSAATKPK-ALPFGDLPNGYQHLHQ 409
 DB 507 TLPLPISSENWMLIRFKTDMENSYG--FKWFSVPKREKFSPLPDDTPT-ISMHLPR 563
 QY 410 ---LQYECISPFYRRILGSSRRRTCLRTGKWSGRAPSCIP-ICGKIENITAPKTQGLRWPMQ 465
 DB 564 AIALDVCGMAPM-----TPKW-----WLPRIVGEE--ASPNS-----WPMQ 598
 QY 466 AAI-YRTSGVHDSGLHKGANFLVCSGALVNRVTVVAAHCVTDLQKVTMTAD---LK 521
 DB 599 VQIFLRT-----PH-----CEGAIISQWILTAAC-----IRAAEFSYWT 635
 QY 522 VVLGKPYRDDR--DEKTIQSLQISAILHPNVDPLLDADIAILKLDKARISTRVQPI 579
 DB 636 VIAG-----DHNRLNSETQIRNIKIRIHDNYSYNDIALLYLEPDLNDFVRV 691
 QY 580 CLAAERDLSFQESHITVAGNVLADVRSPGKNDTLRSVGVSVVDSLLCEQHEHGHG 639
 DB 692 CLPEPEVLT--PASVCVVTGWTAEADGQALGQLQ---LPILDSIICNTSYSG-- 744

QY 640 PVSVDNMFCAWBPETAPSDICTAETGIAAVSPGRASPPRHLWGLVSWSDKTSCH 699
 DB 745 --ELTDHMLCAGFPSSKEKDACQDGSQGLVQC-----NEKEQFSIYGLVSWG--EGCG- 794
 QY 700 RLST--AFTKVLPPKDWIERNMK 720
 DB 795 RVSRPGVYTKVRLFFLTWIONTQQ 817

RESULT 8
 JC6554
 complement subcomponent C1s (EC 3.4.21.42) precursor [similarity] - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 28-Jul-2003
 C:Accession: JC6554
 R:Sakai, H.; Nakashima, S.; Yoshimura, S.; Nishimura, Y.; Sakai, N.; Nozawa, Y.
 A:Title: Molecular cloning of a cDNA encoding a serine protease homologous to complement
 A:Reference number: JC6554; MUID:98192519; PMID:9524231
 A:Accession: JC6554
 A:Molecule type: mRNA
 A:Residues: 1-694 <SAK>
 A:Cross-references: DBJ:D88250; NID:G3080541; PIDN:BAA25797.1; PID:G3080542
 C:Comment: This protein is involved in glial cell differentiation and cartilage remodeling
 C:Genetics:
 A:Gene: r-gp
 C:Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H
 C:Keywords: differentiation; glycoprotein; hydrolase; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:17-133/Domain: C1r/C1s repeat homology <C1R>
 F:22-694/Product: serine protease homolog #status predicted <MAT>
 F:141-177/Domain: EGF homology <EGF>
 F:300-360/Domain: complement factor H repeat homology <FHR>
 F:444-681/Domain: trypsin homology <TRY>
 F:180, 412/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:481, 535, 637/Active site: His, Asp, Ser #status predicted

Query Match 8.6%; Score 340.5; DB 2; Length 694;
 Best Local Similarity 21.2%; Pred. No. 3.6e-14;
 Matches 167; Conservative 98; Mismatches 244; Indels 277; Gaps 40;

QY 44 ECCEYDQTECVCPGKRE-----VVGVTIPCCR-----NEE--- 73
 DB 69 ENCAVDSVQIISGIEERLCQSSKSPNFTVEFQFPYRLQVFTSDFSNERTG 128
 QY 74 -----NECDCLHPGCTIFENCKSRNGSWGTLDDFFVYKPYCAECRAGWYG 123
 DB 129 FAAYSAVDVNECTDFTDVP--CSHF-----CWN-----FIGYFCS-CPPEYFLH 171
 QY 124 DCMR-----CGQVLRAPKQIILLES-----YPLNAHCWTHAKPGFVQLRFLVMSLEF 173
 DB 172 DDMRTCVNGSGDVFTALIGIASPNYPNPENSPENSRCEYQIRLQEGF--RLVLTIRREDF 229
 QY 174 DVMCQDYVVEVRDGNR-----DQIIRKVCNGNERPAP--IOSIGSLHLVPHSDG 222
 DB 230 D-----VEPADSEGNCHDSLTAAKQVQPGYCGNGFPGLTIKTSQNTLDIVFQIDL 282
 QY 223 SKNFDGFHAY-----EETACS-----SPPCFHDGTCVLDKAGSYKACLAGYTG 268
 DB 283 TGQNGKWLRYHGDPIPCPKSISANSIWEPEKAKYFKD-----VVKITC----- 327
 QY 269 QRCENLLEERNCSDPGPNVYQKITGGPGLINGEHAIGITVVSFFCNSYVLSGNEKRT 328
 DB 328 -----VDGFVVEGVNG-----STSPY-----ST 346
 QY 329 COQNGESGK-----OPICIKACREPKISDLVRRKRLPMQVQSRREPLHQLYSAFSAKQKL 384
 DB 347 COSNGQNSRLQCPV--DCGVPE-----PIENGKVEDPDTVPGSV----- 387
 QY 385 QSAPTKPPALPFGDLPNGYQHLTQLOVEICISPFY--RRLGSSRRRTCLRTGKWSG----- 437
 DB 388 -----IHYTCBEPYMYEQUEBGEYHCAANGSVWVDQLGV 422

QY 438 RAPSCIPICG-----KIEN--ITAPKTQGLRWPMQAAIYRTTSGVHDSGLHKGAWFLVC 489
DB 423 ELPCIPCVGVTEPFKQOIRFGYSYKIOSFPQVYFESPRGG-----467
QY 490 SGALVNTVVVAACHVT-DLGKVTMIKTADLVKVLGKFGYRDDDRDEKTIQSLQISAIL 548
DB 468 -GALIDYVWLTAARHVEGSDPNVYVGTLLKI-----ERLNAORLITERVII 516
QY 549 HPNYDP-----ILLDADIALLKLDKARISTRVOPICLAASRDLSLSPQESH-----TV 598
DB 517 HPSWKQEDDLNTRNFDNDIALVQLKDPVKGPVAPICLP---ETSDYNPSEVDLGLI 573
QY 599 AGWNVLADVRGPGFKNDTLRSGVSVVDSLLCE-----EQHEDHGIPVSVTDNMFCAWEP 654
DB 574 SGWG-RTEIRNVIQ---LRGAKLPITSLKXQQQVKNPKRNSDYVFTDNMCAGEKG 629
QY 655 TAPSDICTAETGGAIVAFPGASPEPRHMLGLVSNYSYDKTCHRLSTATTKVLFPKDW 714
DB 630 V---DSCGSDGGAPALFPVN--VKDPKPYVAGLVSMG--KKCG--TYGIYTKVKNYVDW 680
QY 715 IERNMK 720
DB 681 ILKTMQ 686
RESULT 9
C1HUS
complement subcomponent C1s (EC 3.4.21.42) precursor [validated] - human
N/Alcortname names: C1 esterase precursor
C/Specio: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence revision 31-Mar-1992 #text change 28-Jul-2003
C/Accession: A04096; S00224; S26732; S05634; A05140; A25396; A38407; B37820
R/Kusunoto, H.; Hirosewa, S.; Salier, J.P.; Hagen, F.S.; Kurachi, K.
Proc. Natl. Acad. Sci. U.S.A. 85, 7307-7311, 1988
A/Title: Human Genes for complement components C1r and C1s in a close tail-to-tail arrangement
A/Reference number: A04096; MUID:89017187; PMID:2459702
A/Accession: A04096
A/Molecule type: mRNA
A/Residues: 1-688 <KUS>
A/Cross-references: GB:J04080; NID:g179645; PIDN:AAA51852.1; PID:g179646
R/Tosi, M.; Duponchel, C.; Moo, T.; Julier, C.
Biochemistry 26, 8516-8524, 1987
A/Title: Complete cDNA sequence of human complement C1s and close physical linkage of the cDNA
A/Reference number: A27381; MUID:86163522; PMID:2831944
A/Accession: A27381
A/Molecule type: mRNA
A/Residues: 1-688 <TOS>
A/Cross-references: GB:M18767; NID:g179647; PIDN:AAA51853.1; PID:g179648
R/Mackinnon, C.M.; Carter, P.E.; Smyth, S.J.; Dunbar, B.; Fothergill, J.E.
Eur. J. Biochem. 169, 547-553, 1987
A/Title: Molecular cloning of cDNA for human complement component C1s. The complete amino acid sequence
A/Reference number: S00224; MUID:88082788; PMID:3500856
A/Accession: S00224
A/Molecule type: mRNA
A/Residues: 1-688 <MAC>
A/Cross-references: EMBL:X06596; NID:g29542; PIDN:CAA29817.1; PID:g763110
A/Accession: S26732
A/Molecule type: protein
A/Residues: 16-38; 68-116; 170-236; 246-262; 265-280; 282-284; 287-308; 315-363; 384-394; 421-435
R/Tosi, M.; Duponchel, C.; Moo, T.; Couture-Tosi, E.
J. Mol. Biol. 208, 709-714, 1989
A/Title: Complement genes C1r and C1s feature an intronless serine protease domain close to the C1r and C1s
A/Reference number: S05634; MUID:90040704; PMID:2553984
A/Accession: S05634
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 356-513, 'G', 514-688 <TOS>
R/Carter, P.E.; Dunbar, B.; Fothergill, J.E.
Biochem. J. 215, 565-571, 1983
A/Title: The serine proteinase chain of human complement component C1s. Cyanogen bromide cleavage map
A/Reference number: A05140; MUID:84104122; PMID:6362661
A/Accession: A05140

A/Molecule type: protein
A/Residues: 438-483, 'X', 485-500; 503-534; 542-558; 561-572, 'A', 574-601; 617-623; 626-644; 647-654
R/Spycher, S.E.; Nick, H.; Rickli, E.E.
Eur. J. Biochem. 156, 49-57, 1986
A/Title: Human complement component C1s. Partial sequence determination of the heavy chain
A/Reference number: A25396; MUID:86164350; PMID:3007145
A/Accession: A25396
A/Molecule type: protein
A/Residues: 16-61; 168-219; 287-293, 'K', 295-334; 384-445 <SPY>
R/Hess, D.; Schaller, J.; Rickli, E.E.
Biochemistry 30, 2827-2833, 1991
A/Title: Identification of the disulfide bonds of human complement C1s.
A/Reference number: A38407; MUID:9115725; PMID:2007122
A/Accession: A38407
A/Molecule type: protein
A/Residues: 131-134, 'X', 136-146, 'X', 148-150; 155, 'X', 157-162; 166-170, 'X', 172-174, 'X', 176-178, 'X', 387-402, 'X', 404-408; 416-424, 'X', 426-431; 547-556; 592-597; 617, 'X', 619-627, 'X', 629-635.
R/Thielens, N.M.; Aude, C.A.; Lacroix, M.B.; Gagnon, J.; Arlaud, G.J.
J. Biol. Chem. 265, 14469-14475, 1990
A/Title: Ca(2+) binding properties and Ca(2+)-dependent interactions of the isolated NH₂-terminal domain of human complement C1s
A/Reference number: A37820; MUID:90354439; PMID:2387866
A/Accession: B37820
A/Molecule type: protein
A/Residues: 16-25, 'X', 203-207 <THI>
R/Thielens, N.M.; Van Dorsselaer, A.; Gagnon, J.; Arlaud, G.J.
Biochemistry 29, 3570-3578, 1990
A/Title: Chemical and functional characterization of a fragment of C1s containing the epimerase site
A/Reference number: A32672; MUID:90283368; PMID:2141278
A/Contents: annotation; erythro-beta-hydroxyasparagine site, content
A/Note: about half of the A chains contain erythro-beta-hydroxyasparagine
C/Comment: This protein is a serine proteinase that combines with C1q and C1r to form C1s C2 and C4.
C/Comment: C1s is a dimer of identical chains, each of which is activated by cleavage in the C1s chain
C/Genetics:
A/Gene: GDB:C1S
A/Cross-references: GDB:119730; OMIM:120580
A/Map position: 12p13-12p13
A/Introns: 291/1; 329/3; 356/1; 399/1; 424/1
A/Note: the list of introns may be incomplete
C/Superfamily: complement subcomponent C1r; C1r/C1s repeat homology; complement factor H
C/Keywords: acute phase; beta-hydroxyasparagine; calcium binding; complement pathway; dup
F.11-127/Domain: signal sequence #status predicted <SIG>
F.11-127/Domain: C1r/C1s repeat homology <C1R1>
F.116-688/Product: complement subcomponent C1s #status experimental <MAT>
F.116-688/Product: complement subcomponent C1s chain A (heavy chain) #status experimental
F.135-171/Domain: EGF homology <EGF>
F.175-287/Domain: C1r/C1s repeat homology <C1R2>
F.294-354/Domain: complement factor H repeat homology <FHL>
F.359-421/Domain: complement factor H repeat homology <FHL>
F.438-688/Product: complement subcomponent C1s chain B (light chain) #status experimental
F.438-688/Product: tryptsin homology <TRY>
F.65-83, 135-147, 143-156, 158-171, 175-202, 234-251, 294-341, 321-354, 359-403, 386-421, 425-549; 174, 406/Modified site: erythro-beta-hydroxyasparagine (Asn) (partial) #status experimental
F.174, 406/Binding site: carboxylate (Asn) (covalent) #status experimental
F.437-438/Cleavage site: Arg-Ile (complement subcomponent C1r) #status experimental
F.475, 523, 632/Active site: His, Asp, Ser #status predicted
Query Match 8.5%; Score 334; DB 1; Length 688;
Best Local Similarity 21.7%; Pred. No. 9.7e-15;
Matches 163; Conservative 83; Mismatches 246; Indels 260; Gaps 37;
QY 137 GQILL-----ESYPLNACEWTHAKFGVQLRFLVMSLEFDYMCQYDYVEVRGDNEDG 192
DB 21 GEILSPNYQAPYSEVEKSWDIEVPEGYGHLYTHLDIELSENCAYDSVQIISGDTTEG 80
QY 193 QIKRVCNERPAPI-----QSIGSSLVLFPHSDGS---KNFDGFHAIY--EITACS---S 241
DB 81 RLCCGRSSNNPHSPFIVEFQVPYKQLQVIFKSDFSNERFTGFAAYVATDINECTDFD 140
QY 242 SPCHFDTGTVLADKAGSKYACLAGY-----266
DB 141 VPCSHFCNNFI---GGVFCSCPPEYFLHDDMKNGCVNCGSDVFTALIGEIASPNYPKYP 197

Qy 267 TQRCENL-----ERNCS-----PGPVGQYK 294
 Db 198 ENSRCYQIRLEKGFQVVTLRREDFVEAASAGNCLDSLVFVAGDRQFGPCGH-----253
 Qy 295 GGQCLIN-----GRHAK-I 307
 Db 254 GFGPLNIETKSNALDIIFQDLDLTKQKKGKLYRHGDPMPCKBEDTNSVWEPAKAYVF 313
 Qy 308 GTVVSPFCNNY-VLSG-----NEKRTQQNGWSGK-----QPTICAKREPKISDLVRR 357
 Db 314 RDVVQITCLDGFVEVGRGATSPYSTCQNGKWSNKLKQCPV-----DCGIP-----362
 Qy 358 RVLPMQVSRPTPLHLQYSAFSAKQKLSAPTKP-ALPFGDLPMGQHLHLTLQYECIS 416
 Db 363 -----ESIENGKVEDPESTLFGSV-----IRYCEE 388
 Qy 417 PFY--RRLGSSRRRLCTGKWSGRA-----PSCIPIGCKIENTAPKTQGLRWPMQAAIY 469
 Db 389 PYYWNGGGGEYHCAGNSWNEVLGPELPKCPVCG-----VP-----REPFEEK--435
 Qy 470 RRTSGVHDSLHKGAFLV-----CSGALVNERTVVVAHCVTDLGVKVTWKATDLKVL 524
 Db 436 QRIIGSGDADIKNPFQWFFDNPWAGGALINEYVWLTAAHVVEGNREPTW-----YV 487
 Qy 525 GKPYRDDDRDEKTIQSILHLPNVDPIIL-----DADIAILKLDKARISTRVQ 577
 Db 488 GSTSVQTSRLAKS-KMLTPPEHVFTHPGWKULEPVEGRTNFDNDIALVRLKDPVPMGPTVS 546
 Qy 578 PICLAARDLSTSPQESHITVAGNVNADVRSPGFND-----TLRSGVSVVVDLSLLCEQH 634
 Db 547 PICLPSTSYNDMLDGLISGW-----RTE--KEDRAVRLKAARLPVAPLRKCKEVK 599
 Qy 635 EDHGIPVS-----VTNNMCASWEPTAPSDICTAETGGIAAVSPGASPERPHLMGL 688
 Db 600 VEK--PTADAEAYVFTENMTCAGGE--KGMDSCKGDSGGAFVQDP---NDKTKFYAAGL 652
 Qy 689 VSNVDYKTCSHRLSTAFKVLPPKDWIRNNK 720
 Db 653 VSWG--PQCG--TYGLTRVKNYVDWIMKTQW 680
 RESULT 10
 A56318
 N/A:teropetidae (EC 3.4.21.9) precursor [validated] - human
 N/Alternate names: enterokinase
 C/Species: Homo sapiens (man)
 C/Date: 19-May-1995 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003
 C/Accession: A56318; B43090
 R/Kitamoto, Y.; Veille, R.A.; Donis-Keller, H.; Sadler, J.E.
 Biochemistry 34, 4562-4568, 1995
 A/Title: cDNA sequence and chromosomal localization of human enterokinase, the proteolytic
 A/Reference number: A56318; MUID:95234679; PMID:7718557
 A/Accession: A56318
 A/Molecule type: mRNA
 A/Residues: 1-1019 <KIT>
 A/Cross-references: GB:U09860; NID:G746412; PIDN:RAC50138.1; PID:G746413
 R/Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
 Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
 A/Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo
 A/Reference number: A43090; MUID:94329561; PMID:8052624
 A/Accession: B43090
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 749-1019 <KIT>
 A/Cross-references: GB:U09860
 C/Comment: The mechanism of association with the membrane of the intestinal brush border
 (noted below) or with amino-terminal myristoylation of the heavy chain.
 C/Genetics:
 A/Gene: GDB:PRSS7
 A/Cross-references: GDB:384083; OMTM:226200
 A/Map position: 21q21-21q21
 C/Complex: Mature enteropetidae is variously reported to contain two (heavy and light)
 ed by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involv

ducts.
 C/Function:
 A/Description: cleaves activation peptide from trypsinogen to produce active trypsin
 A/Pathway: intestinal digestive hydrolase cascade
 C/Superfamily: enteropetidae; Ctr/Cls repeat homology; LDL receptor ligand-binding rep
 C/Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen
 F:1-784/Product: enteropetidae heavy chain #status predicted <HCH>
 F:22-38/Domain: transmembrane #status predicted <TMM>
 F:184-221/Domain: LDL receptor ligand-binding repeat homology <LDL1>
 F:342-504/Domain: NAM homology <NAM>
 F:526-631/Domain: Ctr/Cls repeat homology <Clr>
 F:643-677/Domain: LDL receptor ligand-binding repeat homology <LDL2>
 F:678-783/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRCF
 F:785-1015/Product: enteropetidae light chain #status predicted <LCH>
 F:785-1015/Domain: trypsin homology <TRY>
 F:116,147,179,328,338,440,470,503,534,630,682,706,725,848,887,909,949/Binding site: c
 F:772-896,810-826,910-977,941-956,967-995/Disulfide bonds: #status predicted
 F:825,876,971/Active site: His, Asp, Ser #status predicted
 Query Match 8.4%; Score 331.5; DB 1; Length 1019;
 Best Local Similarity 22.9%; Pred. No. 2.2e-14;
 Matches 136; Conservative 90; Mismatches 225; Indels 143; Gaps 27;
 Qy 143 SYPLNAHCWTTHAKPGFVIQLRFVMLSLFDFVMCOYDVVVRDGNRQDIIRKVCNE 202
 Db 545 SYPLNAFCVWLNNAQKNIQLHF-----QEFLENINDVVEIRDGEADSLAVVTG--598
 Qy 203 RPAPIQISGSLH-----VLFHSDGSKNF-DGFHAIYEEITACSSSPCFHDGTCV 251
 Db 599 -PGPVKQDFSTTRMTVLLITNDVLARGFGFKANFTTGYHLGIPE-----PC-----643
 Qy 252 LDKAGSYKC---ACLA-----GYTCQRCENLEENRCSDDPGPVNGYQKITGGPGLNG 302
 Db 644 --KADHFQCKNGCEVPLVNLCDGHL--HCEBDSDEAD-----VRFNGTNNNGLVRF 693
 Qy 303 RHAKIGTVVSVFFCNSYVLSGNEKRTCCQNGEWSGKQPIKACRBPKISDLVRRVPLM 362
 Db 694 RIQSIW-----HTACAEWTTQISNDVC-----QLLGL 721
 Qy 363 QVQSRTPHLQYSAFSAKQKLSAPTKPAPLPGDLPNGYQHLHTQLQVECLSPYRRL 422
 Db 722 GSGNSKPISTFDGGPF--VKLNTAPD-----GHLITPSQCLQDSLRL 765
 Qy 423 GSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPMQAAIYRSTGVHDSLHK 482
 Db 766 QCNHKS-----GKCLAAQDITPKI--VGSNAKEGAWPMVVGILY-----YGR--807
 Qy 483 GAWFLVCSGALVNERTVVVAHCVTDLGVKVTWKATDLKVLGKGYRDDDRDEKTIQSILQ 542
 Db 808 ----LLCGASLVSSDWLVSAHCV--YGR--NLEPSKWTAILGLHMKSNLSTPQTVPRL-858
 Qy 543 ISAILHPNVDPIILDADIAILKLDKARISTRVQPICLAASRDLSSTFQESHITVAGWN 602
 Db 859 IDEIVINPHNRRKNDIAMHLEPKVNVTDYIQICLPEENQVPPGK--NCSIAGWG 916
 Qy 603 VLADVSPGKNDTLASGVSVVVDLSLCESEHEDHGPVSVTDNNMCASWEPTAPSDICT 662
 Db 917 T---VVYQGTANILQEAADVPLLSNERCCQMPY-----NITENMICAGYE-BGGIDSCQ 968
 Qy 663 AETGGIAAVSPGASPERPHLMGLVSNYSYDKTCSHRLSTAFKVLPPKDWIE 716
 Db 969 GDSGG-----PLMCQNNRWFLAGVTSFGYKALPNR-PGVYARVSRFTFEMIQ 1015
 RESULT 11
 A53663
 N/A:teropetidae (EC 3.4.21.9) precursor [validated] - pig
 N/Alternate names: enterokinase
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 07-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 28-Apr-2003
 C/Accession: A53663
 R/Watsushima, M.; Ichinose, M.; Yahagi, N.; Kakei, N.; Tsukada, S.; Miki, K.; Kurokawa, T
 J. Biol. Chem. 269, 19976-19982, 1994

A>Title: Structural characterization of porcine enteropeptidase.

A/Reference number: A53663; MUID:94327548; PMID:8051081

A/Accession: A53663

A/Molecule type: mRNA

A/Residues: 1-1034

A/Cross-references: GB:030799; NID:G505122; PID:BAA06459.1; PID:G505123
A/Note: Parts of this sequence, including the amino ends of three chains isolated from C
C/Comment: The mechanism of association with the membrane of the intestinal brush border
ated below) or with amino-terminal myristoylation of the heavy chain.
C/Complex: Mature enteropeptidase is variously reported to contain two (heavy and light)
od by a disulfide bond. Possibly, conversion from membrane-bound to soluble forms involv

C/Function: cleaves activation peptide from trypsinogen to produce active trypsin

A/Pathway: intestinal digestive hydrolyase cascade

C/Superfamily: enteropeptidase; C1r/C1s repeat homology; LDL receptor ligand-binding rep

C/Keywords: glycoprotein; hydrolase; serine proteinase; transmembrane protein; zymogen

F/22-38/Domain: transmembrane #status predicted <TM>

F/52-117/Product: enteropeptidase mini chain #status predicted <MCH>

F/118-799/Product: enteropeptidase heavy chain #status predicted <HCH>

F/199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>

F/357-519/Domain: MAM homology <MAM>

F/541-646/Domain: C1r/C1s repeat homology <C1R>

F/658-692/Domain: LDL receptor ligand-binding repeat homology <LDL2>

F/693-798/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRD

F/800-1034/Product: enteropeptidase light chain #status predicted <LCH>

F/800-1029/Domain: trypsin homology <TRY>

F/116.147.170.194.283.343.350.403.455.485.518.549.645.697.701.721.740.761.804.863.902.96

F/787-911.825-841.925-992.956-971.982-1010/Disulfide bonds: #status predicted

F/840.891.986/Active site: His, Asp, Ser #status predicted

Query Match 8.4%; Score 330.5; DB 1; Length 1034;

Best Local Similarity 22.9%; Pred. No. 2.6e-14;

Matches 137; Conservative 86; Mismatches 224; Indels 151; Gaps 27;

143 SYPLNACEWTIAKPGFVQLRFLVLSDFYMCQDYVEVRDGNDRDGOIIRKVCNCE 202

560 NYNQAFVWNLNAQKKNQLQHP-----EFDLENIADVVEIRDEEDSILLAVYTG-- 613

203 RPAPIQSIGSS---LHLVPHSDGS-----KNF-DGFHAIYEEITACSSSPCFHD---- 247

614 -PGVEDVFSTNRMVTLFTNDALTAKGFKANFTTGYHLGIPE-----PCKEDNFQC 665

248 --GTCVLDKAGSYKACLAGTYGRCENLLEERNCSDFPGPVNGYQKITGGPGLNGRHA 305

666 ENGECVL-----LVNLCDFGSHCKDGSDEAHCVPLNGTANNGLVQPRIQ 711

306 KIGTVSWFFCNNSYVLSGNEKRTCCQNGEWSGKQPICIKACREPKISDLVRRVRLPMQV 365

712 SIW-----HTACAEWTTQTSDVC-----QLLGLGTG 739

366 SRETPLHQLYSAAFSKQLOSAPTKKPPALPGDLPNGYQHLTLQYECISPFYRRLGSS 425

740 NSSMPFFSSGGGP--VKLNTAPNGSLILTASE-----QCFEDSLILLQCN 783

426 RRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLR-----WPQAAIYRRSIVGHDGS 479

784 HKSC--GK-----KQVAQEVSPKIVGNDREGAMPWVALY-----YNGQ 822

480 LHKGAWFLVCSGALVNRVTVAACHCVTDLGKVTMIKTADLKVLGKRYFDRDDREKTIQ 539

823 -----LLCGASIVSRDLVSAACHV--YGR--NLSPSKWAILG-LHMTSNLTSQIV 870

540 SLQISAILHPNYPDPIILLADIATLKLDDKARISTRVQPICLAASRDLSFQESHI-TV 598

871 TRLIDEIVNPHYNNRRKDSIAMMHLFEKVNVDYIOPICLPEENQV---FPDGRICSI 927

599 AGNVLADVSPGPKNDTLASGVSVSDSLICEQHEHDHGIPVSVTNMFCASHEPTAPS 658

928 AGMKVITYQGSFA---DILEADYPLLISNEKCCQOMPEY-----NITENMCAQYB-EGGI 979

659 DICTAETGGIAAIVFPGRASPEPRWHLMLGLVSWSYDKTCSHRLSTAFKVLPPKDWIE 716

980 DSCQDGG-----FLMCLENNRLLAGVTSFGYQCALPNR-PGVVARVPKFTWFIQ 1030

RESULT 12

JX0210

protein C (activated) (EC 3.4.21.69) precursor - mouse

N/Alternate names: vitamin K-dependent serine proteinase

C/Species: Mus musculus (house mouse)

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

C/Accession: JX0210

R/Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.

J. Biochem. 111, 491-495, 1992

A/Title: Isolation and characterization of a mouse protein C cDNA.

A/Reference number: JX0210; MUID:92316897; PMID:1618739

A/Accession: JX0210

A/Molecule type: mRNA

A/Residues: 1-461 <TAB>

A/Cross-references: GB:D10445; NID:G220385; PIDN:BAA01235.1; PID:G220386

A/Experimental source: liver

C/Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that reg

S.

C/Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

C/Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami

F/1-33/Domain: signal sequence #status predicted <SIG>

F/27-85/Domain: Gla domain homology <GLA>

F/34-41/Domain: propeptide #status predicted <PRO>

F/42-196/Domain: product: protein C #status predicted <PRC>

F/42-196/Domain: light chain #status predicted <PCL>

F/91-130/Domain: EGF homology <EG1>

F/139-174/Domain: EGF homology <EG2>

F/199-461/Domain: heavy chain #status predicted <PCH>

F/199-211/Domain: activation peptide #status predicted <ACT>

F/212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>

F/212-445/Domain: trypsin homology <TRY>

F/47.48.55.57.60.61.66.67.70.76/Modified site: gamma-carboxyglutamic acid (Glu) #status I

F/112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted

F/121-130.139-150.146-159.161-174.182-319.238-254.373-387.398-426/Disulfide bonds: #statu

F/214.290.355/Binding site: carbohydrate (Aen) (covalent) #status predicted

F/253.299.402/Active site: His, Asp, Ser #status predicted

Query Match 8.1%; Score 320; DB 1; Length 461;

Best Local Similarity 23.9%; Pred. No. 5.4e-14;

Matches 145; Conservative 70; Mismatches 174; Indels 218; Gaps 29;

152 WTI-----HAKPGF-----VIQLRFVLSLEFDYMCQDYVEVRDGNDRDGOIIRK 198

14 WGSIIPALPDPVPFSSSEHAHQVLRVRRANSFLF-----EMRPG-SLRECEHEE 62

199 CGNERPAPI-QSIGSSLHLVLFHSDGSKNPDGFHAIYEEITACSSSPCFHDGTCVLDKAGS 257

63 CDFEAAQETQFQVEDTLAFWI-----KYFDGQCSAPPDLHQDCSPCCGHGTCT-DGIGS 116

258 YKACLAGYTGRCENLLEERNCSDFPGPVNGYQKITGGPGL-----INGRHAKIGTVV 311

117 FSCSDKMGWKFCQQLRFQDC-----RVNNGGCLHYCLEESNGRCA----- 160

312 SFCNNNSYVLSGNEK-----TCQNGEWSGKQPICIKACREPKISDLVRRVRLPMQV 364

161 ---CAPGYELADHMKCKSTVNPFCGKLGRIEK-----KKIL----- 196

365 QSRETPHLQLYSAAFSKQLOSAPTKKPPALPGDLPNGYQHLTLQYECISPFYRRLG 424

197 -KDDTDL-----EDELPPD----- 210

425 SRETCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSVGHGSLHKA 484

211 -----RVNGLTLTK-QG-DSPWQAILL-----DSKKK-- 235

485 WFLVCSGALVNRVTVAACHCVTDLGKVTMIKTADLKVLGKRYFDRDDREKTIQSIQIS 544

236 --LACGVLHTSWLTAACHVEGTKKLT-----VRLGEE--DLRRRDHLLDLDIK 283

545 AILHPNYPDPIILLADIATLKLDDKARISTRVQPICL-----AASRDLSFQESHITVAG 600

Db 284 EILVHPNRYTRSSDNDIALRLAQAATLSKTIPIVCLPNNGLAQOELTQAGQETVVT--G 341
QY 601 WNVADVRSFGPKNDTL-----RSGVVVVDLSLLCEQEDHGIPVSVTDNMP 649
Db 342 WGVQSDRIKGRNRRTFIITRIPLVARNCEVEMKNV-----VSENMLC 387
QY 650 ASWEPTAPSDICTAETGGIAAIVSPGRASPEPRWHLMLGLVSWYDKTCSHRLSTA-FTKV 708
Db 388 AGIIGNT-RDAGDGDGPGVMVFFRG-----TWPLVGLVSG--EGCGHTNNYGIYTKV 438
QY 709 LPFKDWT 715
Db 439 GSYLKW 445

RESULT 13
A43090
Enteroproteidase (EC 3.4.21.9) precursor [validated] - bovine
N:Alternate names: enterokinase
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 28-Apr-2003
C:Accession: A43090; A48874; A61436
R:Kitamoto, Y.; Yuan, X.; Wu, Q.; McCourt, D.W.; Sadler, J.E.
Proc. Natl. Acad. Sci. U.S.A. 91, 7588-7592, 1994
A:Title: Enterokinase, the initiator of intestinal digestion, is a mosaic protease compo
A:Reference number: A43090; MUID:94329561; PMID:8052624
A:Accession: A43090
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1035 <KIT>
A:Cross-references: GB:U09859; NID:G746410; PIDN:ABA40026.1; PID:G746411
A:Experimental source: small intestine
R:LaValle, E.R.; Rehentulla, A.; Racie, L.A.; DiBlasio, E.A.; Ferenz, C.; Grant, K.L.;
J. Biol. Chem. 268, 23311-23317, 1993
A:Title: Cloning and functional expression of a cDNA encoding the catalytic subunit of E
A:Reference number: A48874; MUID:94043122; PMID:8226855
A:Accession: A48874
A:Molecule type: mRNA
A:Residues: 801-1035 <LAV>
A:Cross-references: GB:L13663; NID:G416131; PIDN:AAA16035.1; PID:G416132
A:Note: Parts of this sequence, including the amino end of the mature protein, were conf
R:Light, A.; Janaka, H.
J. Protein Chem. 10, 475-480, 1991
A:Title: The amino-terminal sequence of the catalytic subunit of bovine enterokinase.
A:Reference number: A61436; MUID:92189715; PMID:1799406
A:Accession: A61436
A:Molecule type: protein
A:Residues: 801-807, 'Y', 809-827 <LIG>
C:Comment: The mechanism of association with the membrane of the intestinal brush border
ombrano attachment using a signal-anchor sequence.
C:Comment: Conversion from membrane-bound to soluble forms may involve further processin
C:Complex: mature enteropeptidase is variously reported to contain two (heavy and light)
lflide linked
C:Function:
A:Description: cleaves propeptide from trypsinogen to produce active trypsin
A:Pathway: intestinal digestive hydrolase cascade
C:Superfamily: enteropeptidase; Clr/Cis repeat homology; LDL receptor ligand-binding rep
C:Keywords: glycoprotein; hydrolase; intestine; serine proteinase; transmembrane protein
F:22-38/Domain: transmembrane #status predicted <TMM>
F:52-117/Product: enteropeptidase mini chain #status predicted <MCH>
F:118-800/Product: enteropeptidase heavy chain #status predicted <HCH>
F:199-236/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F:358-520/Domain: MAM homology <MAM>
F:542-647/Domain: Clr/Cis repeat homology <Clr>
F:659-693/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F:694-799/Domain: scavenger receptor cysteine-rich domain homology #status atypical <SRC
F:801-1035/Product: enteropeptidase light chain #status predicted <LCH>
F:801-1030/Domain: trypsin homology <TRY>
F:116,147,170,194,233,263,264,404,456,486,519,550,646,698,722,741,762,864,903,965/Bindin
F:788-912,826-842,926-993,957-972,983-1011/Disulfide bonds: #status predicted
F:841.892.987/Active site: His, Asp, Ser #status predicted

Query Match 8.0%; Score 317.5; DB 1; Length 1035;

Best Local Similarity 24.6%; Pred. No. 1.9e-13;
Matches 146; Conservative 80; Mismatches 225; Indels 143; Gaps 30;

QY 143 SYPLNAHCETIHKAPGVICQLRFVMLSLFDMYQDYVVRDGDNRDGOIIRKVCNE 202
Db 561 SYPNQAFICIMLNIAQKKNIQHF-----QEPDENIADVIRDEGDDSLFLAVYTG-- 614
QY 203 RPAPIQSIGSS---LHLVFDHSDGSKNFDGPHAIYEEITACS--SGPCFHDG--TCVLDKAGS 257
Db 615 -PGPVNDVFSTNRTMTLVFITDNMLAKQGFANFTTGYGLGIPPECKEDNFQC---KDG- 669
QY 258 YKACLAGYTGORCENLLEERNCSDPGGPVNGYQKITGGPGGLINGRHAKITGVVSFFCNN 317
Db 670 -ECIPLVNL-----CDGPFHCKDGSDEAHCVRLEFNGTTDSSGLVQFRIOSIWHV----- 717
QY 318 SYVLSGNEKRTCOQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQVSRETPLHQLYSA 377
Db 718 -----ACAEN--WT-----TQISDDVCQLL----- 735
QY 378 AFSKOKLOSAPTKPALPFGDLPNGYQHLHTQLQVEICISPFYRRLGSSRRRTCLRTGKWSG 437
Db 736 -----GLGTGSSSVFTFTGGGP--YVNLNT-----APNGSLILTFPSQOCLE----- 775
QY 438 RAPSCIPI-----CGK--IENITAPKTQG-----LRWPOAAIYRRTSGVHDGSLHKG 483
Db 776 --DSLILQCNVKSCKKLVTOEVSFKIVGSDSREGAWPVVADY-----FDDQ----- 823
QY 484 AFWLVCSGALVNERVTVVAAHCVTDLGGKVTMIKTADLVKVLGKGYRDDRDEKTIQSLQI 543
Db 824 ---QVCGASLVSRDVLVSAHCV--YGR--NWEPSKMAVLG-LHMASNLSTPQIETRLI 875
QY 544 SAILIHPNDPILDDADTAIKLKLDKARISTRVQVPCILAAASRDLSSTQESHITVAGWN 602
Db 876 DQIVINPHYNKRNKNDIAMHLEMKVNTYDIQICLFEENQV---FPPGRCISAGNG 932
QY 603 VLADVRSFGKNDTLRSQVSVSDSLCEQEDHGIPVSVTDNMFCAWSEPTAPSDICT 662
Db 933 ALI-----YOGSTADVLQEDVPLLSNEKCCQMPET-----NITENMVCAGYE-AGGVDSQ 984
QY 663 AETGGIAAVSPGRASPEPRWHLMLGLVSWYDKTCSHRLSTAFTKVLPPFKOWIE 716
Db 985 GDSGG-----PLMCQENNRLLAGVTSFGYQCALPNR-PGVYARVPRTTEWIQ 1031

RESULT 14
EXCH
coagulation factor Xa (EC 3.4.21.6) precursor - chicken
N:Alternate names: virus-activating proteinase
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 16-Jul-1999
C:Accession: S15838; S20380; S20381
R:Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Nag
FBBS Lett. 283, 281-285, 1991
A:Title: Primary structure of the virus activating protease from chick embryo. Its ident
A:Reference number: S15838; MUID:91257322; PMID:2044767
A:Accession: S15838
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-475 <SUZ>
A:Cross-references: DDBJ:D00844; NID:G222869; PIDN:BAA00724.1; PID:G222870
R:Gotoh, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
FBBS Lett. 296, 274-278, 1992
A:Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsaib
A:Reference number: S20380; MUID:92164779; PMID:1537403
A:Accession: S20380
A:Molecule type: protein
A:Residues: 41-55 <GO2>
A:Accession: S20381
A:Molecule type: protein
A:Residues: 241-246, 'X', 248-251, 'X', 253-261 <GOT>
C:Function:
A:Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr
A:Pathway: blood coagulation

[illegible]

Db 813 EKDGR1-----EQAGVWSWG--EGCAQRNKPQVYTRIPEVRDIX 850

Search completed: August 18, 2004, 16:25:30
Job time : 26 00cs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 18, 2004, 16:14:22 ; Search time 20 seconds
(without alignments)
1858.535 Million cell updates/sec

Title: US-10-063-546-38

Perfect score: 3945

Sequence: 1 MELGCWTQLGLTFLQLLLIS.....LSTAFKVLPLFKDWIERNMK 720

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 700 summaries

Database : Issued Patents AA.*

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	665	16.9	1019	1	US-08-296-014A-4
2	665	16.9	1019	2	US-08-596-405-4
3	665	16.9	1019	2	US-08-877-820-4
4	665	16.9	1019	4	US-09-287-368-4
5	665	16.9	1083	1	US-08-296-014A-2
6	665	16.9	1083	2	US-08-596-405-2
7	665	16.9	1083	2	US-08-877-820-2
8	665	16.9	1083	4	US-09-287-368-2
9	327	8.3	855	2	US-09-027-337-2
10	327	8.3	855	4	US-09-644-600-2
11	327	8.3	855	4	US-09-654-600A-2
12	321	8.1	460	6	5270178-16
13	317.5	8.0	798	1	US-08-200-900A-2
14	317.5	8.0	798	5	PCT-US94-00616-2
15	311.5	7.9	461	6	5460953-3
16	310.5	7.9	409	3	US-09-065-872-2
17	310.5	7.9	409	4	US-09-667-570A-2
18	310.5	7.9	410	3	US-09-065-872-1
19	310.5	7.9	410	4	US-09-667-570A-1
20	310.5	7.9	419	1	US-08-295-411-1
21	310.5	7.9	419	2	US-08-955-471-1
22	310.5	7.9	419	4	US-09-667-570A-3
23	310.5	7.9	419	5	PCT-US92-10242-1
24	310.5	7.9	419	5	PCT-US92-10242-2
25	310.5	7.9	419	5	US-08-756-506-2
26	310.5	7.9	460	2	US-08-756-506-4
27	310.5	7.9	461	4	US-10-182-263-2

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30	309	7.8	419	4	US-10-182-263-3	Sequence 3, Appl
31	309	7.8	419	4	US-10-182-263-5	Sequence 5, Appl
32	309	7.8	461	6	5270178-2	Patent No. 5270178
33	308	7.8	419	4	US-10-182-263-4	Sequence 4, Appl
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35	305	7.7	460	6	5270178-13	Patent No. 5270178
36	305	7.7	460	6	5270178-14	Patent No. 5270178
37	302.5	7.7	461	6	5270178-17	Patent No. 5270178
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46	281	7.1	492	1	US-08-469-486-2	Sequence 2, Appl
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48	280	7.1	527	1	US-07-609-510B-16	Sequence 16, Appl
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51	280	7.1	527	6	5185259-8	Patent No. 5185259
52	280	7.1	562	2	US-08-811-949-43	Sequence 43, Appl
53	280	7.1	562	2	US-08-560-098A-50	Sequence 50, Appl
54	280	7.1	562	2	US-08-883-795A-38	Sequence 38, Appl
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62	278.5	7.1	466	3	US-09-009-217-14	Sequence 14, Appl
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67	276.5	7.0	655	1	US-08-448-937A-12	Sequence 12, Appl
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77	275.5	7.0	444	2	US-08-537-807-2	Sequence 2, Appl
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89	268.5	6.8	406	1	US-08-293-778-24	Sequence 24, Appl
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97	262.5	6.7	461	6	5521070-2	Patent No. 5521070
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102	258.5	6.6	411	1	US-08-286-748B-18	Sequence 18, Appl	175	238	6.0	237	3	US-08-163-919A-3	Sequence 3, Appl
103	258.5	6.6	411	1	US-08-153-799-18	Sequence 18, Appl	176	238	6.0	237	5	PCT-US94-14073-3	Sequence 3, Appl
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108	255.5	6.5	434	4	US-09-618-259-11	Sequence 11, Appl	181	236.5	6.0	355	1	US-08-427-640-6	Sequence 6, Appl
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112	250.5	6.3	229	2	US-08-557-146-13	Sequence 13, Appl	185	236.5	6.0	355	2	US-08-811-949-47	Sequence 47, Appl
113	250.5	6.3	229	2	US-09-154-344-13	Sequence 13, Appl	186	236.5	6.0	355	3	US-08-794-528-1	Sequence 1, Appl
114	250.5	6.3	411	2	US-08-560-098A-48	Sequence 48, Appl	187	236.5	6.0	355	6	5223256-1	Patent No. 5223256
115	249.5	6.3	986	4	US-09-285-385C-19	Sequence 19, Appl	188	236.5	6.0	356	1	US-08-427-640-4	Sequence 4, Appl
116	249	6.3	251	3	US-08-944-483-47	Sequence 47, Appl	189	236.5	6.0	378	4	US-09-553-498-10	Sequence 10, Appl
117	248.5	6.3	250	3	US-08-944-483-51	Sequence 51, Appl	190	236.5	6.0	378	4	US-09-618-869-10	Sequence 10, Appl
118	248.5	6.3	261	6	5270178-19	Patent No. 5270178	191	236.5	6.0	472	2	US-08-811-949-63	Sequence 63, Appl
119	248.5	6.3	261	6	5270178-20	Patent No. 5270178	192	236.5	6.0	871	3	US-09-245-041-19	Sequence 19, Appl
120	248.5	6.3	262	1	US-07-720-189-1	Sequence 1, Appl	193	236.5	6.0	1013	2	US-08-866-650-3	Sequence 3, Appl
121	248	6.3	230	3	US-08-944-483-62	Sequence 62, Appl	194	236.5	6.0	1013	2	US-09-021-287-3	Sequence 3, Appl
122	248	6.3	231	2	US-09-027-337-6	Sequence 6, Appl	195	236.5	6.0	1013	3	US-09-240-473-3	Sequence 3, Appl
123	248	6.3	231	4	US-09-644-600-6	Sequence 6, Appl	196	236.5	6.0	1350	3	US-08-245-041-17	Sequence 17, Appl
124	248	6.3	231	4	US-09-654-600A-6	Sequence 6, Appl	197	236	6.0	355	2	US-08-811-949-53	Sequence 53, Appl
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127	246.5	6.2	295	2	US-08-944-483-52	Sequence 52, Appl	200	233.5	5.9	252	3	US-08-944-483-72	Sequence 72, Appl
128	246.5	6.2	295	2	US-08-338-368-2	Sequence 2, Appl	201	233.5	5.9	253	2	US-09-027-337-8	Sequence 8, Appl
129	246.5	6.2	276	2	US-08-558-269-10	Sequence 10, Appl	202	233.5	5.9	253	4	US-09-644-600-8	Sequence 8, Appl
130	246.5	6.2	376	3	US-09-410-882-10	Sequence 10, Appl	203	233.5	5.9	253	4	US-08-654-600A-8	Sequence 8, Appl
131	246.5	6.2	579	1	US-08-295-411-4	Sequence 4, Appl	204	233.5	5.9	383	2	US-08-558-269-6	Sequence 6, Appl
132	246.5	6.2	579	2	US-08-955-471-4	Sequence 4, Appl	205	233.5	5.9	383	3	US-09-410-882-6	Sequence 6, Appl
133	246.5	6.2	579	5	US-09-117-708-14	Sequence 14, Appl	206	233.5	5.9	546	6	5200340-6	Patent No. 5200340
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135	246.5	6.2	615	1	US-07-998-972A-3	Sequence 3, Appl	208	232.5	5.9	1013	2	US-09-021-287-5	Sequence 5, Appl
136	246.5	6.2	615	1	US-08-462-261-3	Sequence 3, Appl	209	232.5	5.9	1013	3	US-08-991-408-2	Sequence 2, Appl
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138	246.5	6.2	615	5	PCT-US92-11357-3	Sequence 3, Appl	211	233.5	5.9	1013	4	US-09-432-473-2	Sequence 2, Appl
139	246.5	6.2	622	3	US-08-952-967-8	Sequence 8, Appl	212	233.5	5.9	1013	4	US-08-285-385C-20	Sequence 20, Appl
140	246	6.2	812	4	US-08-991-761A-7	Sequence 7, Appl	213	232	5.9	638	2	US-08-681-151-3	Sequence 3, Appl
141	245	6.2	228	1	US-08-278-091-10	Sequence 10, Appl	214	231.5	5.9	389	2	US-08-811-949-65	Sequence 65, Appl
142	245	6.2	228	1	US-08-483-859-10	Sequence 10, Appl	215	231.5	5.9	417	4	US-08-820-002-4	Sequence 4, Appl
143	245	6.2	228	1	US-08-472-173-10	Sequence 10, Appl	216	231	5.9	365	1	US-08-093-741-83	Sequence 83, Appl
144	245	6.2	228	2	US-08-487-167-10	Sequence 10, Appl	217	231	5.9	365	1	US-08-720-012-83	Sequence 83, Appl
145	245	6.2	228	2	US-08-482-816-10	Sequence 10, Appl	218	231	5.9	393	2	US-08-560-098A-44	Sequence 44, Appl
146	245	6.2	228	2	US-08-296-149-10	Sequence 10, Appl	219	231	5.9	393	3	US-08-967-024C-24	Sequence 24, Appl
147	245	6.2	228	2	US-08-801-499-10	Sequence 10, Appl	220	231	5.9	393	3	US-08-967-024C-25	Sequence 25, Appl
148	245	6.2	228	2	US-08-615-271-10	Sequence 10, Appl	221	231	5.9	1012	4	US-08-285-385C-4	Sequence 4, Appl
149	245	6.2	228	3	US-09-074-660-10	Sequence 10, Appl	222	230.5	5.8	302	3	US-09-220-731-26	Sequence 26, Appl
150	245	6.2	228	3	US-09-074-659-10	Sequence 10, Appl	223	230.5	5.8	302	4	US-09-242-999-22	Sequence 22, Appl
151	245	6.2	228	3	US-09-106-468-10	Sequence 10, Appl	224	230	5.8	248	3	US-08-944-483-63	Sequence 63, Appl
152	245	6.2	228	3	US-09-106-466A-10	Sequence 10, Appl	225	230	5.8	387	3	US-09-032-215-8	Sequence 8, Appl
153	245	6.2	228	3	US-09-106-467-10	Sequence 10, Appl	226	230	5.8	387	3	US-09-032-215-13	Sequence 13, Appl
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155	242.5	6.1	416	2	US-09-000-846-2	Sequence 2, Appl	228	229	5.8	242	3	US-08-749-699-36	Sequence 36, Appl
156	242	6.1	730	3	US-08-872-757-2	Sequence 2, Appl	229	229	5.8	242	4	US-09-004-729-36	Sequence 36, Appl
157	242	6.1	730	3	US-08-872-757-2	Sequence 2, Appl	230	229	5.8	400	3	US-09-004-731-30	Sequence 30, Appl
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159	241.5	6.1	788	1	US-08-572-225-1	Sequence 1, Appl	232	229	5.8	400	3	US-08-749-699-30	Sequence 30, Appl
160	241	6.1	354	2	US-08-811-949-61	Sequence 61, Appl	233	229	5.8	400	3	US-08-749-699-33	Sequence 33, Appl
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162	241	6.1	986	3	US-08-872-757-4	Sequence 4, Appl	235	229	5.8	400	4	US-09-004-729-33	Sequence 33, Appl
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164	240.5	6.1	357	1	US-08-427-640-8	Sequence 8, Appl	237	228.5	5.8	235	4	US-09-478-957-3	Sequence 3, Appl
165	240	6.1	432	2	US-09-911-842A-2	Sequence 2, Appl	238	228	5.8	591	3	US-08-991-408-4	Sequence 4, Appl
166	239.5	6.1	1015	4	US-08-560-098A-47	Sequence 47, Appl	239	228	5.8	591	4	US-09-432-473-4	Sequence 4, Appl
167	239.5	6.1	3594	4	US-09-285-385C-2	Sequence 2, Appl	240	228	5.8	809	4	US-08-991-761A-9	Sequence 9, Appl
168	239	6.1	230	4	US-09-601-318-3	Sequence 3, Appl	241	228	5.8	812	1	US-08-248-629A-1	Sequence 1, Appl
169	239	6.1	356	2	US-08-681-151-1	Sequence 1, Appl	242	228	5.8	812	1	US-08-451-932-1	Sequence 1, Appl
170	239	6.1	389	2	US-08-811-949-67	Sequence 67, Appl	243	228	5.8	812	1	US-08-452-260-1	Sequence 1, Appl
171	238.5	6.0	437	2	US-08-811-949-49	Sequence 49, Appl	244	228	5.8	812	2	US-08-326-785-1	Sequence 1, Appl
172	238.5	6.0	437	2	US-08-811-949-51	Sequence 51, Appl	245	228	5.8	812	2	US-08-612-788-1	Sequence 1, Appl
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259	226	5.7	406	4	US-09-851-588-6	Sequence 6, Appli	332	212.5	5.4	282	3	US-09-025-059-1	Sequence 1, Appli
260	226	5.7	423	4	US-09-656-002-2	Sequence 2, Appli	333	212.5	5.4	289	4	US-09-386-642-14	Sequence 14, Appli
261	226	5.7	433	3	US-09-008-271A-6	Sequence 6, Appli	334	212	5.4	260	3	US-09-025-059-3	Sequence 3, Appli
262	226	5.7	437	4	US-09-851-588-8	Sequence 8, Appli	335	212	5.4	260	4	US-09-618-259-8	Sequence 8, Appli
263	224.5	5.7	275	3	US-08-944-483-65	Sequence 65, Appli	336	212	5.4	814	1	US-08-750-711-1	Sequence 1, Appli
264	224	5.7	275	2	US-09-016-366A-17	Sequence 17, Appli	337	211.5	5.4	232	1	US-08-508-448C-19	Sequence 19, Appli
265	224	5.7	275	2	US-08-978-404B-12	Sequence 12, Appli	338	211.5	5.4	418	1	US-08-508-448C-25	Sequence 25, Appli
266	224	5.7	306	2	US-08-560-098A-45	Sequence 45, Appli	339	211.5	5.4	418	4	US-09-370-838-82	Sequence 82, Appli
267	224	5.7	331	2	US-08-560-098A-46	Sequence 46, Appli	340	211.5	5.4	418	4	US-09-370-838-83	Sequence 83, Appli
268	223.5	5.7	245	3	US-08-944-483-69	Sequence 69, Appli	341	211	5.3	276	2	US-09-016-366A-15	Sequence 15, Appli
269	223	5.6	238	3	US-08-944-483-64	Sequence 64, Appli	342	211	5.3	276	2	US-08-978-404B-21	Sequence 21, Appli
270	222.5	5.6	790	4	US-08-991-761A-13	Sequence 13, Appli	343	211	5.3	300	3	US-08-705-875A-4	Sequence 4, Appli
271	222	5.6	274	2	US-09-016-366A-21	Sequence 21, Appli	344	211	5.3	300	3	US-09-320-731-21	Sequence 21, Appli
272	222	5.6	274	2	US-08-978-404B-16	Sequence 16, Appli	345	211	5.3	300	4	US-09-242-999-4	Sequence 4, Appli
273	222	5.6	407	4	US-09-734-675-4	Sequence 4, Appli	346	211	5.3	1010	3	US-08-882-046-7	Sequence 7, Appli
274	221	5.6	253	3	US-08-944-483-73	Sequence 73, Appli	347	211	5.3	1036	4	US-09-068-740A-6	Sequence 6, Appli
275	221	5.6	273	2	US-08-978-404B-6	Sequence 6, Appli	348	211	5.3	1187	4	US-09-068-740A-7	Sequence 7, Appli
276	221	5.6	300	3	US-08-705-875A-6	Sequence 6, Appli	349	211	5.3	1208	4	US-09-199-865-1	Sequence 1, Appli
277	221	5.6	300	4	US-09-242-999-6	Sequence 6, Appli	350	211	5.3	1218	2	US-08-400-159-6	Sequence 6, Appli
278	220.5	5.6	376	4	US-09-820-002-2	Sequence 2, Appli	351	211	5.3	1218	3	US-08-611-729A-6	Sequence 6, Appli
279	220	5.6	273	2	US-09-016-366A-19	Sequence 19, Appli	352	211	5.3	1218	3	US-08-882-046-2	Sequence 2, Appli
280	220	5.6	273	2	US-08-978-404B-14	Sequence 14, Appli	353	211	5.3	1218	4	US-09-214-278-7	Sequence 7, Appli
281	219.5	5.6	254	3	US-08-944-483-50	Sequence 50, Appli	354	211	5.3	1218	4	US-09-068-740A-11	Sequence 11, Appli
282	219.5	5.6	255	2	US-09-027-337-7	Sequence 7, Appli	355	211	5.3	1218	4	US-09-855-722-7	Sequence 7, Appli
283	219.5	5.6	255	4	US-09-644-600-7	Sequence 7, Appli	356	210.5	5.3	418	3	US-09-370-838-62	Sequence 62, Appli
284	219.5	5.6	255	4	US-09-654-600A-7	Sequence 7, Appli	357	210.5	5.3	1219	3	US-08-882-046-5	Sequence 5, Appli
285	218.5	5.5	244	4	US-09-601-318-4	Sequence 4, Appli	358	210	5.3	154	3	US-09-261-416-5	Sequence 5, Appli
286	218.5	5.5	244	4	US-09-601-318-5	Sequence 5, Appli	359	210	5.3	492	3	US-08-944-483-24	Sequence 24, Appli
287	218.5	5.5	244	4	US-09-601-318-6	Sequence 6, Appli	360	208.5	5.3	442	4	US-09-685-166A-895	Sequence 895, App
288	218.5	5.5	244	3	US-09-601-318-7	Sequence 7, Appli	361	208	5.3	268	1	US-08-270-584A-2	Sequence 2, Appli
289	218.5	5.5	245	3	US-09-079-970A-6	Sequence 6, Appli	362	208	5.3	268	2	US-08-765-192-2	Sequence 2, Appli
290	218.5	5.5	245	4	US-09-601-318-1	Sequence 1, Appli	363	208	5.3	268	1	US-08-944-483-59	Sequence 59, Appli
291	218.5	5.5	249	3	US-09-079-970A-5	Sequence 5, Appli	364	208	5.3	271	1	US-08-467-155A-10	Sequence 10, Appli
292	217.5	5.5	1198	3	US-09-245-041-131	Sequence 131, App	365	208	5.3	271	2	US-08-628-198-10	Sequence 10, Appli
293	217.5	5.5	1198	4	US-09-794-236-3	Sequence 3, Appli	366	208	5.3	271	3	US-09-201-038-10	Sequence 10, Appli
294	217.5	5.5	1429	3	US-09-245-041-130	Sequence 130, App	367	208	5.3	271	5	PCT-US96-07343-10	Sequence 10, Appli
295	217	5.5	239	3	US-08-944-483-61	Sequence 61, Appli	368	207.5	5.3	241	3	US-08-944-483-59	Sequence 59, Appli
296	217	5.5	268	4	US-09-613-822B-2	Sequence 2, Appli	369	206.5	5.2	255	1	US-08-650-129-5	Sequence 5, Appli
297	217	5.5	268	4	US-08-978-404B-3	Sequence 3, Appli	370	206.5	5.2	255	3	US-08-984-417-5	Sequence 5, Appli
298	217	5.5	791	1	US-08-643-219-1	Sequence 1, Appli	371	206.5	5.2	284	4	US-09-387-375-7	Sequence 7, Appli
299	217	5.5	791	3	US-08-851-350-1	Sequence 1, Appli	372	206.5	5.2	316	4	US-09-387-375-9	Sequence 9, Appli
300	217	5.5	2703	1	US-08-185-432-19	Sequence 19, Appli	373	205.5	5.2	235	3	US-08-944-483-48	Sequence 48, Appli
301	217	5.5	2703	4	US-08-899-232-4	Sequence 4, Appli	374	205.5	5.2	269	2	US-08-978-404B-10	Sequence 10, Appli
302	216	5.5	267	2	US-09-016-366A-23	Sequence 23, Appli	375	205.5	5.2	288	4	US-09-386-642-13	Sequence 13, Appli
303	216	5.5	267	2	US-08-978-404B-18	Sequence 18, Appli	376	205.5	5.2	327	4	US-09-386-642-8	Sequence 8, Appli
304	216	5.5	268	1	US-08-568-031-2	Sequence 2, Appli	377	205.5	5.2	492	3	US-09-342-749-2	Sequence 2, Appli
305	216	5.5	268	2	US-09-153-304-2	Sequence 2, Appli	378	205.5	5.2	492	4	US-09-691-840-2	Sequence 2, Appli
306	216	5.5	268	3	US-09-153-304-2	Sequence 3, Appli	379	204	5.2	260	3	US-09-070-526-2	Sequence 2, Appli
307	216	5.5	299	3	US-08-944-483-66	Sequence 66, Appli	380	204	5.2	260	4	US-09-618-259-7	Sequence 7, Appli
308	216	5.5	319	4	US-09-386-642-12	Sequence 12, Appli	381	203.5	5.2	224	3	US-08-944-483-34	Sequence 34, Appli
309	216	5.5	328	4	US-09-386-642-11	Sequence 11, Appli	382	203.5	5.2	3623	4	US-09-341-461-2	Sequence 2, Appli
310	216	5.5	790	1	US-08-469-486-54	Sequence 54, Appli	383	203	5.1	283	3	US-08-807-151-1	Sequence 1, Appli
311	216	5.5	790	2	US-08-469-486-54	Sequence 54, Appli	384	203	5.1	283	4	US-09-478-957-1	Sequence 1, Appli
312	216	5.5	810	6	5200340-8	Patent No. 5200340	385	202	5.1	2321	4	US-09-230-652-2	Sequence 2, Appli
313	215.5	5.5	317	4	US-09-386-629-7	Sequence 7, Appli	386	200.5	5.1	226	1	US-08-650-129-4	Sequence 4, Appli
314	215.5	5.5	317	4	US-09-907-794A-263	Sequence 263, App	387	200.5	5.1	226	3	US-08-984-417-4	Sequence 4, Appli
315	215.5	5.5	317	4	US-09-905-125A-263	Sequence 263, App	388	200.5	5.1	232	1	US-08-278-091-8	Sequence 8, Appli
316	215.5	5.5	317	4	US-09-902-775A-263	Sequence 263, App	389	200.5	5.1	232	1	US-08-483-859-8	Sequence 8, Appli
317	215	5.4	791	2	US-09-131-995-1	Sequence 1, Appli	390	200.5	5.1	232	1	US-08-472-173-8	Sequence 8, Appli
318	215	5.4	791	2	US-08-832-087B-1	Sequence 1, Appli	391	200.5	5.1	232	2	US-08-487-167-8	Sequence 8, Appli
319	215	5.4	791	3	US-09-132-154-1	Sequence 1, Appli	392	200.5	5.1	232	2	US-08-482-816-8	Sequence 8, Appli

393	200.5	5.1	232	2	US-08-296-149-8	Sequence 8, Appl	466	193	4.9	228	3	US-08-944-483-44	Sequence 44, Appl
394	200.5	5.1	232	2	US-08-801-499-8	Sequence 8, Appl	467	193	4.9	253	6	5223425-8	Patent No. 5223425
395	200.5	5.1	232	2	US-08-615-271-8	Sequence 8, Appl	468	193	4.9	268	3	US-09-032-215-42	Sequence 42, Appl
396	200.5	5.1	232	3	US-09-074-660-8	Sequence 8, Appl	469	192.5	4.9	225	2	US-08-557-146-12	Sequence 12, Appl
397	200.5	5.1	232	3	US-09-074-659-8	Sequence 8, Appl	470	192.5	4.9	225	2	US-09-154-344-12	Sequence 12, Appl
398	200.5	5.1	232	3	US-09-106-468-8	Sequence 8, Appl	471	192.5	4.9	281	1	US-08-467-155A-7	Sequence 7, Appl
399	200.5	5.1	232	3	US-09-106-466A-8	Sequence 8, Appl	472	192.5	4.9	281	2	US-08-628-138-7	Sequence 7, Appl
400	200.5	5.1	232	3	US-09-106-467-8	Sequence 8, Appl	473	192.5	4.9	281	3	US-09-201-038-7	Sequence 7, Appl
401	200.5	5.1	247	2	US-08-956-267A-2	Sequence 2, Appl	474	192.5	4.9	281	5	PCT-US96-07343-7	Sequence 20, Appl
402	200.5	5.1	314	4	US-09-636-382A-2	Sequence 104, App	475	192	4.9	149	3	US-09-518-046-20	Sequence 36, Appl
403	200.5	5.1	415	4	US-09-907-794A-104	Sequence 104, App	476	191.5	4.9	224	2	US-08-766-982-13	Sequence 36, Appl
404	200.5	5.1	415	4	US-09-905-125A-104	Sequence 104, App	477	191.5	4.9	224	3	US-08-944-483-36	Sequence 13, Appl
405	200.5	5.1	415	4	US-09-902-775A-104	Sequence 11, Appl	478	191.5	4.9	224	3	US-09-295-219-13	Sequence 5, Appl
406	200.5	5.1	810	4	US-08-991-761A-11	Sequence 16, Appl	479	191.5	4.9	225	2	US-09-027-337-5	Sequence 5, Appl
407	200	5.1	385	4	US-09-163-951-16	Sequence 16, Appl	480	191.5	4.9	225	4	US-09-654-600A-5	Sequence 24, Appl
408	200	5.1	385	4	US-09-345-881-16	Sequence 16, Appl	481	191.5	4.9	225	4	US-09-636-382A-24	Sequence 24, Appl
409	199.5	5.1	1193	2	US-08-400-159-10	Sequence 10, Appl	482	191.5	4.9	830	1	US-08-110-158-4	Patent No. 5223425
410	199.5	5.1	1193	3	US-08-611-729A-10	Sequence 10, Appl	483	191.5	4.9	830	6	5223425-4	Sequence 525, App
411	199.5	5.1	2556	1	US-08-185-432-17	Sequence 17, Appl	484	191	4.8	250	6	US-09-439-313-525	Sequence 525, App
412	199.5	5.1	2556	1	US-08-083-590A-20	Sequence 20, Appl	485	191	4.8	254	4	US-09-636-215-525	Sequence 525, App
413	199.5	5.1	2556	3	US-08-532-384-20	Sequence 20, Appl	486	191	4.8	254	4	US-09-685-166A-525	Sequence 525, App
414	199.5	5.1	2556	4	US-08-899-232-2	Sequence 2, Appl	487	191	4.8	254	4	US-09-261-416-2	Sequence 2, Appl
415	199	5.0	260	3	US-09-008-271A-7	Sequence 7, Appl	488	190	4.8	455	3	US-09-386-642-54	Sequence 54, Appl
416	199	5.0	278	3	US-08-392-828C-4	Sequence 4, Appl	489	190	4.8	284	4	US-09-386-642-54	Sequence 327, App
417	199	5.0	278	3	US-09-330-945-4	Sequence 4, Appl	490	189	4.8	220	4	US-09-439-313-327	Sequence 327, App
418	198.5	5.0	223	1	US-08-278-091-9	Sequence 9, Appl	491	189	4.8	220	4	US-09-352-616A-327	Sequence 327, App
419	198.5	5.0	223	1	US-08-483-859-9	Sequence 9, Appl	492	189	4.8	220	4	US-09-232-149A-327	Sequence 327, App
420	198.5	5.0	223	1	US-08-472-173-9	Sequence 9, Appl	493	189	4.8	220	4	US-09-636-215-327	Sequence 327, App
421	198.5	5.0	223	2	US-08-487-167-9	Sequence 9, Appl	494	189	4.8	220	4	US-09-685-166A-327	Sequence 327, App
422	198.5	5.0	223	2	US-08-482-816-9	Sequence 9, Appl	495	189	4.8	220	4	US-09-688-489-327	Sequence 327, App
423	198.5	5.0	223	2	US-08-296-149-9	Sequence 9, Appl	496	189	4.8	224	3	US-08-944-483-33	Sequence 33, Appl
424	198.5	5.0	223	2	US-08-801-499-9	Sequence 9, Appl	497	189	4.8	225	2	US-09-027-337-4	Sequence 4, Appl
425	198.5	5.0	223	2	US-08-615-271-9	Sequence 9, Appl	498	189	4.8	225	4	US-09-644-600-4	Sequence 4, Appl
426	198.5	5.0	223	3	US-09-074-659-9	Sequence 9, Appl	499	189	4.8	225	4	US-09-654-600A-4	Sequence 4, Appl
427	198.5	5.0	223	3	US-09-106-468-9	Sequence 9, Appl	500	189	4.8	238	6	5223425-5	Patent No. 5223425
428	198.5	5.0	223	3	US-09-106-468-9	Sequence 9, Appl	501	189	4.8	253	2	US-08-557-146-2	Sequence 2, Appl
429	198.5	5.0	223	3	US-09-106-466A-9	Sequence 9, Appl	502	189	4.8	253	2	US-08-824-874-3	Sequence 3, Appl
430	198.5	5.0	223	3	US-09-106-467-9	Sequence 9, Appl	503	189	4.8	253	2	US-09-154-344-2	Sequence 2, Appl
431	198.5	5.0	223	4	US-09-601-318-2	Sequence 2, Appl	504	189	4.8	253	3	US-08-930-188-2	Sequence 3, Appl
432	198.5	5.0	229	3	US-09-120-582-2	Sequence 2, Appl	505	189	4.8	253	3	US-09-210-084-3	Sequence 3, Appl
433	198.5	5.0	232	2	US-08-978-404B-45	Sequence 45, Appl	506	189	4.8	253	5	PCT-US96-04294-2	Sequence 2, Appl
434	198	5.0	242	3	US-08-944-483-57	Sequence 57, Appl	507	189	4.8	312	4	US-09-023-942A-4	Sequence 4, Appl
435	197.5	5.0	221	3	US-08-944-483-54	Sequence 54, Appl	508	189	4.8	449	4	US-09-636-215-617	Sequence 617, App
436	197.5	5.0	222	1	US-08-456-840-46	Sequence 46, Appl	509	189	4.8	449	4	US-09-685-166A-617	Sequence 617, App
437	197.5	5.0	222	1	US-08-266-407A-46	Sequence 46, Appl	510	189	4.8	449	4	US-09-386-653A-7	Sequence 7, Appl
438	197.5	5.0	222	2	US-08-892-544-46	Sequence 46, Appl	511	188.5	4.8	290	4	US-08-744-026-1	Sequence 1, Appl
439	197	5.0	338	4	US-08-991-761A-10	Sequence 10, Appl	512	188	4.8	248	1	US-09-102-732-1	Sequence 1, Appl
440	196.5	5.0	241	3	US-08-944-483-60	Sequence 60, Appl	513	188	4.8	248	2	US-09-261-767-1	Sequence 1, Appl
441	196.5	5.0	248	3	US-08-944-483-71	Sequence 71, Appl	514	188	4.8	248	3	US-09-439-313-523	Sequence 523, App
442	196.5	5.0	300	1	US-08-148-910-1	Sequence 1, Appl	515	188	4.8	254	4	US-09-636-215-523	Sequence 523, App
443	196.5	5.0	300	1	US-08-448-937A-1	Sequence 1, Appl	516	188	4.8	254	4	US-09-685-166A-523	Sequence 523, App
444	196.5	5.0	2523	1	US-08-185-432-18	Sequence 18, Appl	517	188	4.8	263	2	US-08-790-137-4	Sequence 4, Appl
445	196.5	5.0	2523	4	US-08-899-232-3	Sequence 3, Appl	518	188	4.8	263	2	US-08-824-874-5	Sequence 5, Appl
446	195.5	5.0	232	3	US-08-944-483-45	Sequence 45, Appl	519	188	4.8	263	3	US-08-807-151-5	Sequence 5, Appl
447	195.5	5.0	241	1	US-08-330-978-4	Sequence 4, Appl	520	188	4.8	263	3	US-09-210-084-5	Sequence 5, Appl
448	195.5	5.0	241	1	US-08-474-042-4	Sequence 4, Appl	521	188	4.8	263	4	US-09-478-957-5	Sequence 5, Appl
449	195.5	5.0	241	1	US-08-484-558-4	Sequence 4, Appl	522	188	4.8	263	4	US-09-764-762-5	Sequence 5, Appl
450	195.5	5.0	241	1	US-08-774-592-4	Sequence 4, Appl	523	188	4.8	263	4	US-08-991-761A-8	Sequence 8, Appl
451	195.5	5.0	254	1	US-08-330-978-3	Sequence 3, Appl	524	188	4.8	333	4	US-08-944-483-35	Sequence 35, Appl
452	195.5	5.0	254	1	US-08-474-042-3	Sequence 3, Appl	525	187.5	4.8	224	3	US-08-944-483-29	Sequence 29, Appl
453	195.5	5.0	254	1	US-08-484-558-3	Sequence 3, Appl	526	187.5	4.8	242	3	US-08-906-769-83	Sequence 83, Appl
454	195.5	5.0	254	1	US-08-774-592-3	Sequence 3, Appl	527	187.5	4.8	255	3	US-08-906-616-83	Sequence 83, Appl
455	195.5	5.0	306	1	US-08-330-978-1	Sequence 1, Appl	528	187.5	4.8	255	3	US-08-617-795-83	Sequence 83, Appl
456	195.5	5.0	306	1	US-08-474-042-1	Sequence 1, Appl	529	187.5	4.8	255	3	US-08-639-075A-83	Sequence 83, Appl
457	195.5	5.0	306	1	US-08-484-558-1	Sequence 1, Appl	530	187.5	4.8	255	3	US-09-012-431-83	Sequence 83, Appl
458	195.5	5.0	306	1	US-08-774-592-1	Sequence 16, Appl	531	187.5	4.8	255	3	US-09-012-692-83	Sequence 83, Appl
459	195.5	5.0	2471	1	US-08-185-432-16	Sequence 16, Appl	532	187.5	4.8	255	3	US-08-906-613-83	Sequence 83, Appl
460	195.5	5.0	2471	1	US-08-083-590A-19	Sequence 19, Appl	533	187.5	4.8	255	5	PCT-US95-1442A-83	Sequence 83, Appl
461	195.5	5.0	2471	3	US-08-532-384-19	Sequence 19, Appl	534	187.5	4.8	110	4	US-09-341-461-28	Sequence 28, Appl
462	195.5	5.0	2471	3	US-08-899-232-1	Sequence 1, Appl	535	186	4.7	230	1	US-08-456-840-47	Sequence 47, Appl
463	194.5	4.9	246	2	US-08-978-404B-44	Sequence 44, Appl	536	186	4.7	230	1	US-08-266-407A-47	Sequence 47, Appl
464	194.5	4.9	415	3	US-09-032-523-2	Sequence 2, Appl	537	186	4.7	230	1	US-08-892-544-47	Sequence 47, Appl
465	194.5	4.9	415	4	US-09-802-633-2	Sequence 2, Appl	538	186	4.7	230	2		

539	186	4.7	230	2	US-08-766-982-12	Sequence 12, Appl	612	178.5	4.5	468	4	US-09-802-633-8	Sequence 8, Appl
540	186	4.7	230	3	US-08-944-483-53	Sequence 53, Appl	613	178.5	4.5	922	4	US-09-116-473-4	Sequence 4, Appl
541	186	4.7	230	3	US-09-296-219-12	Sequence 12, Appl	614	178.5	4.5	923	3	US-08-936-135-6	Sequence 6, Appl
542	186	4.7	232	2	US-08-887-340-11	Sequence 31, Appl	615	178.5	4.5	923	4	US-09-439-711C-6	Sequence 6, Appl
543	186	4.7	232	3	US-08-232-329-31	Sequence 31, Appl	616	177.5	4.5	248	2	US-08-851-974-3	Sequence 3, Appl
544	186	4.7	326	4	US-09-411-977-3	Sequence 3, Appl	617	177.5	4.5	248	2	US-09-113-390-3	Sequence 3, Appl
545	185.5	4.7	256	3	US-09-032-215-27	Sequence 27, Appl	618	177.5	4.5	1964	4	US-09-467-997-1	Sequence 1, Appl
546	185.5	4.7	261	3	US-08-163-919A-2	Sequence 2, Appl	619	177	4.5	102	3	US-09-374-135-7	Sequence 7, Appl
547	185.5	4.7	261	5	PCT-US94-14073-2	Sequence 2, Appl	620	177	4.5	110	4	US-09-341-461-29	Sequence 29, Appl
548	185.5	4.7	306	4	US-09-386-642-53	Sequence 53, Appl	621	177	4.5	110	4	US-08-378-091-11	Sequence 11, Appl
549	185.5	4.7	711	1	US-08-184-012C-8	Sequence 8, Appl	622	177	4.5	240	1	US-08-483-859-11	Sequence 11, Appl
550	185.5	4.7	711	1	US-08-334-177-2	Sequence 2, Appl	623	177	4.5	240	1	US-08-472-173-11	Sequence 11, Appl
551	185.5	4.7	711	2	US-08-666-082B-1	Sequence 1, Appl	624	177	4.5	240	2	US-08-487-167-11	Sequence 11, Appl
552	185.5	4.7	711	5	PCT-US95-13830-2	Sequence 2, Appl	625	177	4.5	240	2	US-08-482-816-11	Sequence 11, Appl
553	185.5	4.7	713	3	US-08-872-855-5	Sequence 5, Appl	626	177	4.5	240	2	US-08-296-149-11	Sequence 11, Appl
554	185	4.7	247	3	US-08-944-483-49	Sequence 49, Appl	627	177	4.5	240	2	US-08-801-499-11	Sequence 11, Appl
555	185	4.7	258	1	US-08-744-026-3	Sequence 3, Appl	628	177	4.5	240	2	US-08-615-271-11	Sequence 11, Appl
556	185	4.7	258	2	US-09-102-732-3	Sequence 3, Appl	629	177	4.5	240	3	US-09-074-650-11	Sequence 11, Appl
557	185	4.7	258	3	US-08-261-767-3	Sequence 3, Appl	630	177	4.5	240	3	US-09-106-468-11	Sequence 11, Appl
558	185	4.7	314	4	US-09-023-942A-6	Sequence 6, Appl	631	177	4.5	240	3	US-09-106-468A-11	Sequence 11, Appl
559	184	4.7	144	4	US-09-618-259-1	Sequence 1, Appl	632	177	4.5	240	3	US-09-106-467-11	Sequence 11, Appl
560	184	4.7	314	3	US-09-008-271A-3	Sequence 3, Appl	633	177	4.5	240	3	US-08-872-855-8	Sequence 8, Appl
561	184	4.7	314	4	US-09-907-794A-257	Sequence 257, App	634	177	4.5	729	3	US-08-872-855-8	Sequence 8, Appl
562	184	4.7	314	4	US-09-905-125A-257	Sequence 257, App	635	177	4.5	830	6	5378464-2	Patent No. 5378464
563	184	4.7	314	4	US-08-902-775A-257	Sequence 257, App	636	176.5	4.5	232	1	US-07-990-301A-4	Sequence 4, Appl
564	183.5	4.7	711	2	US-08-766-982-2	Sequence 2, Appl	637	176.5	4.5	901	3	US-08-936-135-22	Sequence 22, Appl
565	183.5	4.7	711	3	US-09-296-219-2	Sequence 2, Appl	638	176.5	4.5	901	4	US-09-439-711C-22	Sequence 22, Appl
566	183.5	4.7	711	4	US-08-600-991-10	Sequence 20, Appl	639	176.5	4.5	906	3	US-08-936-135-24	Sequence 24, Appl
567	183.5	4.7	722	3	US-08-981-392-12	Sequence 12, Appl	640	176.5	4.5	906	4	US-09-439-711C-24	Sequence 24, Appl
568	182.5	4.6	258	4	US-09-023-942A-8	Sequence 8, Appl	641	176.5	4.5	909	3	US-08-936-135-8	Sequence 8, Appl
569	182.5	4.6	484	2	US-08-232-433C-9	Sequence 9, Appl	642	176.5	4.5	909	3	US-08-936-135-10	Sequence 10, Appl
570	182.5	4.6	484	3	US-08-196-197-9	Sequence 9, Appl	643	176.5	4.5	909	4	US-09-439-711C-8	Sequence 8, Appl
571	182.5	4.6	720	3	US-08-872-855-4	Sequence 4, Appl	644	176.5	4.5	909	4	US-09-439-711C-10	Sequence 10, Appl
572	182	4.6	405	4	US-08-734-675-2	Sequence 2, Appl	645	176.5	4.5	914	3	US-08-936-135-12	Sequence 12, Appl
573	182	4.6	721	3	US-08-872-855-7	Sequence 7, Appl	646	176.5	4.5	914	4	US-09-439-711C-12	Sequence 12, Appl
574	182	4.6	1055	3	US-09-214-278-2	Sequence 2, Appl	647	176.5	4.5	925	4	US-09-116-473-2	Sequence 2, Appl
575	182	4.6	1055	4	US-08-855-722-2	Sequence 2, Appl	648	176.5	4.5	926	3	US-08-936-135-14	Sequence 14, Appl
576	182	4.6	1065	2	US-08-400-159-8	Sequence 8, Appl	649	176.5	4.5	926	3	US-09-439-711C-14	Sequence 14, Appl
577	182	4.6	1212	3	US-09-214-278-3	Sequence 3, Appl	650	176.5	4.5	931	4	US-08-936-135-16	Sequence 16, Appl
578	182	4.6	1212	4	US-08-855-722-3	Sequence 3, Appl	651	176.5	4.5	931	4	US-09-439-711C-16	Sequence 16, Appl
579	182	4.6	1238	3	US-09-214-278-5	Sequence 5, Appl	652	176	4.5	233	3	US-09-004-731-27	Sequence 27, Appl
580	182	4.6	1238	4	US-08-855-722-5	Sequence 5, Appl	653	176	4.5	233	3	US-08-749-699-27	Sequence 27, Appl
581	182	4.6	1257	3	US-08-611-729A-8	Sequence 8, Appl	654	176	4.5	233	4	US-09-004-729-27	Sequence 27, Appl
582	181.5	4.6	258	1	US-07-990-301A-2	Sequence 2, Appl	655	176	4.5	242	3	US-08-944-483-58	Sequence 58, Appl
583	181.5	4.6	299	1	US-08-467-155A-8	Sequence 8, Appl	656	176	4.5	266	3	US-09-004-731-24	Sequence 24, Appl
584	181.5	4.6	299	2	US-08-628-198-8	Sequence 8, Appl	657	176	4.5	266	3	US-08-749-699-24	Sequence 24, Appl
585	181.5	4.6	299	3	US-09-201-0734-8	Sequence 8, Appl	658	176	4.5	266	4	US-09-004-729-24	Sequence 24, Appl
586	181.5	4.6	299	5	PCT-US96-07343-8	Sequence 8, Appl	659	175.5	4.4	921	4	US-09-439-711C-4	Sequence 4, Appl
587	181	4.6	396	4	US-09-800-729-86	Sequence 86, Appl	660	175	4.4	909	3	US-08-936-135-18	Sequence 18, Appl
588	180	4.6	260	6	5223425-10	Patent No. 5223425	661	175	4.4	909	4	US-09-439-711C-18	Sequence 18, Appl
589	179.5	4.6	205	3	US-09-020-956-176	Sequence 176, App	662	175	4.4	926	3	US-08-936-135-20	Sequence 20, Appl
590	179.5	4.6	205	3	US-09-030-607-176	Sequence 176, App	663	175	4.4	926	4	US-09-439-711C-20	Sequence 20, Appl
591	179.5	4.6	205	4	US-09-439-313-176	Sequence 176, App	664	175	4.4	931	4	US-09-583-638-4	Sequence 4, Appl
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593	179.5	4.6	205	4	US-08-232-149A-176	Sequence 176, App	666	174	4.4	265	2	US-08-687-706-57	Sequence 57, Appl
594	179.5	4.6	205	4	US-08-159-812-176	Sequence 176, App	667	174	4.4	286	1	US-08-467-155A-9	Sequence 9, Appl
595	179.5	4.6	205	4	US-09-636-215-176	Sequence 176, App	668	174	4.4	286	2	US-08-628-198-9	Sequence 9, Appl
596	179.5	4.6	205	4	US-08-685-166A-176	Sequence 176, App	669	174	4.4	286	3	US-09-201-038-9	Sequence 9, Appl
597	179.5	4.6	205	4	US-09-115-453-176	Sequence 176, App	670	174	4.4	286	5	PCT-US96-07343-9	Sequence 9, Appl
598	179.5	4.6	205	4	US-09-688-489-176	Sequence 176, App	671	173.5	4.4	294	4	US-09-800-729-146	Sequence 146, App
599	179.5	4.6	259	6	5223425-2	Patent No. 5223425	672	173.5	4.4	717	3	US-08-872-855-9	Sequence 9, Appl
600	179.5	4.6	728	3	US-08-981-392-2	Sequence 2, Appl	673	173	4.4	211	3	US-09-220-731-25	Sequence 25, Appl
601	179.5	4.6	830	5	PCT-US91-05059-2	Sequence 2, Appl	674	173	4.4	211	4	US-09-242-999-20	Sequence 20, Appl
602	179	4.5	230	1	US-08-379-621-2	Sequence 2, Appl	675	172.5	4.4	449	2	US-08-839-008-9	Sequence 9, Appl
603	179	4.5	230	1	US-08-147-000B-2	Sequence 2, Appl	676	172.5	4.4	449	2	US-08-839-008-9	Sequence 9, Appl
604	179	4.5	230	2	US-08-889-078-2	Sequence 2, Appl	677	172.5	4.4	1248	3	US-08-882-046-6	Sequence 6, Appl
605	179	4.5	253	4	US-08-578-303-4	Sequence 4, Appl	678	172	4.4	721	3	US-08-981-392-5	Sequence 5, Appl
606	179	4.5	384	3	US-09-032-215-22	Sequence 22, Appl	679	171.5	4.3	238	3	US-08-944-483-39	Sequence 39, Appl
607	178.5	4.5	315	3	US-08-944-483-68	Sequence 68, Appl	680	171.5	4.3	259	3	US-08-906-769-190	Sequence 190, App
608	178.5	4.5	315	4	US-09-386-653A-9	Sequence 9, Appl	681	171.5	4.3	259	3	US-08-906-616-190	Sequence 190, App
609	178.5	4.5	401	2	US-08-839-008-5	Sequence 5, Appl	682	171.5	4.3	259	3	US-08-639-075A-190	Sequence 190, App
610	178.5	4.5	468	2	US-08-839-008-7	Sequence 7, Appl	683	171.5	4.3	259	3	US-09-004-731-85	Sequence 85, Appl
611	178.5	4.5	468	3	US-09-032-523-8	Sequence 8, Appl	684	171.5	4.3	259	3	US-09-012-431-190	Sequence 190, App

685 171.5 4.3 259 3 US-08-749-699-85 Sequence 85, Appl
686 171.5 4.3 259 3 US-09-012-692-190 Sequence 190, App
687 171.5 4.3 259 3 US-08-906-613-190 Sequence 190, App
688 171.5 4.3 259 4 US-09-004-729-85 Sequence 85, Appl
689 171.5 4.3 262 2 US-08-790-137-1 Sequence 1, Appl
690 171.5 4.3 262 2 US-08-790-137-3 Sequence 3, Appl
691 171.5 4.3 262 2 US-08-681-151-4 Sequence 4, Appl
692 171.5 4.3 262 2 US-08-824-874-4 Sequence 4, Appl
693 171.5 4.3 262 3 US-08-807-151-4 Sequence 4, Appl
694 171.5 4.3 262 3 US-09-210-084-4 Sequence 4, Appl
695 171.5 4.3 262 4 US-09-478-957-4 Sequence 4, Appl
696 171.5 4.3 262 4 US-09-764-762-4 Sequence 4, Appl
697 171.5 4.3 262 4 US-09-618-259-9 Sequence 9, Appl
698 171.5 4.3 666 4 US-09-341-587-1 Sequence 1, Appl
699 171.5 4.3 1785 4 US-09-341-587-3 Sequence 3, Appl
700 171 4.3 262 3 US-09-025-059-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-08-296-014A-4
; Sequence 4, Application US/08296014A
; Patent No. 5716834
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/296,014A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-296-014A-4

Query Match 16.9%; Score 665; DB 1; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;
QY 34 PGAEWNIMRECCEYDQIEVCVCKE-----VVGTYIPCCRNNEECDSCLIH 82
DB 184 PNGQSNFFPKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSDDS----- 229
QY 83 PGCTIFENCKSCR-NGSWGCTL----- 103

230 PYLLIGQTTLCQNGQNGQIPCKKNLVFCPDLDPVNAEHKVKIGVEQKVGPPQSTE 289
104 -----DDFYKGYFCACR--AGMYGG--DCMR-----CGOVLK-- 133
290 VTYTCGNYFLMGFTLKCNDPDGSMGSGQSCVKVADREVDCDSKAVDFLDVGEVPIRH 349
134 APKGOILLES-----YPLNAHCEWTIHA---KGFVI----- 162
350 CPAGCSLTAGTVMGTATYIHELSSVCAHAGLKPNSGAVHVVNNGPYSDFLGSDLNGI 409
163 ---OLRFVMLSLEFDYM-----COYDVVEVRD-----GNRDQIIKRVCGN--E 202
410 KSEELKSLARFRDYVRSSTAGSKGCDGDFEVDENCYVYTSKORAWERAQGVCTNMAA 469
203 RPAPIQS--IGSSLHVLPHSDG--SKNFDGFH-----AIYEEITACSS 241
470 RLAVLDKDVIPNSLTETLRGKGLATTWIGLHRLDAEKPIWELMDRNSVNLNDLNTFWAS 529
242 SPCPHDGTCLV-----DKAGS--YKCACLAGYTGQRCENLLEERN---CSDPGPVNGYQKI 293
530 GEPGNETCVYMDIQDQLOQSVWTKSCQPSFACMDLSDRNKAKACDDPSLENGHATL 589
294 TGGPGLINGRAKIGTVVSFFCNNSYVLSGNEKRTCOQNGEWSGKQPCIK--ACREPKI 351
590 HQQS--IDGFYA--GSSIRYSCVHLVLSGTYTCTTGTNGTWSAPKPRCIKVIITCQNPV 645
352 SDLVRRVLPQVOSRETPHLQLYSAAFSKOKLO---SAPTKKPPALPFGD----- 398
646 PSYGSVEIKP---PSRTNSISRVSFPFLRLPLPLPLARAAPKPPKPRSSQPSSTDVLSK 702
399 ---LPMGYOHLATLOQYECISPFYRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
703 VKLPEGHYRVGSRALYTCESRYELLGQGRCDNSNGWSGRPASCIPVCGRSDSPRSPF 762
456 -----KTQGLRPMQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVAHAHCVTDLG 510
763 IWNNGNSTEIGQWPMQAGISRWLA-----DHNMMFLQCGGSLNKEWIVTAAHCVTYSA 815
511 KVTMIKTADLVKLGKFYRDDREKTIQSIQISAILHPNYDPIILLDADTALILKLDKA 570
816 TAEIIPNQFKYLGKYYRDSRDDYVQVREALEIHVNPYNDPGLNFDLIALIQLKTPV 875
571 RISTRVQPICLAASRDLSTSFQESH-----TVAGWNVLADVRSPGKNDTLRSGVSV 624
876 TLTRVQPICLPT--DITT---REHLKEGTLLAVTGWG-----LNENNTYSETIQOAVLPV 926
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927 VAASTCEGKYKEADLPLVTENMFCAGYK-KGRYDACSDDSGG--PLVFADDSRTERRWV 983
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984 LEGIVSWGSPSGCGKANQYGGFTKYNVFLSWIRQ 1017

RESULT 2
US-08-596-405-4
; Sequence 4, Application US/08596405
; Patent No. 5858706
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA


```

; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-596-405-4

Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNIMRECCEYDQIEVCVCKRE-----VVGYYIPCCRNENECDSCLIH 82
DB 184 PNGQWSNFPKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCDS----- 229

QY 83 PGCTIFENCKSCR-NGSWGTL----- 103
DB 230 PYLIGETITCQNGQWNGQIPCKNLVFCPLDPVNHAEHKVIGVEKYGQFPQGT 289

QY 104 -----DDFYVKGFCYACER--AGWYGG--DCMR-----CGQVLR-- 133
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QY 134 APKGQILLES-----YPLNAHCEWTHA-----KGFVI----- 162
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QY 163 ---OLRFVLSLEFDYM-----COYDYVERD-----GMDRGQIIRKVCNG--E 202
DB 410 KSEELKSLARSFREDYVRSSTAGSGCPDGFVFDENCYVYTSKQRAWERAQGVCTNMAA 469

QY 203 RPAPIQS--IGSSLHVLFHSDG--SKNFDGPH-----AYIEBITACSS 241
DB 470 RLAVLKDVIPNSLTETLRGKGLTTTWIGLRLDAEKPFITWELMDRNVNVLNDNLTFWAS 529

QY 242 SPCHDGTCLV-----DKAGS--YKACACLAGYTGQRCENLLERN---CSDPGGPVNGYQKI 293
DB 530 GEPGNETNCVYMDIQDLQSVWTKSCFPQSSPFACMDLSDRNKAKCDDPGLSLENGHATL 589

QY 294 TGGPGLNGRHAKITGVVVFPCNNSYVLGNEKRTCOONGEWSGKQPICIK--ACREPKI 351
DB 590 HGQS--IDGFA--GSSIRSVCEVLHLSGTETVCTTNGTWSAPKRCIKVITCQPPV 645

QY 352 SDLVRRVLPVQVRSRTPHLQLYSAAFSOKLO---SAPTKPALPFGD----- 398
DB 646 PSYGSVEIKP---PSRTNISIRVSGSPFLRLPLRLPLARAAKPPKPRSSQSPSTVDLASK 702

QY 399 ---LPMGQHLHTQLQYECISPFYRLGSSRRTCLRTGWSGRAPSCIPICGKIENITAP- 455
DB 703 VKLPEGHYRVSGRAIYTCESRYELLGSGQRCDSNGWSGRPASCIPVCGRSRSPSPF 762

QY 456 -----KTQGLRWPQAAIYRTSGVHDSGLHKGAWFLVCSGALVNERTVVVAACHVTDLGL 510
DB 763 IWNGNTEIGQWPHQAGISRWLA-----DHNWVFLQCGSLNLNEXWIVTAAHCVITYSA 815

; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-596-405-4

Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 511 KVTMIKTADLKVVLGKFRDDEKTIQSLQISAILHPNYPDPIILLDADIALKLLDKA 570
DB 816 TABIIDPNQFKWLGKVRDSDRDDYQVREALEIHVNENYDPGNLNFIDIALIQLKTPV 875

QY 571 RISTRVOPICLAASRDLSFQESH-----TVAGMNVLADVRSPGPKNDTLRSQVSV 624
DB 876 TLTTRVQICLPT--DITT---REHLKEGTAVVVGW---LNENNTYSETIQQAVLPV 926

QY 625 VDSLCEQHEHDGIPVSTDNMFCASMEPTAPSDICTAETGCIAGVSPFGRASPPRMH 684
DB 927 VAASTCEEGYKEADLPLTVTENMFCAGYK-KGRYDACSGDSGG--PLVFADDSRTERRWV 983

QY 685 LMGLVSWSDTKTCSH--RLSTAFTKVLPFKDWIER 717
DB 984 LEGIVSWGSPSGCGKANQYGGFTKVNFLSWIRQ 1017

RESULT 3
US-08-877-620-4
; Sequence 4, Application US/08877620
; Patent No. 5985590
; GENERAL INFORMATION:
; APPLICANT: Ding, Jeak Ling
; APPLICANT: Ho, Bow
; TITLE OF INVENTION: The Cloned Factor C cDNA of the
; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpis
; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolaesch & Birch
; STREET: 8110 Gatehouse Road, Suite 500 East
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,620
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/596,405
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1781-105P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1019 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-877-620-4

Query Match 16.9%; Score 665; DB 2; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAEWNIMRECCEYDQIEVCVCKRE-----VVGYYIPCCRNENECDSCLIH 82
DB 184 PNGQWSNFPKICR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCDS----- 229

QY 83 PGCTIFENCKSCR-NGSWGTL----- 103
DB 230 PYLIGETITCQNGQWNGQIPCKNLVFCPLDPVNHAEHKVIGVEKYGQFPQGT 289

QY 104 -----DDFYVKGFCYACER--AGWYGG--DCMR-----CGQVLR-- 133
DB 290 VVTCTSGNYFLMGFDLTKCNPDGWSGSPQSVKVAADREVDKCDKAVDFDDVGEPIRIH 349

QY 134 APKGQILLES-----YPLNAHCEWTHA-----KGFVI----- 162
DB 350 CPAGCSLTAGTVMGTATYHELSSVCRAAIHAGKLPNSGGAVHVVNNGPYSDFLGSLNIGI 409

QY 163 ---OLRFVLSLEFDYM-----COYDYVERD-----GMDRGQIIRKVCNG--E 202
DB 410 KSEELKSLARSFREDYVRSSTAGSGCPDGFVFDENCYVYTSKQRAWERAQGVCTNMAA 469

QY 203 RPAPIQS--IGSSLHVLFHSDG--SKNFDGPH-----AYIEBITACSS 241
DB 470 RLAVLKDVIPNSLTETLRGKGLTTTWIGLRLDAEKPFITWELMDRNVNVLNDNLTFWAS 529

QY 242 SPCHDGTCLV-----DKAGS--YKACACLAGYTGQRCENLLERN---CSDPGGPVNGYQKI 293
DB 530 GEPGNETNCVYMDIQDLQSVWTKSCFPQSSPFACMDLSDRNKAKCDDPGLSLENGHATL 589

QY 294 TGGPGLNGRHAKITGVVVFPCNNSYVLGNEKRTCOONGEWSGKQPICIK--ACREPKI 351
DB 590 HGQS--IDGFA--GSSIRSVCEVLHLSGTETVCTTNGTWSAPKRCIKVITCQPPV 645

QY 352 SDLVRRVLPVQVRSRTPHLQLYSAAFSOKLO---SAPTKPALPFGD----- 398
DB 646 PSYGSVEIKP---PSRTNISIRVSGSPFLRLPLRLPLARAAKPPKPRSSQSPSTVDLASK 702

QY 399 ---LPMGQHLHTQLQYECISPFYRLGSSRRTCLRTGWSGRAPSCIPICGKIENITAP- 455
DB 703 VKLPEGHYRVSGRAIYTCESRYELLGSGQRCDSNGWSGRPASCIPVCGRSRSPSPF 762

QY 456 -----KTQGLRWPQAAIYRTSGVHDSGLHKGAWFLVCSGALVNERTVVVAACHVTDLGL 510
DB 763 IWNGNTEIGQWPHQAGISRWLA-----DHNWVFLQCGSLNLNEXWIVTAAHCVITYSA 815

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QY 104 -----DDFYVKGFCACER--AGWYGG--DCMR-----CGQVLR-- 133
Db 290 VYTTCGNTFLMGFTLCKNPDGSGSQSPSCVKVADREVDCSKAVDFLDVGEFVRIH 349
QY 134 APKGOILLES-----YPLNAHCEWTIHA-----KPGFVI----- 162
Db 350 CPAGCSLTAGTVMGTATYHELSSVCRAAIHAGKLPNSGGAVHVNNGPYSDPLGSLNGI 409
QY 163 ----QLRFVWLSLEFDYM-----COYDYVEVD-----GDRDGOIIRKVCN--E 202
Db 410 KSEELKSLARSTRFYRVSSTAGSGCPDGFVENDENCYVVTSKORAWERAGQVCTNMAA 469
QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNFDGFH-----AIYEETACSS 241
Db 470 RLAVLDKDVIPNSLTETLKGKLTWTLGLHRLDAEKPIWELMDRSNVVLDNLTFWAS 529
QY 242 SPCFHDGTCVL-----DKAGS--YKACLAGYTGQRCENILLEBN-----CSDPGPVNGYQKI 293
Db 530 GEPGNETNCVYMDIQDQLQSVWKTSCFPSSFACMDLSDRNKAACDDPGSLENGHATL 589
QY 294 TGGPGLINGRAKIGTVVVSFFCNNSYVLSGNEKRTCCQNGWSGKQPICIK--ACREPKI 351
Db 590 HQQS--IDGFYA--GSSIRYCEVLHYLSGTETVCTTNGTWSAPKPRCIKVIITQNPVP 645
QY 352 SDLVRRRLVPMQVQSRRETLPHQLYSAAFSKQKLO---SAPTKKPALPFGD----- 398
Db 646 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLPLAARAKPPPKPRSSQSTVDLASK 702
QY 399 --LPMGYOHLHTQLOVECI--SPFYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
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Db 763 IWNGNSTEIGQWPQAGISRWLA-----DHNMFLOCGGSLNKEKIVTAAHCVTYSA 815
QY 511 KYTMIKTADLVKLVGKFYRDDDRDEKTIQSLQISAILHPNYDPTILLDADIALKLLDKA 570
Db 816 TAEIIDPNQFKMVLGKYRYDDSDDDYVQVREALEIHVNPNYDGNLNFIDIALIQLKTPV 875
QY 571 RISTRVQPICLAASRLDSTSFQESHI-----TVAGNVLADVRSPGKNDTLRSQVSV 624
Db 876 TLTRVQPICLPT--DITT---REHLKEGTAVVTGNG---LNENNTYSETIQQAVLVP 926
QY 625 VDSLLCEEHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGAIAVSPFGGRASPEPRWH 684
Db 927 VAASCTEEGYKEADLPVTIENMFCAGYK--KGRYDACSDDSG--PLVFAADSRTERRWV 983
QY 685 LMGLVSWSYDKTCSH--RLSTAFKVLPPFKDWIER 717
Db 984 LEGIVSWGSPSGCGKANQYGGFTKVNVLFWIRQ 1017
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RESULT 4

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US-09-287-368-4
; Sequence 4, Application US/09287368A
; Patent No. 6645724
; GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; APPLICANT: HO, Bow
; TITLE OF INVENTION: Assays for Endotoxin and Methods for Removal of Endotoxin
; TITLE OF INVENTION: from a Sample Using Recombinant Factor C
; FILE REFERENCES: 1781-0165P
; CURRENT APPLICATION NUMBER: US/09/287,368A
; CURRENT FILING DATE: 1999-04-07
; EARLIER APPLICATION NUMBER: 09/201,786
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/081,767
; EARLIER FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 60/058,816
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; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Carinoscorpius rotundicauda
; FEATURE:
; OTHER INFORMATION: any n or Xaa = Unknown
US-09-287-368-4
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Query Match 16.9%; Score 665; DB 4; Length 1019;
Best Local Similarity 25.4%; Pred. No. 1.2e-46;
Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGAENIMCRCECEYDQIECVCPGKRE-----VVGYTIPCCRNEENECDCLIH 82
Db 184 PNGQWSPFPKICR---ECAMVSSPEHGKVALSGDMIEGATL-----RFSDDS----- 229
QY 83 PGCTIFENCKSCR--NGSWGTL----- 103
Db 230 PYLIGQETLTCCGNGQNGQIPQCKNLVFCPLDLPVNAHAEHKVIGVEQKYQPPQOTE 289
QY 104 -----DDFYVKGFCACER--AGWYGG--DCMR-----CGQVLR-- 133
Db 290 VYTTCGNTFLMGFTLCKNPDGSGSQSPSCVKVADREVDCSKAVDFLDVGEFVRIH 349
QY 134 APKGOILLES-----YPLNAHCEWTIHA-----KPGFVI----- 162
Db 350 CPAGCSLTAGTVMGTATYHELSSVCRAAIHAGKLPNSGGAVHVNNGPYSDPLGSLNGI 409
QY 163 ----QLRFVWLSLEFDYM-----COYDYVEVD-----GDRDGOIIRKVCN--E 202
Db 410 KSEELKSLARSTRFYRVSSTAGSGCPDGFVENDENCYVVTSKORAWERAGQVCTNMAA 469
QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNFDGFH-----AIYEETACSS 241
Db 470 RLAVLDKDVIPNSLTETLKGKLTWTLGLHRLDAEKPIWELMDRSNVVLDNLTFWAS 529
QY 242 SPCFHDGTCVL-----DKAGS--YKACLAGYTGQRCENILLEBN-----CSDPGPVNGYQKI 293
Db 530 GEPGNETNCVYMDIQDQLQSVWKTSCFPSSFACMDLSDRNKAACDDPGSLENGHATL 589
QY 294 TGGPGLINGRAKIGTVVVSFFCNNSYVLSGNEKRTCCQNGWSGKQPICIK--ACREPKI 351
Db 590 HQQS--IDGFYA--GSSIRYCEVLHYLSGTETVCTTNGTWSAPKPRCIKVIITQNPVP 645
QY 352 SDLVRRRLVPMQVQSRRETLPHQLYSAAFSKQKLO---SAPTKKPALPFGD----- 398
Db 646 PSYGSVEIKP---PSRTNSISRVGSPFLRLPLPLPLAARAKPPPKPRSSQSTVDLASK 702
QY 399 --LPMGYOHLHTQLOVECI--SPFYRLGSSRRRTCLRTGKWSGRAPSCIPICGKIENITAP- 455
Db 703 VKLPEGHYRVGSRATYTCESRYELLGSGRRCDNSNGMWSGRPASCIPVCGRSDSRSPF 762
QY 456 -----KTQGLRWPQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNNRTVVAACHVTDLG 510
Db 763 IWNGNSTEIGQWPQAGISRWLA-----DHNMFLOCGGSLNKEKIVTAAHCVTYSA 815
QY 511 KYTMIKTADLVKLVGKFYRDDDRDEKTIQSLQISAILHPNYDPTILLDADIALKLLDKA 570
Db 816 TAEIIDPNQFKMVLGKYRYDDSDDDYVQVREALEIHVNPNYDGNLNFIDIALIQLKTPV 875
QY 571 RISTRVQPICLAASRLDSTSFQESHI-----TVAGNVLADVRSPGKNDTLRSQVSV 624
Db 876 TLTRVQPICLPT--DITT---REHLKEGTAVVTGNG---LNENNTYSETIQQAVLVP 926
QY 625 VDSLLCEEHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGAIAVSPFGGRASPEPRWH 684
Db 927 VAASCTEEGYKEADLPVTIENMFCAGYK--KGRYDACSDDSG--PLVFAADSRTERRWV 983
QY 685 LMGLVSWSYDKTCSH--RLSTAFKVLPPFKDWIER 717
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Db 984 LEGIVSWGSPGCGKANQYGGFTKVNFLSWIRQ 1017

RESULT 5

US-08-296-014A-2
 ; Sequence 2, Application US/08296014A
 ; Patent No. 5716834
 ; GENERAL INFORMATION:
 ; APPLICANT: Ding, Jeak Ling
 ; APPLICANT: Ho, Bow
 ; TITLE OF INVENTION: The Cloned Factor C cDNA of the
 ; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
 ; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch
 ; STREET: 8110 Gatehouse Road, Suite 500 East
 ; CITY: Falls Church
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22042
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/296.014A
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murphy, Jr., Gerald M.
 ; REGISTRATION NUMBER: 28,977
 ; REFERENCE/DOCKET NUMBER: 1781-105P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 205-8000
 ; TELEFAX: (703) 205-8050
 ; TELEX: 248345
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1083 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-296-014A-2

Query Match 16.9%; Score 665; DB 1; Length 1083;
 Best Local Similarity 25.4%; Pred. No. 1.3e-46;
 Matched 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;
 Qy 34 PGAENINMRECCBYDQIEVCYCPGKRE-----VVGTYTPCCRNENECDSCLIH 82
 Db 248 PNGQWSNFPKCIKIR-----ECAMVSSPEHGKYNALSGDMIEGATL-----RFSCDS--- 293
 Qy 83 PGCTIFENCKSCR-NGSWGTL----- 103
 Db 294 PYLLIGETLTTCOGNGWNGQIPQCKNLVFCPLDPVNHAEKVKIGVEQKYGFPGQTE 353
 Qy 104 -----DDFYVKGFCACR--AGWYGG--DCMR-----CGQVLR-- 133
 Db 354 VTYTCNGNYFLMGFDTLKCPDNGSWSGSPSCVKVADREVDGCDKAVDFLDDVGEPRHI 413
 Qy 134 APKQIILLES-----YPLNAHCEWTIHA-----KPGFVI----- 162
 Db 414 CPAGCSLTAGTVGWTGTAIYHVELSSVCRAAHAGKLPNSGGAVHVNNGFYSDFLGSDLNGI 473
 Qy 163 ---QLRPFWLSLEFDYM-----COYDYVEYRD-----GDRDQIIRKVCN--E 202
 Db 474 KSEELKSLARSFRFDYVSSSTAGSKGCPDGFVEYDNCVYVTSKQAWERAQGVCTNMAA 533
 Qy 203 RPAPIQS--IGSSHLVLFHSDG--SKNFDGPH-----AIYEETACSS 241
 Db 534 RLAVLDKDVIFNSLTETLURGKGLTTTWIGLRLDAEKPFIMELMDSRVNLNDLITWAS 593

Qy 242 SPCFHDGTCVLT-----DKAGS--YKACACLAGYTGQRCENILLEERN---CSDPGGVPNGYQKI 293
 Db 594 GEPGNETNCYMDIQDQLQSVMTKSCFOFSSFACWMDLSRKNKAKCDDPFGSLENGHATL 653
 Qy 294 TGGPGLINGHAKIGTVVFFCNSVYLSNGEKRTCOONGENSGKQIPICIK--ACREPKI 351
 Db 654 HGQS--IDGYA--GSSIRYSCEVLHLSGTETVCTTNGTWSAPKRCIKVITQNPVP 709
 Qy 352 SDLVRRRLPMQVQSRTPHLQLYSAAFSKQLQ---SAPTKKPALPFGD----- 398
 Db 710 PSVGSVEIKP---PSRTNSISRVGSPFLRLPLRLPLARAAPKPPKPRSSQSPSTVDLASK 766
 Qy 399 --LPMGQHLHLTLQYECISPFYRRLGSSRRRTCLRTGKNSGRAPSCIPICGKIENITAP- 455
 Db 767 VKLPEGHYRVGSRAIVTCESRYVELLGSQGRCDSDNGNWSGRPASCIPVCGRSDSPSPF 826
 Qy 456 -----KTQGLRWQAAIYRTSGVHDGSLHKAFLVCSGALVNVRTVVAAHCVTDLG 510
 Db 827 IWNGNSTEIQGWPQAGISRWLA-----DHNMFLOCGGSLNKKWIVTAAHCVTYS 879
 Qy 511 KVTMIKTADLVKVLGKPYRDDDEKTIQSLQISAILHPNYDPILLADAILKLDKA 570
 Db 880 TAEIIDPNQFMYLGYKYRDRDDYVQVREALEIHVWNYDFGNLNFIALIQLKTPV 939
 Qy 571 RISTRVQPICLAAASRLDLSFSQSHI-----TVAGNVLADVRSPGKNDTLRSGVVSV 624
 Db 940 TLATRVQPICLPT--DITT---REHLKEGTAVVVTGNG---LNENNTYSETIQQAVLPV 990
 Qy 625 VDSLLCEEHEDHGIPUSVTDNMFCASWEPTASDICTAETGGIAVSPFGRASPEPRWH 684
 Db 991 VAASTCEEGYKEADPLVTVTENMFCAGYK-KGRYDACSDDSGG--PLVFADDSRTERRW 1047
 Qy 685 LMGLVSMYDKTCSH-RLSTAFKTVLPFKDWIER 717
 Db 1048 LEGIVSWGSPGCGKANQYGGFTKVNFLSWIRQ 1081

RESULT 6

US-08-596-405-2
 ; Sequence 2, Application US/08596405
 ; Patent No. 5858706
 ; GENERAL INFORMATION:
 ; APPLICANT: Ding, Jeak Ling
 ; APPLICANT: Ho, Bow
 ; TITLE OF INVENTION: The Cloned Factor C cDNA of the
 ; TITLE OF INVENTION: Singapore Horseshoe Crab, Carinoscorpius
 ; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch
 ; STREET: 8110 Gatehouse Road, Suite 500 East
 ; CITY: Falls Church
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22042
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/596.405
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murphy, Jr., Gerald M.
 ; REGISTRATION NUMBER: 28,977
 ; REFERENCE/DOCKET NUMBER: 1781-105P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 205-8000
 ; TELEFAX: (703) 205-8050
 ; TELEX: 248345

INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1083 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-596-405-2

Query Match 16.9%; Score 665; DB 2; Length 1083;
 Best Local Similarity 25.4%; Pred. No. 1.3e-46;
 Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGEWNNIMRECCEYDQIECVCPGKRE-----VVGTYTPCCRNENECDCLIH 82
 DB 248 PNGQSNFPKCIKIR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCHS----- 293
 QY 83 PCTTFENCKSCR-NGSWGTL----- 103
 DB 294 PYLLIGQETLTCCGNGQWNGQIPQCKNLVFCPLDPVNHAEHKVIGVEQKYGPFPQGT 353
 QY 104 -----DDFYVKGFCYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
 DB 354 VTYTCGNYFLMGFTLCKNPDGWSGSPSCVKVADREVDCCSKAVDFLDDVGFVRH 413
 QY 134 APKQILLES-----YPLNAHCEWTIHA-----KPGFVI----- 162
 DB 414 CPAGCSLTAGTVMGTAIYHELSSVCRAAHAGKLPNSGGAVHVNNGPYSDFLGSLNGI 473
 QY 163 ---QLRFVMLSLEFDYM-----COYDYVEVRD-----GDNRDGQIIKRVCGN--E 202
 DB 474 KSEELKSLARSFRFDYVSSSTAGKSGCPDGFVEVDENCYVYTSKORAWERAGQVCTNMAA 533
 QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNFDGFH-----AIYEETACSS 241
 DB 534 RLAVLDKDVIPNSLTETLGRKGLTTTWIGLHRLDAEKPFIMELMDSNVVLDNLTFWAS 593
 QY 242 SPCFHDGTCLV-----DKAGS--YKACLAGYTGQRCENLLEERN-----CSDPGGPNVNGYK 293
 DB 594 GEPNETNCTVYMDIQDQLOSVMKTKSCFQPSFACMMDLSRNTAKACDDPGLSLENGHATL 653
 QY 294 TGGPGLINRHAKIGTVVFFCNNSVVLGSGNEKRTCCQNGEWSGKQPICIK--ACREP 351
 DB 654 HQQS--IDGYA--GSIIRYSEVLHYLSTGTEVTCTTNGTWSAPKPRCIKIVITQNPV 709
 QY 352 SDLVRRVLPVQSRRETLHQLYSAFSGKQLQ-----SAPTKKPALPFGD----- 398
 DB 710 PSYGSVEIKP--PSRTNSISRVGSPFLRLPLPLPLARAAPPPKPRSSQSPSTVDLASK 766
 QY 399 --LPMGYQHLHTQLQYECISPFYRRLGSSRRCLRTGKWSGRAPSCIPICGKIENITAP- 455
 DB 767 VKLPEGHYRVGSRAIYTCESRYELIGSQGRCDNSGNMWSGRAPSCIPYVCGRSDSPSPF 826
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 DB 827 INWNGSTEIGQWPWQAGISRWLA-----DHNWFLQCGGSLNLEKNIYTAHCVTYSA 879
 QY 511 KYTMIKTADLVKVLGKFRDORDEKTIQSLOISAILHPNYDPIILLDADIALKLLDKA 570
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 QY 685 LMLGLVSWSYDKTCSH--RLSTAFPTKVLFPKDWIER 717
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RESULT 7

US-08-877-620-2
 ; Sequence 2, Application US/08877620
 ; Patent No. 5985590
 ; GENERAL INFORMATION:
 ; APPLICANT: Ding, Jeak Ling
 ; APPLICANT: Ho, Bow
 ; TITLE OF INVENTION: The Cloned Factor C cDNA of the
 ; TITLE OF INVENTION: Singapore Horsehoe Crab, Carinoscorpius
 ; TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Birch, Stewart, Kolasch & Birch
 ; STREET: 8110 Gatehouse Road, Suite 500 East
 ; CITY: Falls Church
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22042
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: 1781-105P
 ; APPLICATION NUMBER: US/08/877,620
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/596,405
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murphy, Jr., Gerald M.
 ; REGISTRATION NUMBER: 28,977
 ; REFERENCE/DOCKET NUMBER: 1781-105P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 205-8000
 ; TELEFAX: (703) 205-8050
 ; TELEX: 248345
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1083 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-877-620-2

Query Match 16.9%; Score 665; DB 2; Length 1083;
 Best Local Similarity 25.4%; Pred. No. 1.3e-46;
 Matches 222; Conservative 118; Mismatches 304; Indels 230; Gaps 37;

QY 34 PGEWNNIMRECCEYDQIECVCPGKRE-----VVGTYTPCCRNENECDCLIH 82
 DB 248 PNGQSNFPKCIKIR-----ECAMVSSPEHGKVNALSGDMIEGATL-----RFSCHS----- 293
 QY 83 PCTTFENCKSCR-NGSWGTL----- 103
 DB 294 PYLLIGQETLTCCGNGQWNGQIPQCKNLVFCPLDPVNHAEHKVIGVEQKYGPFPQGT 353
 QY 104 -----DDFYVKGFCYCAECR--AGWYGG--DCMR-----CGQVLR-- 133
 DB 354 VTYTCGNYFLMGFTLCKNPDGWSGSPSCVKVADREVDCCSKAVDFLDDVGFVRH 413
 QY 134 APKQILLES-----YPLNAHCEWTIHA-----KPGFVI----- 162
 DB 414 CPAGCSLTAGTVMGTAIYHELSSVCRAAHAGKLPNSGGAVHVNNGPYSDFLGSLNGI 473
 QY 163 ---QLRFVMLSLEFDYM-----COYDYVEVRD-----GDNRDGQIIKRVCGN--E 202
 DB 474 KSEELKSLARSFRFDYVSSSTAGKSGCPDGFVEVDENCYVYTSKORAWERAGQVCTNMAA 533
 QY 203 RPAPIQS--IGSSLHVLPHSDG--SKNFDGFH-----AIYEETACSS 241
 DB 534 RLAVLDKDVIPNSLTETLGRKGLTTTWIGLHRLDAEKPFIMELMDSNVVLDNLTFWAS 593


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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of TAGD-15 encoded by nucleotides
; Patent No. 5972616
US-09-027-337-2

Query Match      8.3%; Score 327; DB 2; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-18;
Matched 144; Conservative 69; Mismatches 224; Indels 230; Gaps 27;

QY 128 CGOVLRAKPGQI-----LLESYPLNAHCETTHAKPGFVIQLRFVMLSLFDFM----- 176
DB 340 CGRLRKAQGTNSPYPGHYPPNIDCTWNE-----VFNQHVKVSKFFYLLEPGVPA 394
QY 177 --COYDVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNFDGPHAIYE 234
DB 395 GTCPKDYVEING-----EKYCGERSQFVVTNSNKITVRFHSDQSYTDTGFLAEY- 444
QY 235 EITACSSSPCFHDGTC-----VLDKAGSYKCACLAGY----- 266
DB 445 -LSYDSSDPCPGQFTCRGCIKRELRCGWDADCTDHSDELNCSCDAGHQFTCKNKFCKP 503
QY 267 -----TGORCENLLERNCSDPGPGVNGYQKITGGPGLNGRHAIGTVVSVFFCNSYV 320
DB 504 LFWVCDVNDGNSDEQGCSCP-----AQTFRCSNGKC 537
QY 321 LSG-----NEKRTCCQNGESGKQPICIKACREPKISDLVRRVLPVQVQSRRTPLHLQYS 376
DB 538 LSKSQCNCKDCCGSDGSDGSCPKVNVVTC-----CLSKGN-- 584
QY 437 GRAPSCIPICGKIENITAPKTO-----GLR-----WPMQAAIYRRTS 473
DB 585 -----PECCKEDCSDGSDGSDGSCPKVNVVTC-----WPMQAAIYRRTS 473
QY 474 GVHDSLHGKAWFLVCSGALVNRVTVVAACHVTDLGKVTMIKTADLVKVLGKFRDDDR 533
DB 638 G-----H-----ICGASLISPNWLVSAHACYIDDRGFRYSPTQWTAFLG-LHDQSOR 684
QY 594 SH-ITVAGNVNVLADVRSPGKNDTLRSQVSVVSDSLCEBQHDHGIPVSVTDNMFCAW 652
DB 742 GKAIWVTG-----GHTQVGGTGALILQKGEIRVINQTTCNL-----LPQOITPRMVCVGF 793
QY 653 EPTAPSDICTAETGG-IAAVSPFGASPEPRHMLGLVSWSYDKTCSHRLSTAFKVLPLF 711
DB 794 -LSGGVDSQCGSGGSLSSVEADGRI-----FQAGVWSWG-DGCAQRNKPQGVYTRPLPLF 845
QY 712 KDWIERN 718
DB 846 RDWIEN 852

RESULT 10
US-09-644-600-2
; Sequence 2, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
; TITLE OF INVENTION: TAGD-15: An Extracellular Serine Protease
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
```

```
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 2
; LENGTH: 855
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TAGD-15
US-09-644-600-2

Query Match      8.3%; Score 327; DB 4; Length 855;
Best Local Similarity 21.6%; Pred. No. 1.3e-18;
Matches 144; Conservative 69; Mismatches 224; Indels 230; Gaps 27;

QY 128 CGOVLRAKPGQI-----LLESYPLNAHCETTHAKPGFVIQLRFVMLSLFDFM----- 176
DB 340 CGRLRKAQGTNSPYPGHYPPNIDCTWNE-----VFNQHVKVSKFFYLLEPGVPA 394
QY 177 --COYDVEVRDGNRDGQIIKRVCGNERPAPIQSIGSSLHVLPHSDGSKNFDGPHAIYE 234
DB 395 GTCPKDYVEING-----EKYCGERSQFVVTNSNKITVRFHSDQSYTDTGFLAEY- 444
QY 235 EITACSSSPCFHDGTC-----VLDKAGSYKCACLAGY----- 266
DB 445 -LSYDSSDPCPGQFTCRGCIKRELRCGWDADCTDHSDELNCSCDAGHQFTCKNKFCKP 503
QY 267 -----TGORCENLLERNCSDPGPGVNGYQKITGGPGLNGRHAIGTVVSVFFCNSYV 320
DB 504 LFWVCDVNDGNSDEQGCSCP-----AQTFRCSNGKC 537
QY 321 LSG-----NEKRTCCQNGESGKQPICIKACREPKISDLVRRVLPVQVQSRRTPLHLQYS 376
DB 538 LSKSQCNCKDCCGSDGSDGSCPKVNVVTC-----CLSKGN-- 584
QY 377 AAFSKQKLSAPTKPKPALPFGDLPNGYQHLHTQLOYECISPFYRLGSSRRRTCLRTGKWS 436
DB 568 -----TK-----HT-----YRCLNGL-----CLSKGN-- 584
QY 437 GRAPSCIPICGKIENITAPKTO-----GLR-----WPMQAAIYRRTS 473
DB 585 -----PECCKEDCSDGSDGSDGSCPKVNVVTC-----WPMQAAIYRRTS 473
QY 474 GVHDSLHGKAWFLVCSGALVNRVTVVAACHVTDLGKVTMIKTADLVKVLGKFRDDDR 533
DB 638 G-----H-----ICGASLISPNWLVSAHACYIDDRGFRYSPTQWTAFLG-LHDQSOR 684
QY 534 DEKTIQSLQISAILHPNVDPILLADIAILKLDKARISTRVQPICLAASRDLSFQE 593
DB 685 SAPGVQERRLRIISHPPFNDFDYDIALLELEKPAEYSSMVRPCLP---DASHVFP 741
QY 594 SH-ITVAGNVNVLADVRSPGKNDTLRSQVSVVSDSLCEBQHDHGIPVSVTDNMFCAW 652
DB 742 GKAIWVTG-----GHTQVGGTGALILQKGEIRVINQTTCNL-----LPQOITPRMVCVGF 793
QY 653 EPTAPSDICTAETGG-IAAVSPFGASPEPRHMLGLVSWSYDKTCSHRLSTAFKVLPLF 711
DB 794 -LSGGVDSQCGSGGSLSSVEADGRI-----FQAGVWSWG-DGCAQRNKPQGVYTRPLPLF 845
QY 712 KDWIERN 718
DB 846 RDWIEN 852

RESULT 11
US-09-654-600A-2
; Sequence 2, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotooshi
```

; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
 ; FILE OF INVENTION: Overexpressed in Carcinomas
 ; FILE REFERENCE: D6064CIP/D
 ; CURRENT APPLICATION NUMBER: US/09/654.600A
 ; CURRENT FILING DATE: 2000-09-01
 ; PRIOR APPLICATION NUMBER: 09/421,213
 ; 09/027,337
 ; PRIOR FILING DATE: 1999-10-20
 ; NUMBER OF SEQ ID NOS: 98
 ; SEQ ID NO 2
 ; LENGTH: 855
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: TADG-15
 ; US-09-654-600A-2

Query Match 8.3%; Score 327; DB 4; Length 855;
 Best Local Similarity 21.6%; Pred. No. 1.3e-18;
 Matches 144; Conservative 69; Mismatches 224; Indels 230; Gaps 27;
 QY 128 CGVLRAPKGOI-----LLESYPLNAHCETTHAKPGFVIQLRFVYMLSLFEDYM----- 176
 Db 340 CGRLRKAQGFNSPYPGHPNIDCTWNE-----VNNQHVKVFKFYLLEPGVPA 394
 QY 177 --COYDVEVRDGNRDQIIIRKVCGRNERPAPIQISGSLHVLPHSPGSKNFDGFHAIYE 234
 Db 395 GTCPKDYVEING-----EKYCGERSQFVVTNSNKITVRFHSDQSYTDTGFLAEY- 444
 QY 235 EITACSSSPCHDGTG-----VLDKAGSYKACLAGY----- 266
 Db 445 -LSYDSSDPGQFCTGTCIRKELRCDGWADCTDHSDELNCSCDAGHQBTCKNKFCKP 503
 QY 267 -----TGQRNLEERNCSDPGCPYNGYKITGGPGLNGRHAKIGTVVSPFCNNSYV 320
 Db 504 LFWCDSVNDGDSDEGGCCP-----AGTFCRSGKC 537
 QY 321 LSG-----NEKRTCOONGSWGSKQPICIKACREPISDLVRRVLPVMOVQSGRETPLHLQYS 376
 Db 538 LSKSQCGKDKDCGDSDEASCPKVVVTC-----YRCLNGL----- 567
 QY 377 AAFSKQKLSAPTKKPPALPGDLPMGYQHLHTQIYECISPFYRLGSSRRTCLRTGKWS 436
 Db 568 -----TK-----HT-----YRCLNGL----- 584
 QY 437 GRAPSCIPICGKIENITAPKTQ-----GLR-----WPMQAAIYRRTS 473
 Db 585 -----PECQKEDSCSGDEKDCDGLRFTQARVVGCTDADGEWPMQVSLHALGQ 637
 QY 474 GVHDSLHKGAWFLVCSGALVNERTVVVAHCVTDLKGVTMKTADLKVVLGKPYRDDDR 533
 Db 638 G-----H-----ICGASLISPNWLVSAAHCYIDDRGRYSDDPTQWTAFLG-LHDQSOR 684
 QY 534 DEKTIQSLQISAILHPNYDPIILDADIAIKLDKARISTRVQPICLAAASRDISTFQOE 593
 Db 685 SAPGVQERLRKRIISHPFNFDDFTFYDIALLEKPAEYSSMVRPCLP-----DASHVPPA 741
 QY 594 SH-ITVAGMNVLDVRSFGKNDTLRSQVSVSDLSLCEEHEDHGIPVSVTDNMFCASW 652
 Db 742 GKALWVTGW-----GHTQYGGTALLQKEIRVINQTTCENTL-----LPQOITPRMVCVF 793
 QY 653 EPTAPSDICTAETGG-IAAVSFPGRASPEPRHMLGLVSWSYDKTCSHRLSTAFTKVLPF 711
 Db 794 -LSGGVDSQCGSGGLSSVEADGRI-----FQAGVVSWG-DGCAQRNKPQVTVTLPLF 845
 QY 712 KDWIERN 718
 Db 846 RDWIKEN 852

RESULT 12
 5270178-16

; Patent No. 5270178
 ; APPLICANT: GELITZ, BRUCE E.; GRINNELL, BRIAN W.
 ; TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
 ; ZYMOGEN FORMS OF HUMAN PROTEIN C
 ; NUMBER OF SEQUENCES: 21
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/484,133
 ; FILING DATE: 23-FEB-1990
 ; SEQ ID NO:16:
 ; LENGTH: 460
 ; 5270178-16

Query Match 8.1%; Score 321; DB 6; Length 460;
 Best Local Similarity 25.1%; Pred. No. 1.8e-18;
 Matches 138; Conservative 62; Mismatches 170; Indels 180; Gaps 27;
 QY 193 QIIKRVCGNERPAPI-QSIGSSHLVLFHSDGSKNFDGFHAIYEEIT-ACSSSPCFHDGTC 250
 Db 58 ECIEEICDFEAEKEIFQVDDTL-----AFWSKHVDGQCLVPLEHPCASLCCGH-GTC 111
 QY 251 VLDKAGSYKACLAGYTGQRCENLBERNCS-DPGGPVN-----GYQKITGGFGLNGR 303
 Db 112 I-DGIGSFCDCRSWEGRFQREVSLNCLDNGGCTHYCLEEVGWRRCSAPGY----- 166
 QY 304 HAKIG-----TVVSFFCNSYVLSGNEKRTCOONGSWGSKQPICIKACREPISDLVR 356
 Db 167 --KLGDLLQCHPAVPPCGRPW-----KR-----MEKRSHL-- 197
 QY 357 RRVLPMOVQSRREPLHOLYSAAFSSKQKLOSAPTKKPPALPGDLPMGYQHLHTQIYECIS 416
 Db 198 -----KEDTELH-----KQI----- 208
 QY 417 PFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAPKTQGLRMPWQAAIYRRTSGVH 476
 Db 209 --YPRL-----NGKMTRRGDS-----PMQVLL----- 229
 QY 477 DGSLLHKGAWFLVCSGALVNERTVVVAHCVTDLKGVTMKTADLKVVLGKPYRDDDRDEK 536
 Db 230 -DSKCK-----LAGAVLIHPSWVLTAAHCDSEK-----LIVRIGY--DLRWEK 274
 QY 537 TIQSLQISAILHPNYDPIILDADIAIKLDKARISTRVQPICL-----AASRDLSTSFQ 592
 Db 275 WELDDDIKEVFVHPNYSKSTTDNDIALHLAQAATLSQITVPICLPDSGLAERLNAQGO 334
 QY 593 ESHITVAGMNVLDVRSFGKNDT--LRSGVSVSDLSLCEEHEDHGIPVSVTDNMFC 650
 Db 335 ETLVT--GMGYHSSREKEAKRNRFTVLNFIKIPVPHNECSEVMSN-----MVSENMLCA 387
 QY 651 SWEPTAPSDICTAETGGIAAVSFPGRASPEPRHMLGLVSWSYDKTCSHRLSTAFTKVLP 710
 Db 388 GILGDR-QDACEGSGGPVAVSFHG-----TWFLVGLVSWGEGCGLLHNVG-VYTHVSR 439
 QY 711 FKDWIERNMK 720
 Db 440 YLDWIHGHIR 449

RESULT 13
 US-08-200-900A-2
 ; Sequence 2, Application US/08200900A
 ; Patent No. 5655566
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,900A
FILING DATE: 23-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinent, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5201-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 X8574
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US-08-200-900A-2

Query Match 8.0%; Score 317.5; DB 1; Length 798;
Best Local Similarity 24.6%; Pred. No. 7.4e-18;
Matches 146; Conservative 80; Mismatches 225; Indels 143; Gaps 30;

QY 143 SYPLNAHCEWTIHAKPGFVIQIRFVMSLEFDYMCQYDVEVRDGNRQIIRKVCNE 202
DB 324 SYPNQAFICIMNLNAQKGNKIQHF-----QEPDENIADVVEIRDEGDDSLFLAVYTG-- 377

QY 203 RPAPIQSIGSS---LHVLFDHSGSKNFDGFHAIYEITACS--SSPCFHDG--TCVLDDKAGS 257
DB 378 -PGPVNDFSTNRTMTVLTITDNMLAKQGFKANFTTGYGLGPIPECKEDNFQC---KDG- 432

QY 258 YKACLAGTGTGRCENLLEERNCSDEGPGVNGYQKITGGPGLNGRHAQIGTVVFFCEN 317
DB 433 -ECIPLVNL-----CDGPFHCKDGSDEAHCVRLEFNGTTDSSGLVQFRIQSIWHV----- 480

QY 318 SYVLSGNEKRTCOQNGEWSGKQICIKACREPKISDLVRRVRLPMQVQSRRETPHLQLYSA 377
DB 481 -----ACAEN--WT-----TQISDDVCQLL----- 498

QY 378 AFSKQKLOSAPTKKPPALPGDLPNGYOHLLTQLOVEICISPFYRRLGSSRRRTCLRTGKWSG 437
DB 499 -----GLGTGNSVPTFTSTGGP--YVNLNT-----APNGSLILTPSQOCLE----- 538

QY 438 RAPSCIP-----CGK--IENITAPKTG-----LRWPQAAIYRRTSGVHDGSLHKG 483
DB 539 --DSLILLQCNKSKGKLVTOEVSPIKVGSDSREGAPWVVALY-----FDDQ----- 586

QY 484 AWFVCSGALVNERVTVAACHVTDLGKVTMIKADLVKLVGKFYRDDDRDEKTIQSLQI 543
DB 587 ---QVCGASLVSRDLVSAACHV--YGR--NMEPSKWKAVLG-LHMASNLTPSQIETRLI 638

QY 544 SAILHPNVDPIILDADIAILKLLDKARISTRVQPICLAASRDLSSTFQESH--TVAGWN 602
DB 639 DQIVINPHYNKRKNNDIAMHLEKVNVTYDQICLPEENQV---FPPGRICSIAAGW 695

QY 603 VLADVRSPGFKNDLRSVSVVDSLLCEQHEHDGIPVSVTDNMFCAWETAPSDICT 662
DB 696 ALI---YQGSTADVLQEADVPILLSNEKQQQMPY-----NITENMVCAGYE--AGGVDSQ 747

QY 663 AETGGIAAVSPPGRASPEPRHMLGLVSWSYDKTCSHRLSTAFKTLVLPFKDWIE 716
DB 748 GDSSG-----PLMCOENNRWLLAGVTSFGYQCALPNR-PGVYARVPRFTENIQ 794

RESULT 14
PCT-US94-00616-2
; Sequence 2, Application PC/TUS9400616
; GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
NUMBER OF SEQUENCES: 33
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00616
FILING DATE:
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-00616-2

Query Match 8.0%; Score 317.5; DB 5; Length 798;
Best Local Similarity 24.6%; Pred. No. 7.4e-18;
Matches 146; Conservative 80; Mismatches 225; Indels 143; Gaps 30;

QY 143 SYPLNAHCEWTIHAKPGFVIQIRFVMSLEFDYMCQYDVEVRDGNRQIIRKVCNE 202
DB 324 SYPNQAFICIMNLNAQKGNKIQHF-----QEPDENIADVVEIRDEGDDSLFLAVYTG-- 377

QY 203 RPAPIQSIGSS---LHVLFDHSGSKNFDGFHAIYEITACS--SSPCFHDG--TCVLDDKAGS 257
DB 378 -PGPVNDFSTNRTMTVLTITDNMLAKQGFKANFTTGYGLGPIPECKEDNFQC---KDG- 432

QY 258 YKACLAGTGTGRCENLLEERNCSDEGPGVNGYQKITGGPGLNGRHAQIGTVVFFCEN 317
DB 433 -ECIPLVNL-----CDGPFHCKDGSDEAHCVRLEFNGTTDSSGLVQFRIQSIWHV----- 480

QY 318 SYVLSGNEKRTCOQNGEWSGKQICIKACREPKISDLVRRVRLPMQVQSRRETPHLQLYSA 377
DB 481 -----ACAEN--WT-----TQISDDVCQLL----- 498

QY 378 AFSKQKLOSAPTKKPPALPGDLPNGYOHLLTQLOVEICISPFYRRLGSSRRRTCLRTGKWSG 437
DB 499 -----GLGTGNSVPTFTSTGGP--YVNLNT-----APNGSLILTPSQOCLE----- 538

QY 438 RAPSCIP-----CGK--IENITAPKTG-----LRWPQAAIYRRTSGVHDGSLHKG 483
DB 539 --DSLILLQCNKSKGKLVTOEVSPIKVGSDSREGAPWVVALY-----FDDQ----- 586

QY 484 AWFVCSGALVNERVTVAACHVTDLGKVTMIKADLVKLVGKFYRDDDRDEKTIQSLQI 543
DB 587 ---QVCGASLVSRDLVSAACHV--YGR--NMEPSKWKAVLG-LHMASNLTPSQIETRLI 638

QY 544 SAILHPNVDPIILDADIAILKLLDKARISTRVQPICLAASRDLSSTFQESH--TVAGWN 602
DB 639 DQIVINPHYNKRKNNDIAMHLEKVNVTYDQICLPEENQV---FPPGRICSIAAGW 695

QY 603 VLADVRSPGFKNDLRSVSVVDSLLCEQHEHDGIPVSVTDNMFCAWETAPSDICT 662
DB 696 ALI---YQGSTADVLQEADVPILLSNEKQQQMPY-----NITENMVCAGYE--AGGVDSQ 747

QY 663 AETGGIAAVSPPGRASPEPRHMLGLVSWSYDKTCSHRLSTAFKTLVLPFKDWIE 716
DB 748 GDSSG-----PLMCOENNRWLLAGVTSFGYQCALPNR-PGVYARVPRFTENIQ 794

RESULT 15
5460953-3
; Patent No. 5460953
; APPLICANT: GERLITZ, BRUCE E.; GRINNELL, BRIAN W.
; TITLE OF INVENTION: VECTORS AND COMPOUNDS FOR EXPRESSION OF
; GLYCOSYLATION MUTANTS OF HUMAN PROTEIN C
; NUMBER OF SEQUENCES: 3

FIG. 38 is a graph showing the binding of the antibody of Claim 1 to the polypeptide shown in Figure 38 (SEQ ID NO:38). The graph shows the binding of the antibody of Claim 1 to the polypeptide shown in Figure 38 (SEQ ID NO:38). The graph shows the binding of the antibody of Claim 1 to the polypeptide shown in Figure 38 (SEQ ID NO:38).

Claims

- [c1] An antibody that binds to the polypeptide shown in Figure 38 (SEQ ID NO:38).
- [c2] The antibody of Claim 1 which is a monoclonal antibody.
- [c3] The antibody of Claim 1 which is a humanized antibody.
- [c4] The antibody of Claim 1 which is an antibody fragment.
- [c5] The antibody of Claim 1 which is labeled.
- [c6] The antibody of Claim 1 which specifically binds to the polypeptide shown in Figure 38 (SEQ ID NO:38).

8/19/04

Score 5.4

Trans 0.15
91.3%
id. 0.5

MELGCMWTLGLFTLQLLLISSLPREYTVINEACPGAEWMINMCRCECEYDQIECVCPGKREVVGYT
 IPCRNENEENECDSCLIHPCCTIIFENCKSCRNCSWGGLDLDYVKGFFYCAECRAAGWGGDCMRGCG
 VLRAPKGOILLSESYPLNAHCEWTHAKPGFVIQLRFMVLSLEFDYMCQYDYVEVRDGDNRDGOII
 KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHHDGTCVLDKAGSYKC
 ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGGLINGRHAHAKIGITVVSFFCINNYSYLSGNE
 KRTCCQNGEWSGKQPIKACREPKISDLVRRRVLPMDQVQSRFETPLHQLYSAAFSKQKLSAPTK
 KPALPFGDLPMGYQHHLHTQLQYECISPFYRRRLGSSRRCTCRLTGKWSGRAPSCIPICGKIENITAP
 KTQGLRWQPAIYRRTSGVHHDGSLHKGAWFLVCSGALVNERITVVAHACVTDLGGKVTMIKTADL
 KVLGKRYRDDRDDEKTIQSLQISAIILHPNYDPIILLDADAIILKLLDKARISTRVQPICLAAASR
 DLSTSFQESHITVAGWNVLAADVRSPPGFKNDTLRSGVSVVSDLLCEEQHEHDHGIPVSVITDNMFCA
 SWEPITAPSDICTAEETGGIAAVSFPGRASPEPRWHLMGLVSMSCYCKTCSHRLSTIAFTKVLPEKDWI
 ERNMK

Important features of the protein:
 Signal peptide:
 amino acids 1-23
 EGF-like domain cysteine pattern signature.
 amino acids 260-272
 N-glycosylation sites.
 amino acids 96-100, 279-283, 316-320, 451-455, 614-618
 N-myristoylation sites.
 amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314,
 474-480, 491-497, 638-644, 666-672
 Amidation site.
 amino acids 56-60
 Serine proteases, trypsin family.
 amino acids 489-506
 CUB domain proteins profile.
 amino acids 150-167

FIGURE 38

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